

Parallel Numerical Algorithms

Chapter 7 – Differential Equations

Section 7.3 – Particle Methods

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Outline

- 1 Particle Simulations
 - N-Body Problems
 - Symplectic Integrators
 - Potentials
- 2 All-Pair Interactions
 - Particle Decomposition
 - Force Decomposition
- 3 Distance-Limited Interactions
 - Spatial Decomposition
 - Neutral Territory Methods
 - Smooth Particle Mesh Ewald Method
 - Hierarchical Methods

N-Body Problems

- Many physical systems can be modeled as collection of interacting particles
- “*Particles*” vary from atoms in molecule to planets in solar system or stars in galaxy
- Particles exert mutual *forces* on each other, such as gravitational or electrostatic forces

N-Body Model

- Newton's Second Law

$$F = m a$$

- Force between particles at positions x_i and x_j

$$f(x_i, x_j)$$

- Overall force on i th particle

$$F(x_i) = \sum_{j=1}^n f(x_i, x_j)$$

N-Body Simulation

- System of ODEs

$$F(x_i) = m_i \frac{d^2 x_i}{dt^2}$$

- *Verlet* time-stepping scheme

$$x_i^{k+1} = 2x_i^k - x_i^{k-1} + (\Delta t)^2 F(x_i^k)/m_i$$

- For long time integration, *symplectic* integrators are appropriate (preserve geometric properties, such as orbits)
- Velocity Verlet scheme used in molecular dynamics to preserve energy
- $\mathcal{O}(n^2)$ cost of evaluating force at each time step dominates overall computational cost

Molecular Dynamics

A molecular dynamics simulation performs the following calculations at every *timestep*

- 1 Calculate non-bonded forces F_{ij} for each pair (i, j) of particles (atoms)
- 2 Integrate non-bonded forces $f_i = \sum_j F_{ij}$
- 3 Consider local bonded many-particle interactions and update f_i
- 4 Update acceleration $a_i = f_i/m_i$ and velocity v_i using a_i
- 5 Compute new particle position x_i using v_i and a_i

Van der Waals Forces

Short-range atomic interactions governed by electronic coupling (Pauli exclusion principle)

- Molecular bonds typically treated specially
- Short-range 'non-bonded' forces modelled by *Van der Waals (dipole) potential*
- These are based on approximations to the electronic wavefunction
- A popular simple formulation is the Lennard-Jones potential

$$F_{\text{LJ}}(x_i, x_j) = \frac{1}{x_i - x_j} \left(\frac{\sigma_{ij}^{(A)}}{|x_i - x_j|^{12}} - \frac{\sigma_{ij}^{(B)}}{|x_i - x_j|^6} \right)$$

where $\sigma_{ij}^{(A)}$ and $\sigma_{ij}^{(B)}$ depend on the types of atoms

Electrostatic Forces

Electrostatic potentials describe Coulomb's law for electric fields due to charge

- They decay slowly relative to Van Der Waals interactions

$$F_{\text{EC}}(x_i, x_j) = (x_i - x_j) \frac{q_i q_j}{|x_i - x_j|^3}$$

where q_i and q_j are the charges of particles at x_i and x_j

- Coulomb potential interactions are well-approximated using fast solvers

Particle Decomposition

The simplest way to parallelize MD is by *particle decomposition*

- Fine-grained tasks are particles, each processor is assigned n/p of them
- Processors exchange particles in a ring, computing forces from received particles to original n/p
- Parallel execution time is

$$T_p(n) = O(p\alpha + n\beta + (n^2/p)\gamma)$$

- Memory footprint is minimal $M_p = \Theta(n)$
- Can reduce latency cost by working with larger subsets of particles

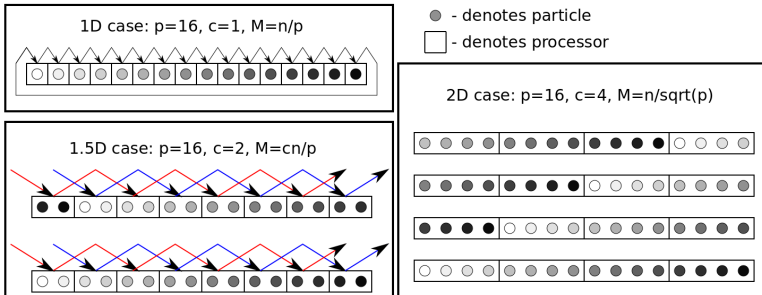
Force Decomposition

Force decomposition achieves lower communication volume

- Fine-grained tasks are forces, coarse-grained (aggregated) tasks are square blocks of forces
- Assignment/scheduling of aggregated tasks on processors must control for memory usage
- Each processor gets $s \times t$ block ($st = n^2/p$), accumulates forces for $\min(s, t)$ particles, by streaming in $\max(s, t)$ other particle data
- Memory footprint per processor is $M_p = p \min(s, t)$, time is

$$T_p(s, t) = O\left(\frac{\max(s, t)}{\min(s, t)}\alpha + \max(s, t)\beta + st\gamma\right)$$

