Michela Mapelli

N-body techniques for astrophysics: Lecture 5 – N-body methods for collisionless systems

PhD School in Astrophysics, University of Padova November 19-30, 2018

OUTLINE of this lecture:

- 1 Softening
- 2 Tree code (tree building)
- 3 Particle Mesh (PM), Particle-Particle (PP)/PM and Fast Multipole Moment (FMM) algorithms
- **4 Clusters of computers**
- **5 Example of tree code: gasoline**

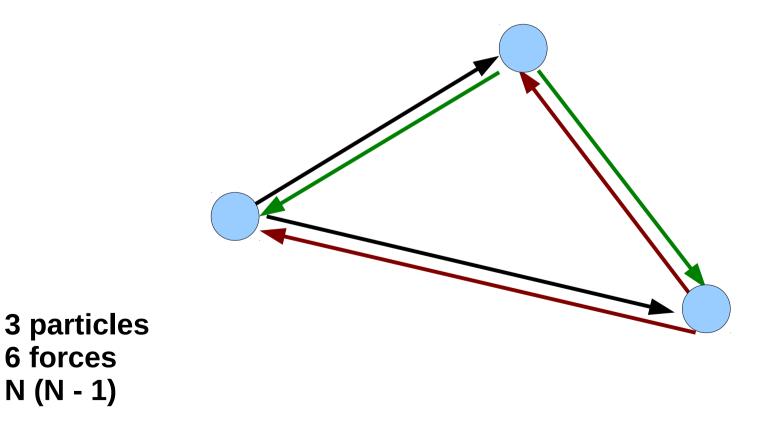
1. WHAT IS an N-Body SIMULATION?

SCALING of a NUMERICAL PROBLEM:

Numerical complexity:

$$\ddot{\vec{r}}_{i} = -G \sum_{j \neq i} m_{j} \frac{\vec{r}_{i} - \vec{r}_{j}}{|\vec{r}_{i} - \vec{r}_{j}|^{3}}$$

How many calculations I have to do for N-particles



1. WHAT IS an N-Body SIMULATION?

SCALING of a NUMERICAL PROBLEM:

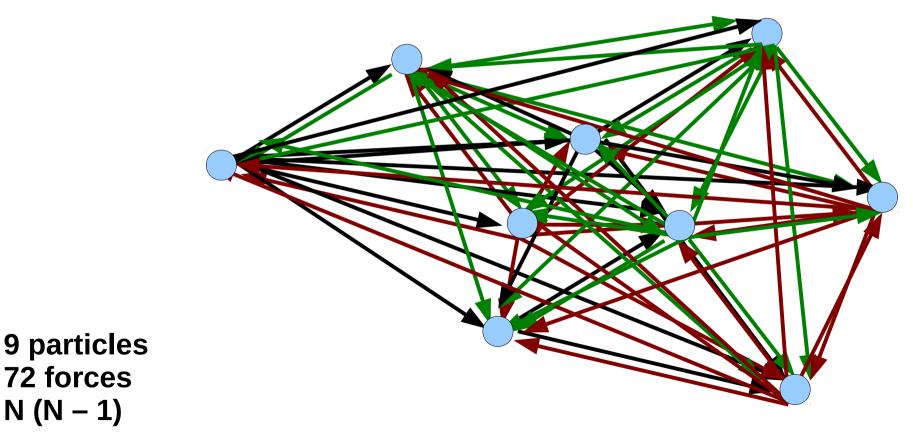
Numerical complexity:

72 forces

N(N - 1)

$$\ddot{\vec{r}}_{i} = -G \sum_{j \neq i} m_{j} \frac{\vec{r}_{i} - \vec{r}_{j}}{|\vec{r}_{i} - \vec{r}_{j}|^{3}}$$

How many calculations I have to do for N-particles



COMPLEXITY GROWS as N² - VERY FAST !!!!

1. WHAT IS an N-Body SIMULATION?

SCALING of a NUMERICAL PROBLEM:

COMPLEXITY GROWS as N² - VERY FAST !!!!

- CAN I REDUCE COMPLEXITY?

YES, BUT IT IS NOT ALWAYS THE RIGHT CHOICE → See direct vs indirect N-body LECTURE 2

 HOW CAN I REDUCE COMPLEXITY?
 E.G. with BARNES-HUT TREE METHOD and/or with MULTIPOLE EXPANSION
 → See LECTURE 3

1. SOFTENING:

In most N-body simulations (except for those in Lecture 2)

 MASS of a PARTICLE >> MASS of a true star, or gas, or dark matter particle
 particles are point-like (no physical radius)

If 2 particles approach each other, $F(r_i-r_j) \propto (r_i - r_i)^{-2}$ becomes very large (unphysical)

→ particles spuriously scatter each other

 \rightarrow wrong kinetic energy distribution in the simulation

We need a substitute of the physical radius, a radius over which the force is SOFTENED, smoothed to a smaller value :=

The SOFTENING

NB: The softening does not slow down two-body relaxation (does not affect far encounters), but the softening KILLS impulsive 3-body encounters → should not be used in direct N-body (apart from limited cases), → must be used in large (cosmological-, galaxy cluster- galaxies, galaxy-) scale simulations

1. SOFTENING:

Calculate softening in practice:

Substituting point potential with Plummer potential (Aarseth 1963) at small scales

$$F_{ij} = -G m_i m_j \frac{\mathbf{r}_i - \mathbf{r}_j}{(|\mathbf{r}_i - \mathbf{r}_j|)^3}$$

$$F_{ij} = -G m_i m_j \frac{\mathbf{r}_i - \mathbf{r}_j}{(|\mathbf{r}_i - \mathbf{r}_j|^2 + \epsilon^2)^{3/2}}$$

Or with a more general Kernel:

$$F_{ij} = -G \, \frac{m_i \, m_j}{\epsilon^2} \, \frac{\mathrm{d}}{\mathrm{d}t} \phi \left(\frac{|\mathbf{r}_i - \mathbf{r}_j|}{\epsilon} \right) \, \frac{|\mathbf{r}_i - \mathbf{r}_j|}{|\mathbf{r}_i - \mathbf{r}_j|}$$

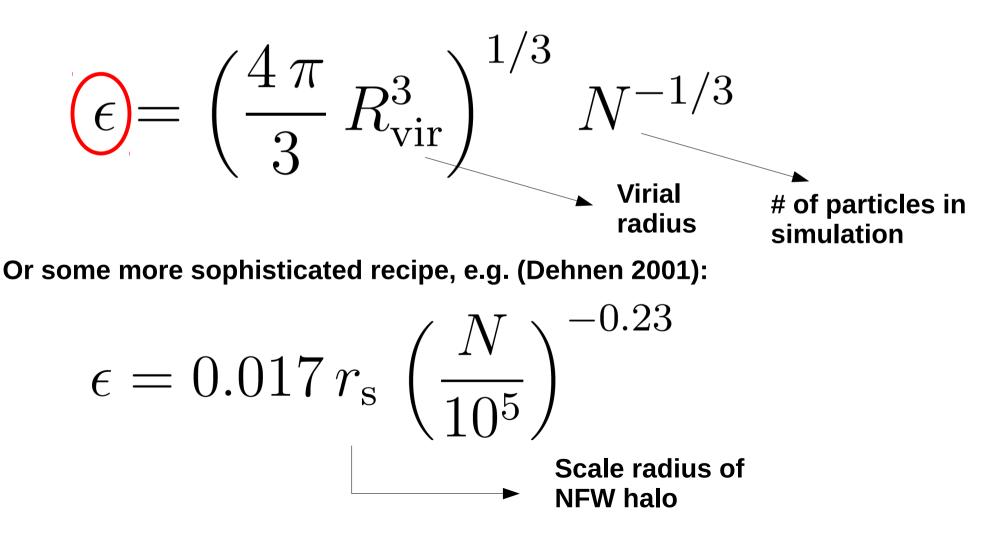
Dehnen 2001, MNRAS, 324, 273

1. SOFTENING:

<u>Calculate softening in practice -2:</u>

Which is the most reasonable value of epsilon? Sort of magic..

