

# Improving PME on distributed computer systems



Carsten Kutzner

Max-Planck-Institut für Biophysikalische Chemie, Göttingen Theoretical and Computational Biophysics Department





# Outline

- how to get optimum performance from MD simulations with PME
  - Recap: Particle-Mesh-Ewald (PME)
  - parallel PME in GROMACS
  - understanding the PME parameters
  - tuning the performance of an example benchmark

# Recap: PME

- N atoms at r<sub>i</sub> with charges q<sub>i</sub> in neutral box (PBC)
- electrostatic potential (conditionally convergent, s-l-o-w)

$$U = \frac{1}{2} \sum_{i,j=1}^{N} \sum_{\vec{n} \in \mathbb{Z}^{3}}^{'} \frac{q_{i}q_{j}}{|\vec{r}_{ij} + \vec{n}L|}$$

- Coulomb: strong variation at small r, smooth at large r
- Ewald summation: split up U with



+  $\rho \rightarrow \,$  discrete mesh (DFT / FFT)









# PME time step

- I. SR part can be directly calculated
- 2. LR part: need FT charge density
  - I. spread charges on grid: each charge is spread on pme\_order grid points in x,y,z
  - 2. FFT to reciprocal space
  - 3. solve PME
  - 4. FFT back yields potential on grid points
  - 5. extrapolate forces on the particles from grid with splines of order pme\_order

## Parallel PME time step

particle redistribution
 xyz-domains → x-slabs



- communicate grid overlaps
- parallel data transpose within FFT needs all-to-all communication (2x to and from reciprocal space)

force redistribution
 slabs → domains



interpolate forces on local atoms

# Parallel PME: scaling bottlenecks

- all-to-all communication becomes increasingly expensive with N (latency increases by N<sup>2</sup>)
- all-to-all might overload network,
  MPI\_Alltoall performance = f(N, MPI lib, network type, ...)
- PME grid cannot always be distributed evenly among all processors:
  90 points → 64 CPUs?



N•(N-I) messages



N=3

N=6

# Multiple-Program Multiple-Data PME

- direct and reciprocal space contributions can be computed independently
- assign a subset of the processors for recip. space with -npme mpirun -np 5 mdrun -npme 2



- + MPI\_Alltoall on only 1/4 to 1/2 of the processors, reducing the communication to 1/16 to 1/4
- + better distribution of PME grid onto processors

# Multiple-Program Multiple-Data PME

- today typically 2, 4, or 8 CPUs share a network interconnect
- PP/PME node interleaving
- higher bandwidth on multi-CPU nodes
- let the LR processors use all available network bandwidth



mpirun -np 8 mdrun -npme 4 -ddorder pp\_pme ... -ddorder interleave

## Knobs to turn

#### same accuracy:

- node separation yes/no,# of PME nodes
- node order: PP\_PME, interleaved,...
- DD grid, dlb yes/no

#### Second compiler & MPI library!



#### affects accuracy:

- PME grid points
- Cutoff radius
  - to shift real/recip load @ same accuracy: multiply both r<sub>c</sub> and fourierspacing by factor



PME order 4, 6, 8, ... but we don't want to enlarge the grid overlap in the parallel case!

## Example benchmark system



- SBMV in water, 4.5 M particles
- cutoffs I nm
- PME order 4, grid spacing 0.135 nm (275<sup>3</sup> grid)
- Intel 2.66 GHz, 8 cores / node
- Infiniband Interconnect

# Easy GROMACS benchmarking

- performance measurement in GROMACS: build-in timers
- e.g. ns/day output from log file
- make a "short" test tpr ... but not too short!







mpirun -np N mdrun



mpirun -np N mdrun -v



mpirun -np N mdrun -dlb yes





mpirun -np N mdrun -npme 0



## Shifting load to real space



	r <sub>c</sub> / nm	grid spacing / nm	grid dimensions
Α	١,00	0,135	275^3
В	١,07	0,144	256^3
С	١,20	0,160	231^3





# **Tuning Howto**

□ make a short (>>100 steps) benchmark tpr, run with -v

start with automatic settings, **apply performance hints** 

few CPUs:

 $\hfill\square$  turn on dlb if there is a load imbalance in the force

turn on/off PME nodes

many CPUs:

**adjust # of PME nodes** if an imbalance pme mesh/force is reported

adjust real/reciprocal space workload by multiplying both r<sub>c</sub> and fourierspacing by (same) factor near I

might want to try other DD grids:

hight # of x-slabs mimicks the data organization for PME



can be favourable NOT to decompose in one direction (no x/f communication pulse needed in that direction)



# Acknowledgments



- The GROMACS developers
  - David van der Spoel
  - Erik Lindahl
  - Berk Hess
- The Theoretical and Computational Biophysics Department
  - Mareike Zink
  - Gerrit Groenhof
  - Bert de Groot
  - Helmut Grubmüller