Algorithms for All-pairs Force Calculation



- 1D – particle decomposition ($c = 1, s = n/p, t = n$)
- 2D – force decomposition ($c = \sqrt{p}, s = n/\sqrt{p}, t = n/\sqrt{p}$)
- 1.5D – memory-constrained force decomposition
 ($M_p = cn^2, s = cn/p, t = n/c$)

Decay of Forces with Distance

Molecular dynamics is typically done without explicitly computing all particle interactions

- Van der Waals interactions decay very rapidly and can be ignored for far-away particles
- Electrostatic forces can be computed by fast solvers
 - Electrostatic potential obeys the Poisson equation
 - The gravitational potential (used for cosmological simulation) is also Poisson
 - While pairwise interactions decay slowly, the aggregate potential due to long-range forces will be a smooth function

Cutoff Radius

For molecular dynamics, interactions decoupled as follows

- Compute Van der Waals interactions of all particle pairs (i, j) within distance $|x_i - x_j| \leq r_c$
- Fit a 3D charge density grid to the particle charges
- Solve the 3D Poisson equation on the grid via 3D FFT or Multigrid to obtain potential at grid-points
- Extrapolate potential from grid to compute electrostatic forces on particles
 - Force is given by the spatial gradient of potential
 - *B-splines* provide a basis with compact spatial support and easy computation of derivatives

Spatial Decomposition

Domain is $n^{1/3} \times n^{1/3} \times n^{1/3}$ box with uniform density

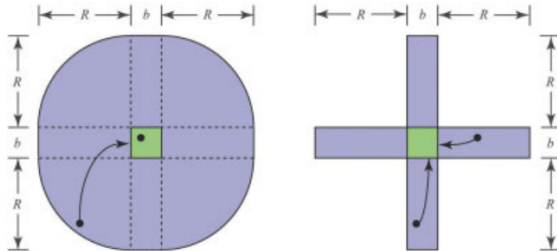
- MD simulations are typically done inside ‘solute’ (water), and have uniform density
- Uniform density does not necessarily hold in other domains, e.g. cosmological simulations
- Fine-grained tasks are unit-volume boxes
- Aggregated-tasks (boxes) are mapped to processors
- Each processor can have subdomain of dimensions $(n/p)^{1/3} \times (n/p)^{1/3} \times (n/p)^{1/3}$
- To compute forces onto all these particles, need all particles within r_c away from subdomain

$$W_p(n, r_c) = O((r_c + (n/p)^{1/3})^3 - n/p) = O(r_c^3 + r_c(n/p)^{2/3})$$

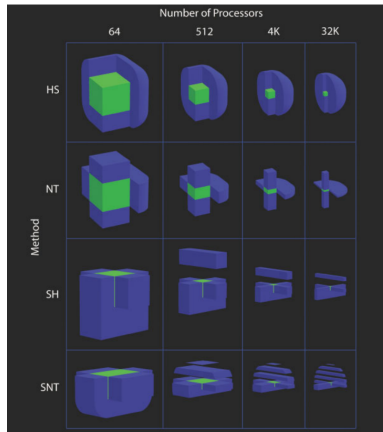
Neutral Territory Methods

Spatial decomposition leverage locality of particles, *neutral territory methods* directly exploit locality of forces

- Allow interactions between particles owned by two different processors to be computed on a third, in *neutral territory*



3D Neutral Territory Methods



Diagrams taken from D. Shaw, “A Fast, Scalable Method for the Parallel Evaluation of Distance-Limited Pairwise Particle Interactions”, 2005

Minimal Import Regions

Assign each processor k is assigned a unique subvolume $X_k \times Y_k \times Z_k$ of dimensions $b_{xy} \times b_{xy} \times b_z$ such that $b_{xy}^2 b_z = n/p$

- Processor k computes interactions of particle pair (i, j) if
 - i and j have a z -coordinate in Z_k and x, y -coordinates within r_c of some element in X_k, Y_k , respectively
 - i and j have x, y -coordinates in X_k, Y_k and a z -coordinate within r_c of some element in Z_k
- The volume of the region (amount of communication) is

$$W_p(n, r_c, b_{xy}, b_z) = O(r_c b_{xy}^2 + r_c b_z b_{xy} + r_c^2 b_z)$$

- Minimizing the import region with respect to b_{xy} and b_z

$$W_p(r_c) = O(r_c (n/p)^{2/3} + \sqrt{r_c^3 n/p})$$

Smooth Particle Mesh Ewald (SPME)