Rule of thumb: average distance between particles or a bit less



IDEA:

We do not need to estimate the force exerted by each single particle

We can estimate the cumulative force exerted by groups of particles if they are sufficiently far

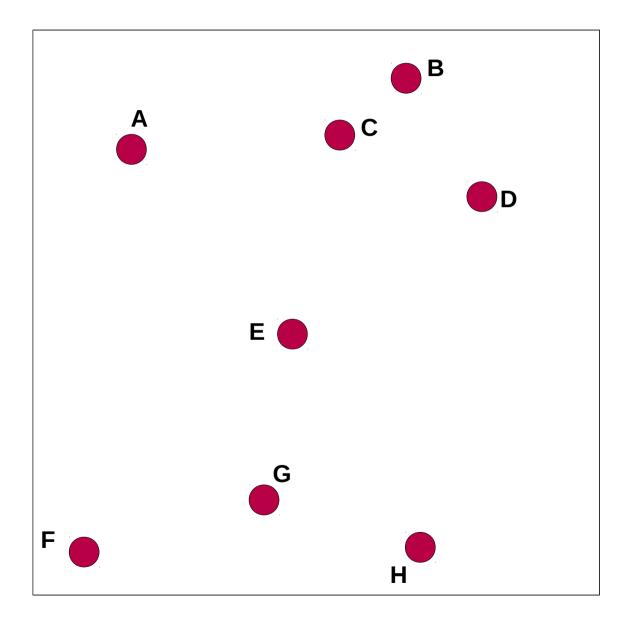
Particles that are far-off can be grouped into a single particle with mass = total mass and position/velocity = the position/velocity of the centre of mass

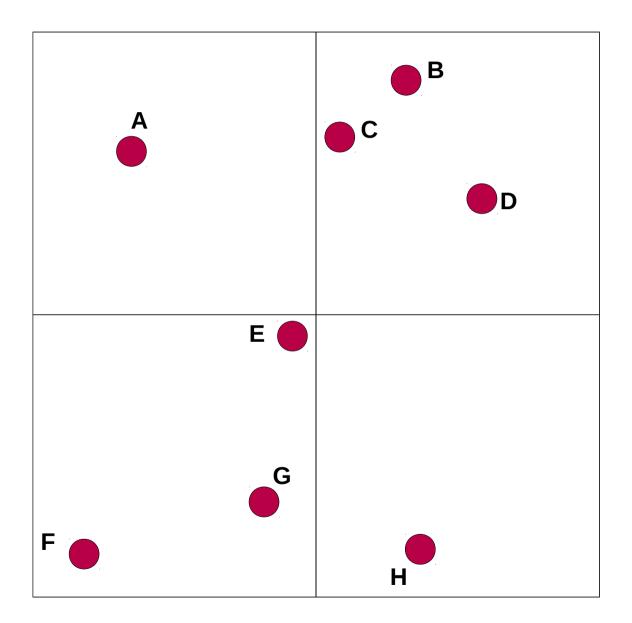
Why tree?

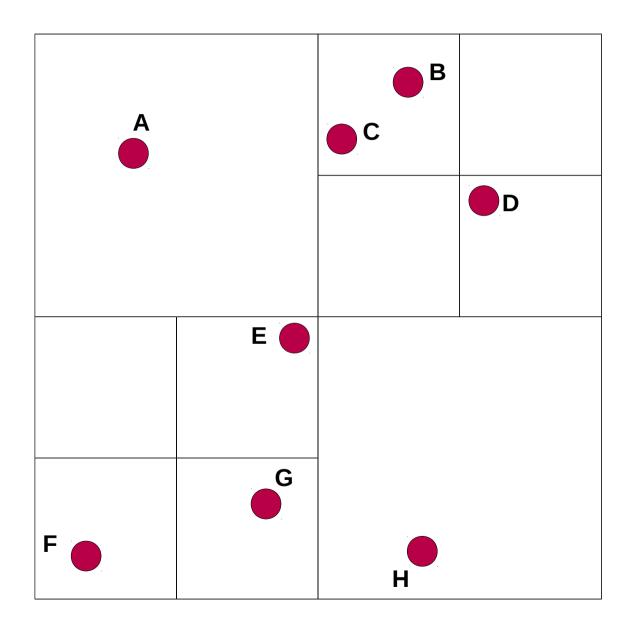
Divide simulation box into sub-boxes and then divide the sub-boxes into sub-sub-boxes and so on, down to the smallest sub-boxes that still have particles

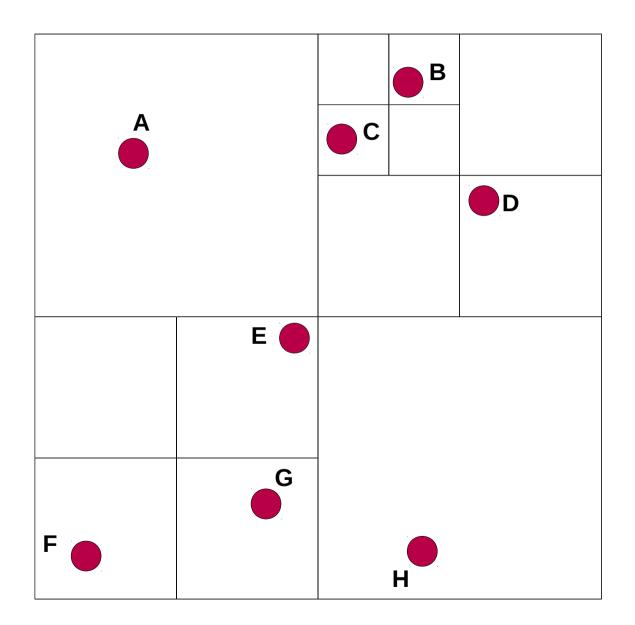
The big box is the ROOT of the tree The sub-boxes are BRANCHES The smallest sub-boxes are LEAVES



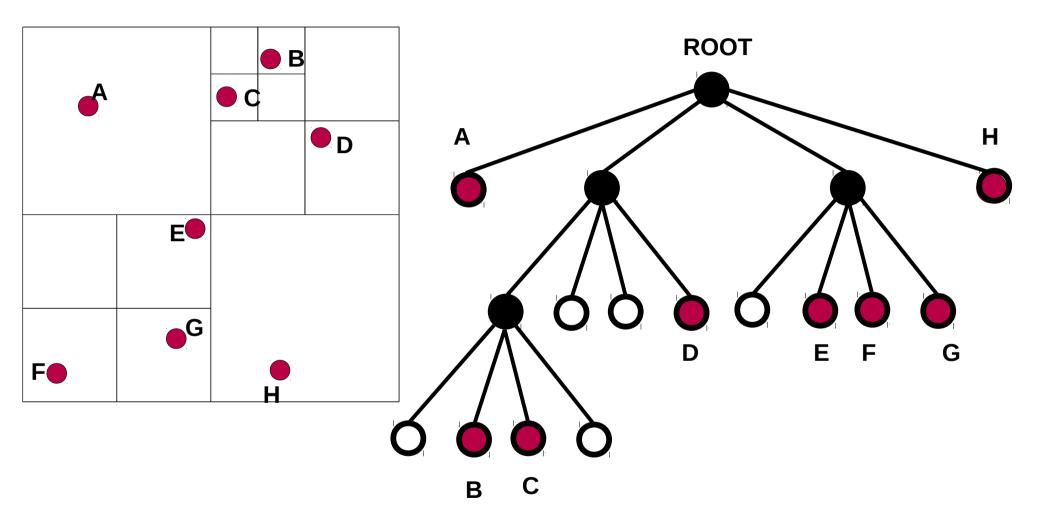








Example: quad-tree with 8 particles





O Empty daughter node



Daughter node

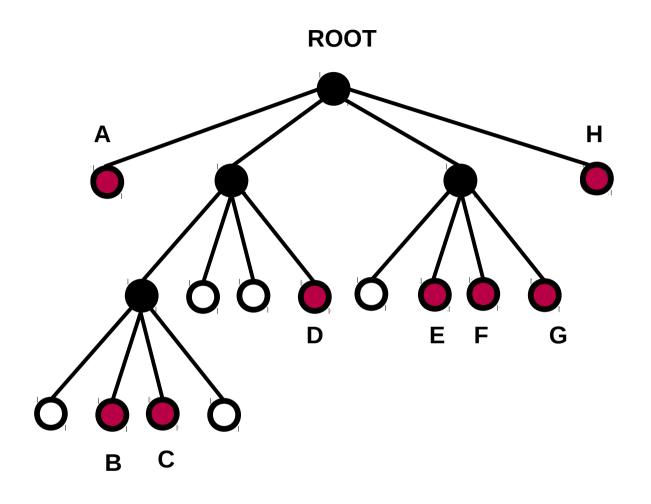
with 1 particle

Force between nearby particles is calculated directly.

e.g. the force exerted by F on E

Force between distant particles is approximated with centre of mass

e.g. the force of E, F, G on D is approximated by the centre of mass of E, F and G



HOW DO I DECIDE THAT A PARTICLE IS FAR ENOUGH TO AVOID DIRECT CALCULATION?

If $s/d < \theta$

s = width of the region represented by the considered node,

d = distance between the body and the node's center-of-mass

 θ = threshold value

(θ = 0.5 commonly used in practice;

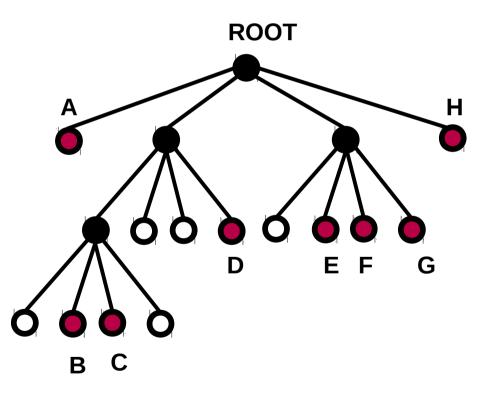
 θ = 0 means no internal node is treated as a single body, and the algorithm degenerates to brute force)

$\boldsymbol{\theta}$ is called OPENING ANGLE

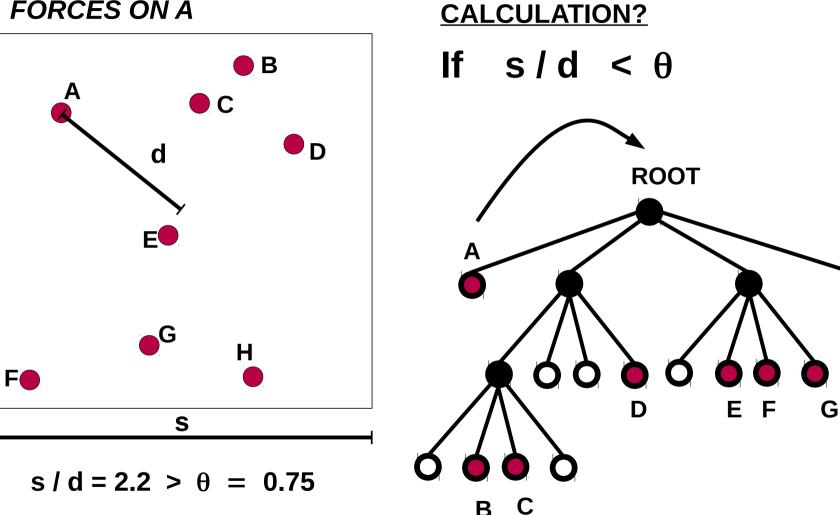
Example: CALCULATE FORCES ON A

HOW DO I DECIDE THAT A PARTICLE IS FAR ENOUGH TO AVOID DIRECT CALCULATION?

If $s/d < \theta$



Example: CALCULATE FORCES ON A



HOW DO I DECIDE THAT A PARTICLE IS

н

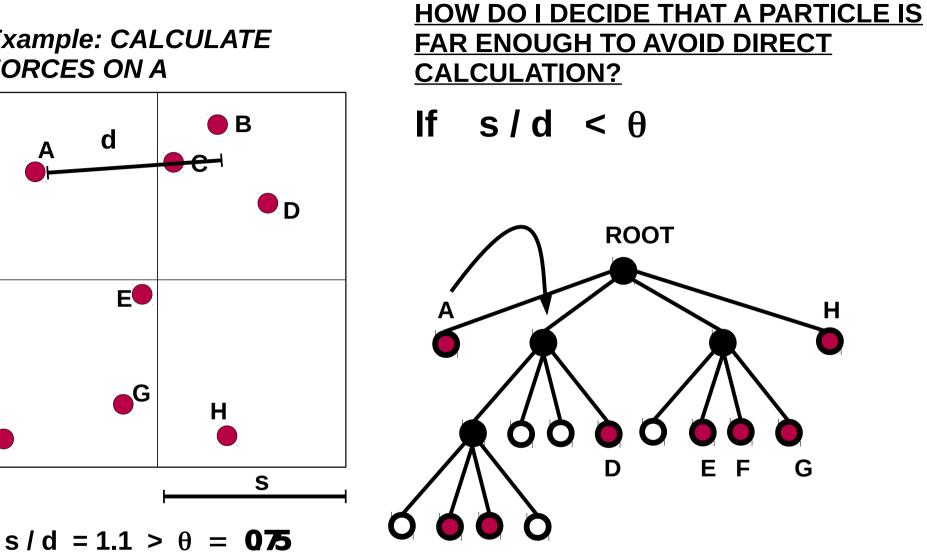
FAR ENOUGH TO AVOID DIRECT

I walk the tree to calculate forces (I split cells)

Α

F

Example: CALCULATE FORCES ON A



B

С

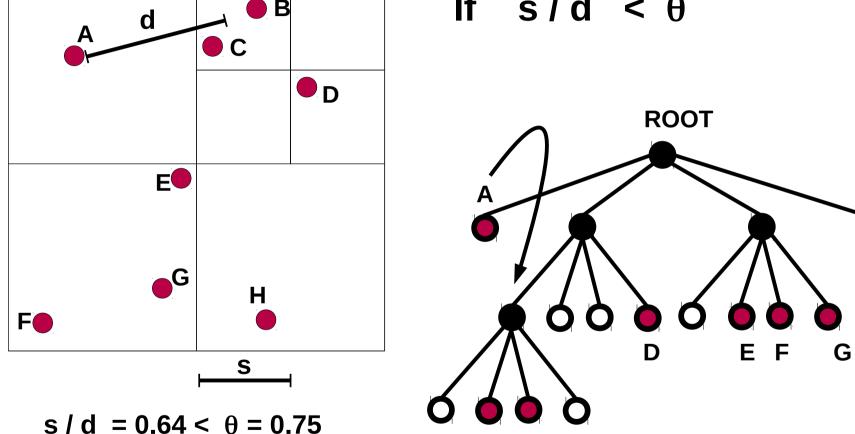
I walk the tree to calculate forces (I split cells)