Solve for long range interactions on a $m \times m \times m$ charge grid

- System assumed periodic, which is often valid in MD
- *Ewald summation* is used to split the total potential energy

$$E = \frac{1}{2} \sum_{c \in \mathbb{Z}^3} \sum_{i=1}^n \sum_{j=1}^n \frac{q_i q_j}{|x_i - x_j + cn|^{1/3}}$$

into two parts (the form here is slightly simplified)

Ewald Summation

- The first part is a dampened direct summation

$$E_{\text{dir}} = \frac{1}{2} \sum_{c \in \mathbb{Z}^3} \sum_{i=1}^n \sum_{j=1}^n \frac{q_i q_j \text{erfc}(\beta |x_i - x_j + cn^{1/3}|)}{|x_i - x_j + cn^{1/3}|}$$

the function $\text{erfc}(y)$ is the probability a uniform random variable with mean 0 and variance $1/2$ falls outside of the range $[-y, y]$, so pairs with sufficiently large $x_i - x_j$ or in distant cells can be ignored

- The reciprocal (second part) is a convolution over all charge grid cells, except $c = (0, 0, 0)$ is contracted based on β

SPME Computational Structure

The forces on particles in SPME are obtained by equations that are derivatives of the energy with respect to position

- SPME with $m \times m \times m$ grid calculates the reciprocal portion as follows
 - B-splines interpolate charge from nearby region of particles

$$T_p(n, m) = O(\alpha + (n/p)^{2/3}\beta + (m^3/p)\gamma)$$

- The grid convolution by 3D FFT for $p \leq m^{5/2}$ takes time

$$T_p(m) = O(\log p\alpha + (m^3/p)\beta + (m^3 \log(m)/p)\gamma)$$

- Extrapolating potential from grid to particles

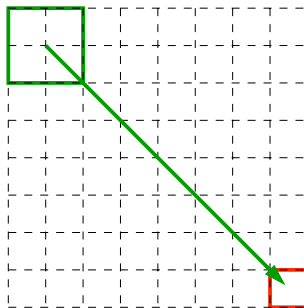
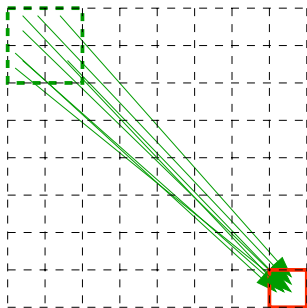
$$T_p(m) = O(\log p\alpha + (m^2/p^{2/3})\beta + (m^3/p)\gamma)$$

Alternative Methods

- Poisson equation on grid can theoretically be solved fastest by multigrid
- SPME can outperform multigrid in practice, achieving high accuracy with a small grid
- Advantage in part due to sensibility of periodicity condition
- Particle simulations with unbalanced particle distributions require different methods
- The *Barnes-Hut* method and the *Fast Multipole Method (FMM)* leverage hierarchical domain partitioning

Tree Partitioning for N-Body Problems

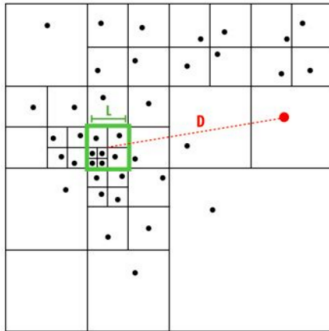
- Tree-based methods such as Barnes-Hut and FMM replace *a set* of forces from far-away particles with *a single* aggregate approximate force



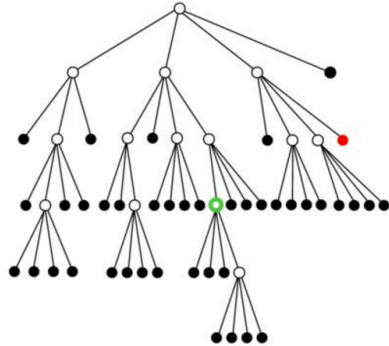
Barnes-Hut

- Barnes-Hut simulations provide a hierarchical spatial decomposition suitable for unbalanced distributions
- Subdivide space recursively until cells contain $O(k)$ particles
 - in 1D, obtain *binary tree*
 - in 2D, obtain *quad tree*
 - in 3D, obtain *oct tree*
- Compute a centered mass/charge for each tree node or r terms of a Taylor series for higher accuracy
- Calculate forces between far-away particles in far-away cells, based on interaction with particle and a mass/charge at a higher-level tree node