Example: CALCULATE FORCES ON A

HOW DO I DECIDE THAT A PARTICLE IS FAR ENOUGH TO AVOID DIRECT **CALCULATION?**

Н

If
$$s/d < \theta$$



B

С

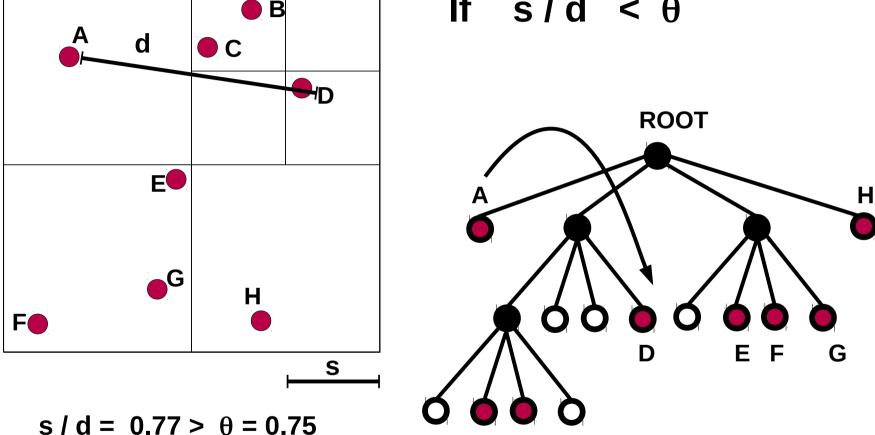
I STOP WALKING the tree and CALCULATE the **FORCE** between A and the centre-of-mass of B+C

B and **C** are sufficiently far from A

Example: CALCULATE FORCES ON A

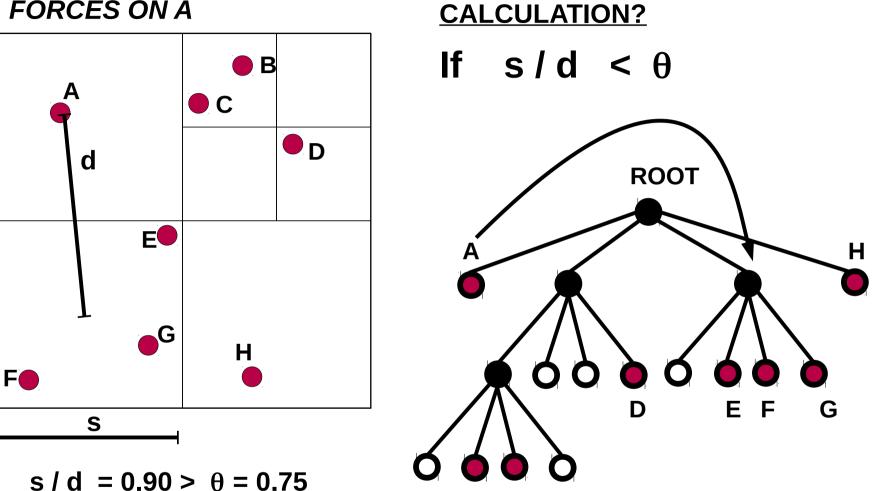
HOW DO I DECIDE THAT A PARTICLE IS FAR ENOUGH TO AVOID DIRECT **CALCULATION?**

If
$$s/d < \theta$$



I should split a cell, but D is already a single particle → I calculate force between A and D

Example: CALCULATE FORCES ON A

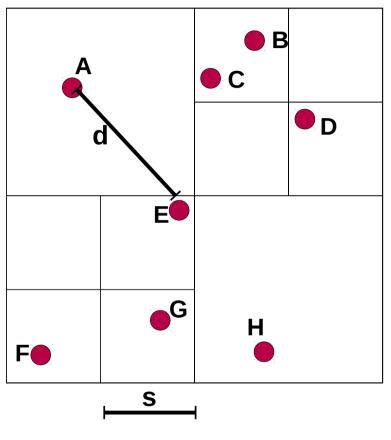


HOW DO I DECIDE THAT A PARTICLE IS

FAR ENOUGH TO AVOID DIRECT

I walk the tree to calculate forces (I split cells)

Example: CALCULATE FORCES ON A

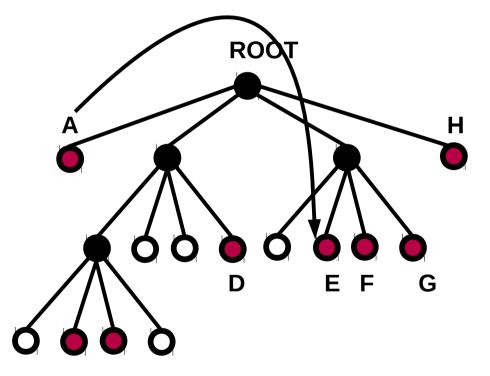


$s / d = 0.63 < \theta = 0.75$

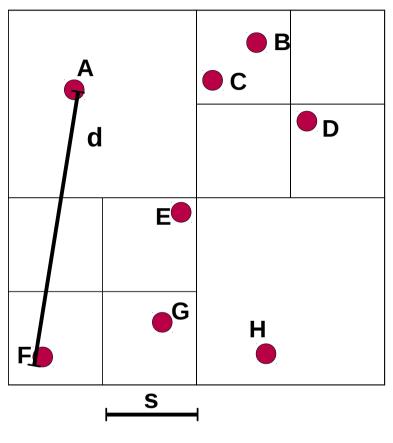
I should stop splitting cells, and besides E is a single particle: I calculate force between A and E

HOW DO I DECIDE THAT A PARTICLE IS FAR ENOUGH TO AVOID DIRECT CALCULATION?

If $s/d < \theta$



Example: CALCULATE FORCES ON A

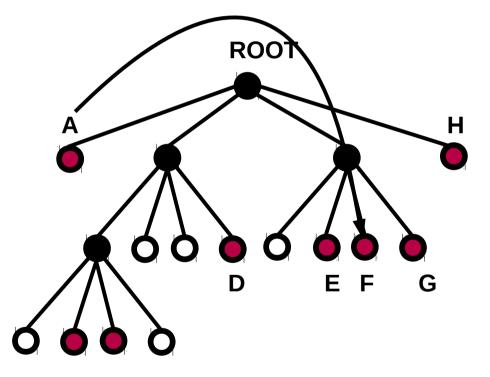


$s / d = 0.25 < \theta = 0.75$

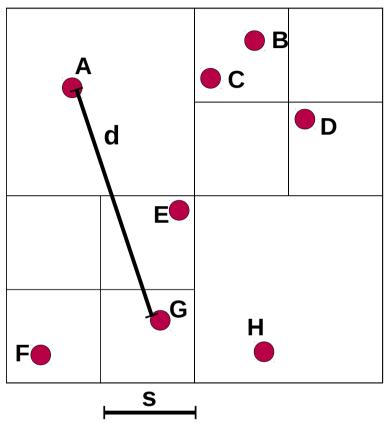
I should stop splitting cells, and besides F is a single particle: I calculate force between A and F

HOW DO I DECIDE THAT A PARTICLE IS FAR ENOUGH TO AVOID DIRECT CALCULATION?

If $s/d < \theta$

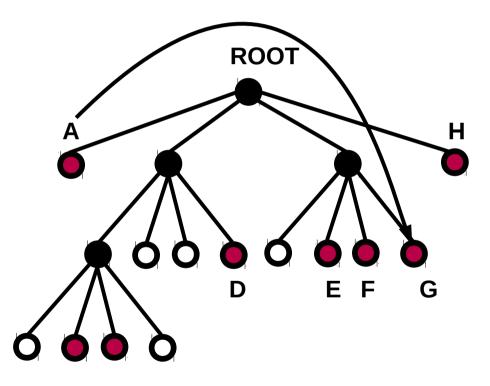


Example: CALCULATE FORCES ON A



HOW DO I DECIDE THAT A PARTICLE IS FAR ENOUGH TO AVOID DIRECT CALCULATION?

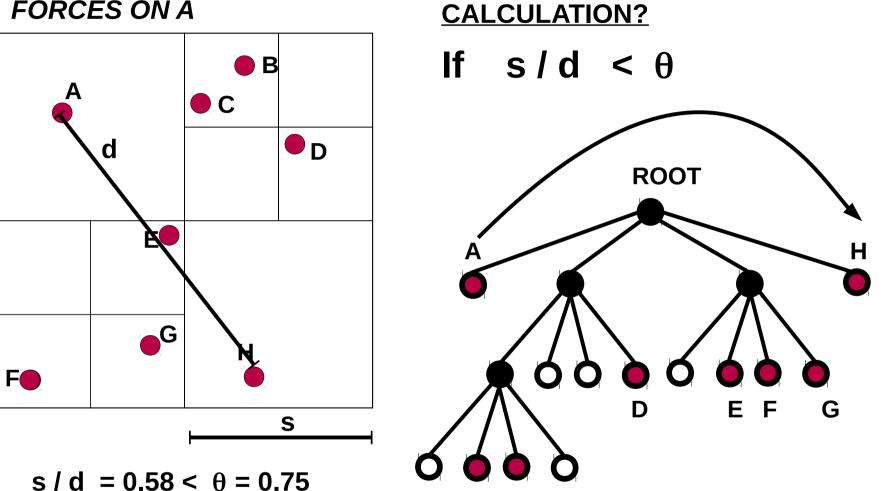
If $s/d < \theta$



 $s / d = 0.35 < \theta = 0.75$

I should stop splitting cells, and besides G is a single particle: I calculate force between A and G

Example: CALCULATE FORCES ON A



HOW DO I DECIDE THAT A PARTICLE IS

FAR ENOUGH TO AVOID DIRECT

I should stop splitting cells, and besides H is a single particle: I calculate force between A and H

<u>What is the advantage of building a tree?</u> Evaluation of force scales as O (N logN) rather than O(N^2) as an effect of cell opening criterion

Which kind of integrator for force? In most codes a LEAPFROG (see Lecture 1)



Which kind of time-stepping criterion?

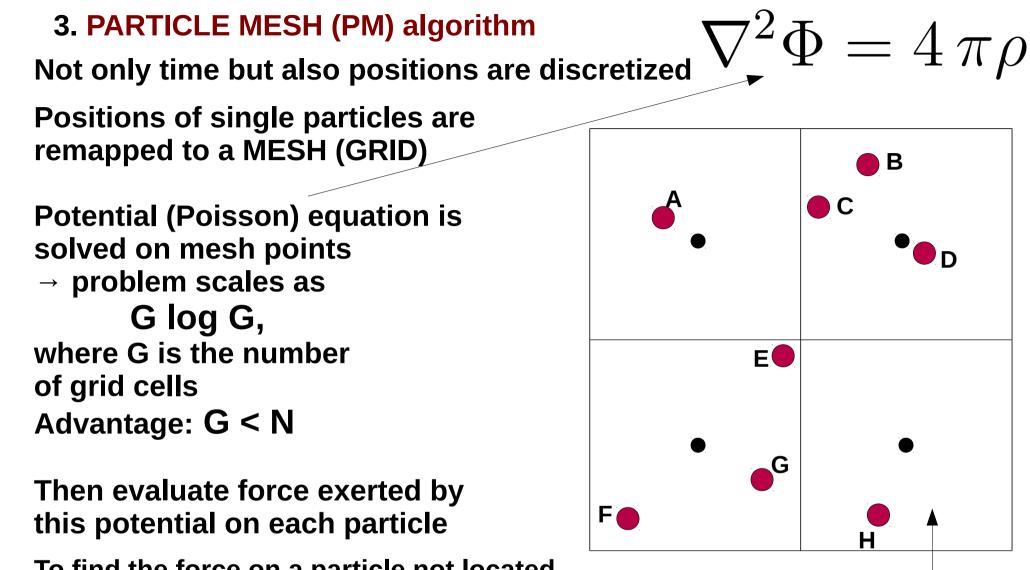
Generally same time-step for all particles (since the system is collisionless) but multiple time-stepping is possible. Most

used criterion

$$\Delta t = \min\left(\Delta t_{max}, \left(\frac{2\eta\,\epsilon}{|a|}\right)^{1/2}\right)$$

where η = accuracy parameter, ε = softening, A = acceleration of particle, Δt_{max} = max. timestep

Tree codes can be pure Barnes-Hut trees, or combined with Particle-Mesh and Fast Multipole algorithms. See next discussion



Meshpoints

Particles

Mesh cell

(G=4)

(N=8)

To find the force on a particle not located at a meshpoint we can either use the force at the nearest meshpoint, or interpolate the force from the closest meshpoints

→ Complexity O(N G log G) ~ O(N)

3. PARTICLE-PARTICLE (PP)/ PARTICLE MESH (PM) algorithm

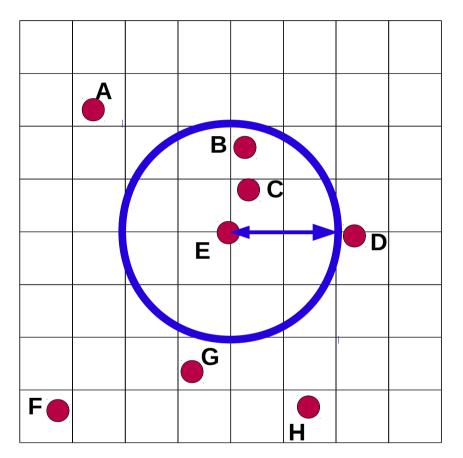
PM algorithm is fast – O(N) - but inaccurate for nearby particles

PP PM is a HYBRID algorithm:

-PP on short range forces: within a critical distance particle-particle forces are calculated directly

-PM on long-range forces: outside critical distance particlemesh algorithm is used

- critical distance~ 2 – 3 cell sizes



Critical distance for particle E PP used for force of B and C on E PM for all other forces on E

3. FAST MULTIPOLE MOMENT (FMM) algorithm

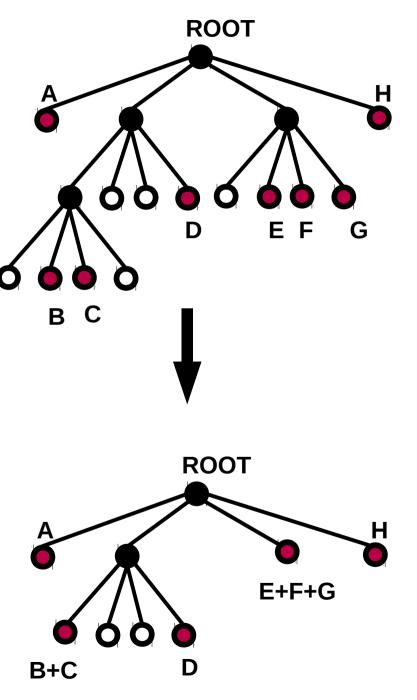
Similar to tree code but based on POTENTIAL INSTEAD OF FORCE

Implications:

1) Multipole expansions of the potential of a box is <u>more accurate</u> than center of mass substitution, but computationally <u>heavier</u>,

2) leaves can have > 1 particle(2 compensates 1),

3) force needs to be evaluated only at leaf level



 Barnes-Hut tree code (where leaves can be > 1 particle and there is multipole expansion for far away particles)

- Softening not as Plummer but cubic spline
- In gravity only mode seems to work well for > 128k cores

 Multi-stepping for timesteps allowed (which does not mean it is smart to use it)