Barnes-Hut



Spatial Domain



Quad-Tree Representation

Diagram taken from course webpage of Mowry and Railing (CMU)

Fast Multipole Method (FMM)

FMM obtains linear complexity for integral equations

- Derivations specific to equations, Greengard and Rokhlin originally focused on 2D electrostatics
- In Barnes-Hut leaves interact with tree nodes, in FMM, tree nodes interact with $O(1)$ other tree nodes
- Each node has a *multipole (inner)* and *Taylor (outer)* expansion consisting of $O(\log(1/\epsilon))$ terms for accuracy ϵ
 - Error is controlled by number of terms in expansion
 - A multipole expansion is a special type of Taylor expansion
- *Transformation* operators are defined to 'shift' multipole and Taylor expansions, and to convert between the two

FMM Algorithm

The computation in FMM proceeds as follows

- 1 Perform interactions among particles in neighboring blocks
- 2 Upward pass – generate multipole expansion for every tree node starting from leaves
- 3 Downward pass – generate local expansion for every tree node starting from root

Structure and execution time model is analogous to HSS matrices, but with some differences

- 1 All neighboring cells interact directly
- 2 Amount of work associated with each tree node may vary

References - Particle Simulations

- M. P. Allen and D. J. Tildesley, *Computer Simulation of Liquids*, Oxford University Press, 1987
- D. Frenkel and B. Smit, *Understanding Molecular Simulation: From Algorithms to Applications*, 2nd ed., Academic Press, 2002
- M. Griebel, S. Knapek, and G. Zumbusch, *Numerical Simulation in Molecular Dynamics: Numerics, Algorithms, Parallelization, Applications*, Springer, 2007
- J. M. Haile, *Molecular Dynamics Simulations: Elementary Methods*, Wiley, 1992
- E. Hairer, C. Lubich, and G. Wanner, *Geometric Numerical Integration: Structure-Preserving Algorithms for Ordinary Differential Equations*, 2nd ed., Springer, 2006

References - Particle Simulations

- R. W. Hockney and J. W. Eastwood, *Computer Simulation Using Particles*, Institute of Physics, 1988
- B. Leimkuhler and S. Reich, *Simulating Hamiltonian Dynamics*, Cambridge University Press, 2005
- J. A. McCammon, B. M. Pettitt, and L. R. Scott, Ordinary differential equations of molecular dynamics, *Comput. Math. Appl.*, 28:319-326, 1994
- S. Pfalzner and P. Gibbon, *Many-Body Tree Methods in Physics*, Cambridge University Press, 1996
- D. C. Rapaport, *The Art of Molecular Dynamics Simulation*, Cambridge University Press, 1995
- T. Schlick, *Molecular Modeling and Simulation: An Interdisciplinary Guide*, 2nd ed., Springer, 2010

References - Parallel Particle Simulations

- M. Driscoll et al., A communication-optimal n-body algorithm for direct interactions, IPDPS, Boston, May 2013
- B. A. Hendrickson and S. J. Plimpton, Parallel many-body simulations without all-to-all communication, *J. Parallel Distrib. Comput.* 27:15-25, 1995
- S. Plimpton, Fast parallel algorithms for short-range molecular dynamics, *J. Comput. Physics* 117:1-19, 1995
- H. Schreiber, O. Steinhauser, and P. Schuster, Parallel molecular dynamics of biomolecules, *Parallel Comput.* 18:557-573, 1992
- W. Smith, Molecular dynamics on hypercube parallel computers, *Comp. Phys. Comm.* 62:229-248, 1991
- M. Snir, A note on n-body computations with cutoffs, *Theory Comput. Sys.* 37:295-318, 2004

References - Parallel Particle Simulations

- D. E. Shaw, A fast, scalable method for the parallel evaluation of distance-limited pairwise particle interactions, *Journal of Computational Chemistry*, 26(13), pp.1318-1328, 2005
- J. C. Phillips, R. Braun, W. Wang, J. Gumbart, E. Tajkhorshid, E. Villa, C. Chipot, R. D. Skeel, L. Kale and K. Schulten, Scalable molecular dynamics with NAMD, *Journal of computational chemistry*, 26(16), pp.1781-1802, 2005
- U. Essmann, L. Perera, M. L. Berkowitz, T. Darden, H. Lee and L. G. Pedersen, A smooth particle mesh Ewald method, *The Journal of chemical physics*, 103(19), pp.8577-8593, 1995