- Excellent work-load balance (= integrations and particles are well distributed between the used CPUs)
- GAS treatment through smoothed-particle hydrodynamics (see Lecture 6)
- Lot of extra-physics (star formation, supernovae, ... see Lecture 7)

<u>OBTAIN mdl libraries and gasoline:</u> git clone https://github.com/N-BodyShop/mdl git clone https://github.com/N-BodyShop/gasoline

<u>BUILD and COMPILE gasoline:</u> cd gasoline cp Makefile.default Makefile

IF YOU HAVE MPI: make mpi

IF YOU DO NOT HAVE MPI: make pthread

YOUR EXECUTABLE NAME: gasoline

<u>RUN gasoline WITH MPI:</u> mpirun -np 2 ./gasoline parameterfileDM.par

RUN gasoline without MPI: ./gasoline parameterfileDM.par

EXAMPLE of a PARAMETER FILE (parameterfileDM.par):

bPeriodic = 0 # periodic boundaries: use only for cosmo bParaRead = 0 # read input file in parallel (usually safe) bParaWrite = 0 # write outputs in parallel

nSteps = 20 #number of time steps iStartStep = 0 # starting step number of simulation (for output numbering) dDelta = 0.01 # length of base timestep ("Rung 0") in Nbody units

achInFile = ./cond_init_DM.std #input file
achOutName = ./out #output file

dTheta = 0.7 # opening angle for gravity (standard value)

| iCheckInterval = 1 | # do a checkpoint every N timesteps |
|--------------------|--|
| IOutInterval = 1 | # print an output every N timesteps |
| dExtraStore = 3 | # extra memory storage per node |
| bKDK = 1 | # kick-drift-kick, leave like this |
| iMaxRung = 15 | # max number of "rungs", i.e. sub-timestep |

EXAMPLE of a PARAMETER FILE - continued:

| bStandard | = 1 | # snapshots in standard binary |
|-----------------------|--|--------------------------------|
| bDoGravity | = 1 | # ok |
| dMsolUnit dKpcUnit | = 2.225e5 # mass scale in Msun (for Nbody units) = 1.0 # length scale in kpc (for Nbody units) # → with this choice timescale is 1 Gyr | |

bVDetails=1 # write verbose stdout

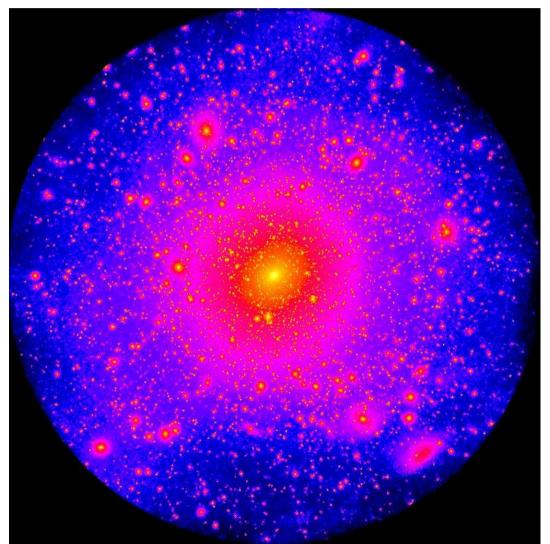
http://www-hpcc.astro.washington.edu/tools/tipsy/tipsy.html

Installation: follow readme on the website

Usage: Type tipsy on the terminal

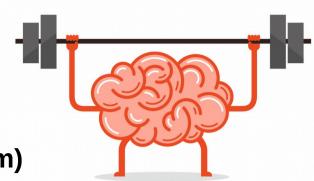
openb namefile loads 1 xall boxstat 0 all

and so on..



Exercise # 13:

*** RUN A BLOB OF DARK MATTER WITH UNIFORM DENSITY** (velocity field is Gaussian, with a power spectrum) 10⁵ DM particles for 2 Myr



mpirun -np 2 ./gasoline parameterfileDM.par

(initial conditions: cond_init_DM.std and parameter file: parameterfileDM.par are provided by me)

* Visualize with tipsy

hard movie out20

openb out.000020 loads 1 zall boxstat 0 all gasify 1 1 10 1.001 0 0 0 zall viewgas logrho 2 10

xall or yall depending on projection

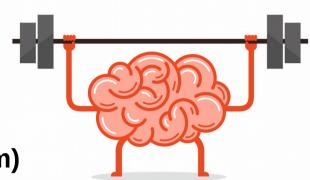
to use plot options of gas for DM

to see projected density in code units, log scale

create an image in tipsy image format shell convert out20 out20.jpg # convert image to jpg

Exercise # 13:

* RUN A BLOB OF DARK MATTER WITH UNIFORM DENSITY (velocity field is Gaussian, with a power spectrum) 10^5 DM particles for 2 Myr



its.

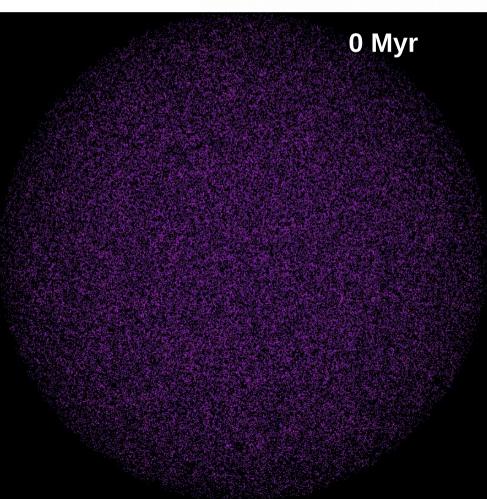
at

mpirun -np 2 ./gasoline paramet

(initial conditions: cond_init_DI parameter file: parameterfileDM

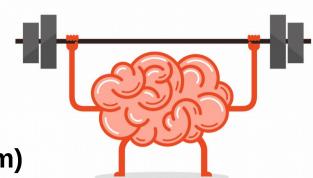
* Visualize with tipsy openb out.000020 loads 1 zall boxstat 0 all gasify 1 1 10 1.001 0 0 0 zall viewgas logrho 2 10

hard movie out20 shell convert out20 out20.jpg



Exercise # 13:

* RUN A BLOB OF DARK MATTER WITH UNIFORM DENSITY (velocity field is Gaussian, with a power spectrum) 10^5 DM particles for 2 Myr

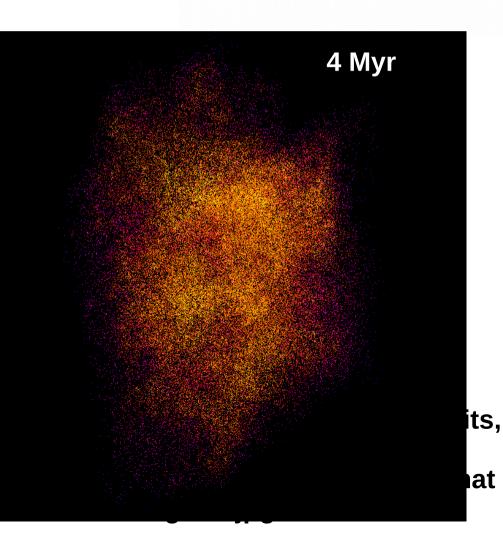


mpirun -np 2 ./gasoline paramet

(initial conditions: cond_init_DI parameter file: parameterfileDM

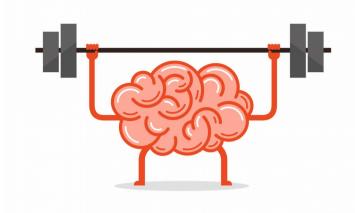
* Visualize with tipsy openb out.000020 loads 1 zall boxstat 0 all gasify 1 1 10 1.001 0 0 0 zall viewgas logrho 2 10

hard movie out20 shell convert out20 out20.jpg



Exercise # 14:

* Use the code you developed for Exercise # 8 and generate a Plummer sphere with Total mass = 10^10 Msun Mass of a single particle = 10^5 Msun



* convert it to a tipsy standard file with python convert_to_tipsy_ascii.py ascii2bin <plummer_000.tip >plummer_000.bin totipstd <plummer_000.bin >plummer_000.std

* run it for 20 Myr

* visualize the system with tipsy

7. COMPUTER CLUSTERS: problems of N-body codes

- The need for parallel computing
- HPC architectures
- MPI: basic concepts and main issues
- Intrinsic problems of scaling
- The queues and the scheduler (example: PBS)

7. COMPUTER CLUSTERS: THE NEED FOR PARALLEL COMPUTING

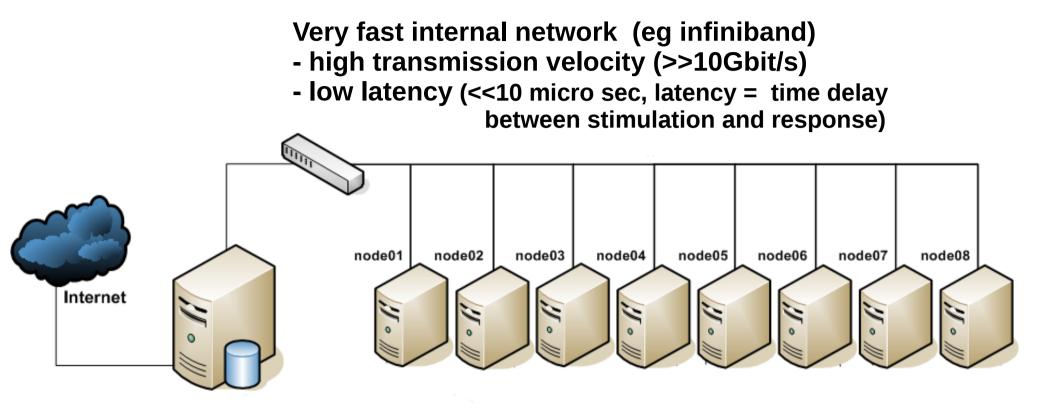
Systems with >10⁵ particles subject to gravity (long-range force, we cannot neglect forces on distant particles)

- \rightarrow beyond clock and RAM performance of a single CPU
- \rightarrow need to do same calculation in parallel

BASIC CONCEPTS:

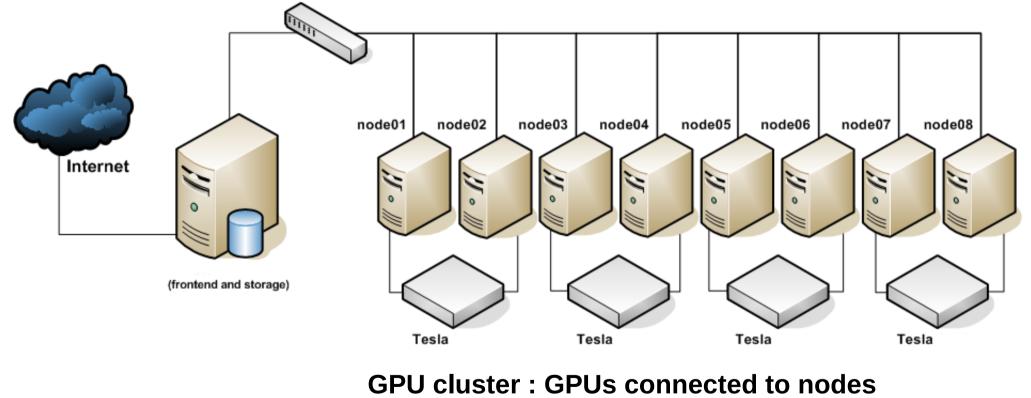
- *N* particles must be distributed between *p* processors with a suitable algorithm (simplest one : *N/p*)
- each processor calculates a portion of forces (those on local particles)
- since gravity is long-range, information about calculated forces must be sent to all other processors

- 1. the more processors I have the better (unless *N~p*)
- 2. <u>communication</u> between processors is critical: must be fast, otherwise is <u>bottleneck</u>
 - \rightarrow useless to increase *p* if communication saturates



(frontend and storage)

One front-end (master) for -user access (via internet) -compiling -launching jobs Many computing nodes (slaves): `normal' CPUs but connected by fast network



(usually 2-4)

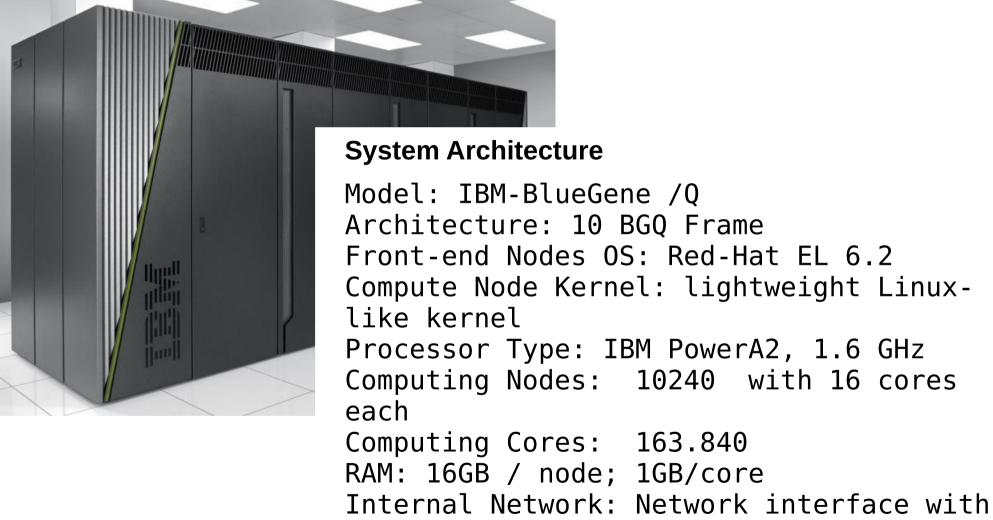
SOME EXAMPLES of CLUSTERS: GALILEO @ CINECA



System Architecture

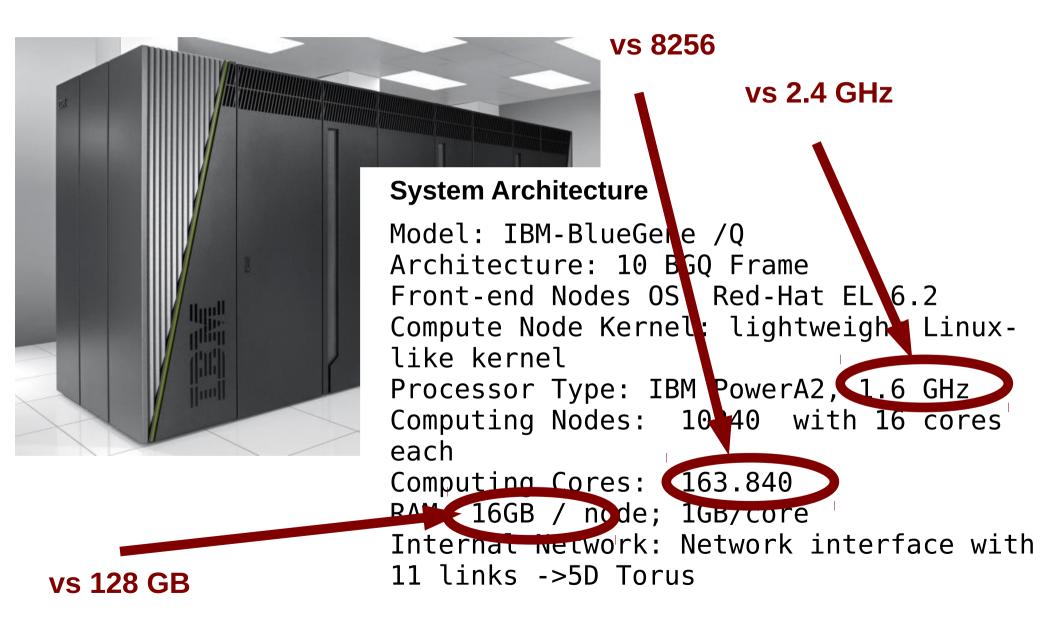
Model: IBM NeXtScale Architecture: Linux Infiniband Cluster Nodes: 516 Processors: 8-cores Intel Haswell 2.40 GHz (2 per node) Cores: 16 cores/node, 8256 cores in total Accelerators: 2 Intel Phi 7120p per node on 384 nodes (768 in total) + 2 NVIDIA K80 per node on 40 nodes RAM: 128 GB/node, 8 GB/core Internal Network: Infiniband with 4x QDR switches

SOME EXAMPLES of CLUSTERS: FERMI @ CINECA



11 links ->5D Torus

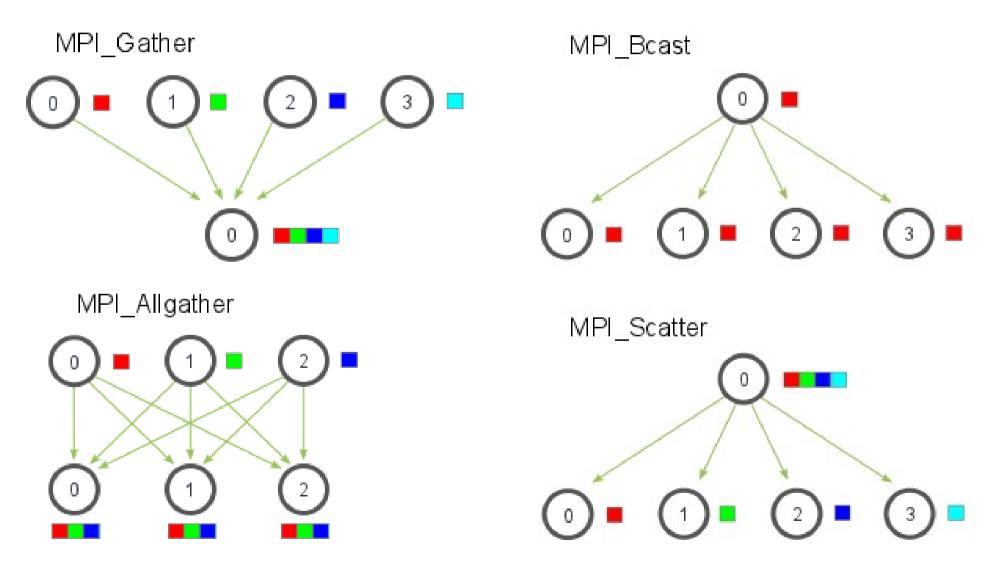
SOME EXAMPLES of CLUSTERS: FERMI @ CINECA



7. COMPUTER CLUSTERS: MPI basic concepts

How does MPI work?

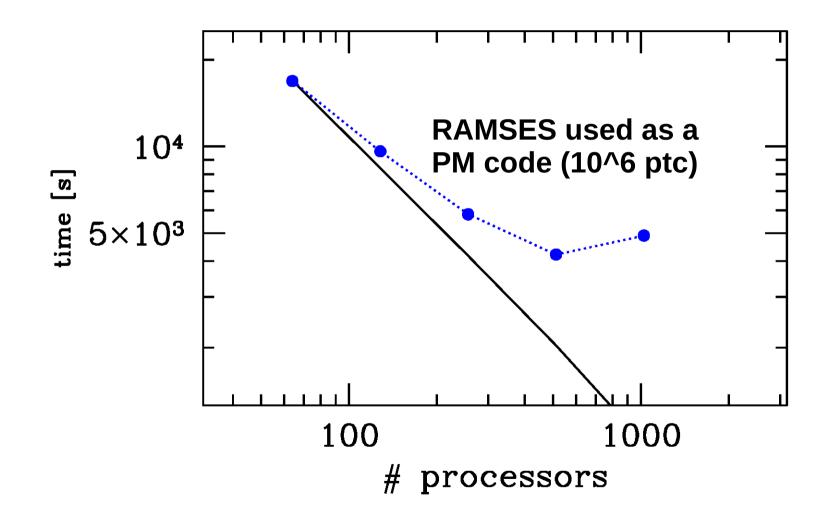
Library that organizes communication of commands, variables, information between nodes



7. COMPUTER CLUSTERS: intrinsic problems of scaling

How do I measure the scaling?

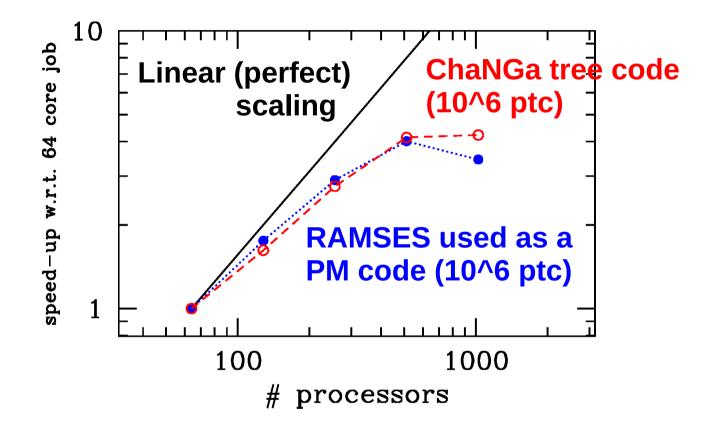
Time for running a job versus number of cores



7. COMPUTER CLUSTERS: intrinsic problems of scaling

How do I measure the scaling?

SPEED UP: sequential execution time / parallel execution time



EFFICIENCY or LINEARITY: ratio of speed up to number of processors

The problems are 1. gravity is long-range → communication is necessary 2. gas physics, sub-grid physics, binaries or other things that require even more communication! 7. COMPUTER CLUSTERS: queues and scheduler

on a cluster you cannot run by typing mpirun -np 16 mycode because there are other 100s of users

- **1. You submit a job to a scheduler**
- **2.** The scheduler assigns a priority to the job
- **3.** The job is QUEUED according to this priority
- 4. The run starts when priority is higher than any other job

HOW TO SUBMIT A JOB?

Note: the University of Padova pays CPU time at CINECA You might want to use such hours....

7. COMPUTER CLUSTERS: queues and scheduler

PBS (Portable Batch System) is the most used scheduler

1. prepare a submission script, e.g.

```
#!/bin/bash
#PBS -A NAME-OF-YOUR-PROJECT
#PBS -N changaprova2
#PBS -I walltime=00:59:00
#PBS -I select=1:ncpus=2
```

cd /gpfs/scratch/userexternal/mmapelli/sphere/dm_changa/ NPROCS=`wc -I < \$PBS_NODEFILE`

./charmrun -machinefile \$PBS_NODEFILE -np \$NPROCS ./ChaNGa ./newpar.par

This is the example pbs_script.sh

7. COMPUTER CLUSTERS: queues and scheduler

PBS (Portable Batch System) is the most used scheduler

2. submit job with

qsub pbs_script.sh

3. check the status

qstat -u username

4. delete wrong job

qdel job_identifier

NOW we can go back to section 5. of Lecture 2 and understand it better..