NBODY6++GPU ready for million-body globular cluster simulation - black hole evolution

The paper of NBODY6++GPU implementation is submitted to MNRAS

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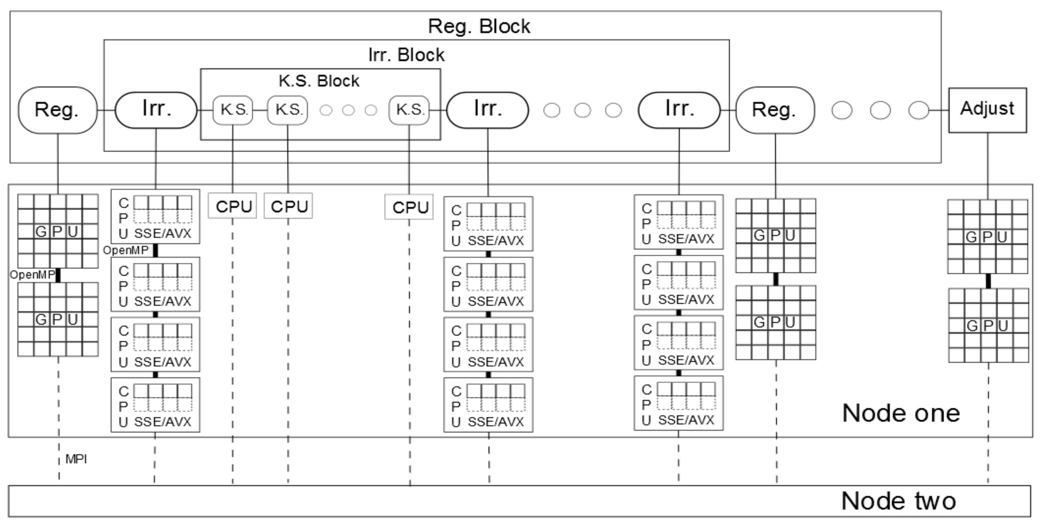
Abstract

Direct N-body simulation help to obtain accurate and detailed information about the dynamical evolution of star clusters. They enable comparisons with analytical models and Fokker-Planck or Monte-Carlo methods. NBODY6++ is the extension of well-known NBODY6 code. It's designed for large particle number simulation on supercomputers. We present NBODY6++GPU, an optimized version of NBODY6++ with improved hybrid parallelization methods (MPI, GPU, OpenMP and AVX/SSE), to accelerate large direct N-body simulation and in particular to solve the million-body problems. We provide the first results of black hole evolution from 4 realistic globular cluster simulations with initially a million particles.

NBODY6++GPU parallelization structure

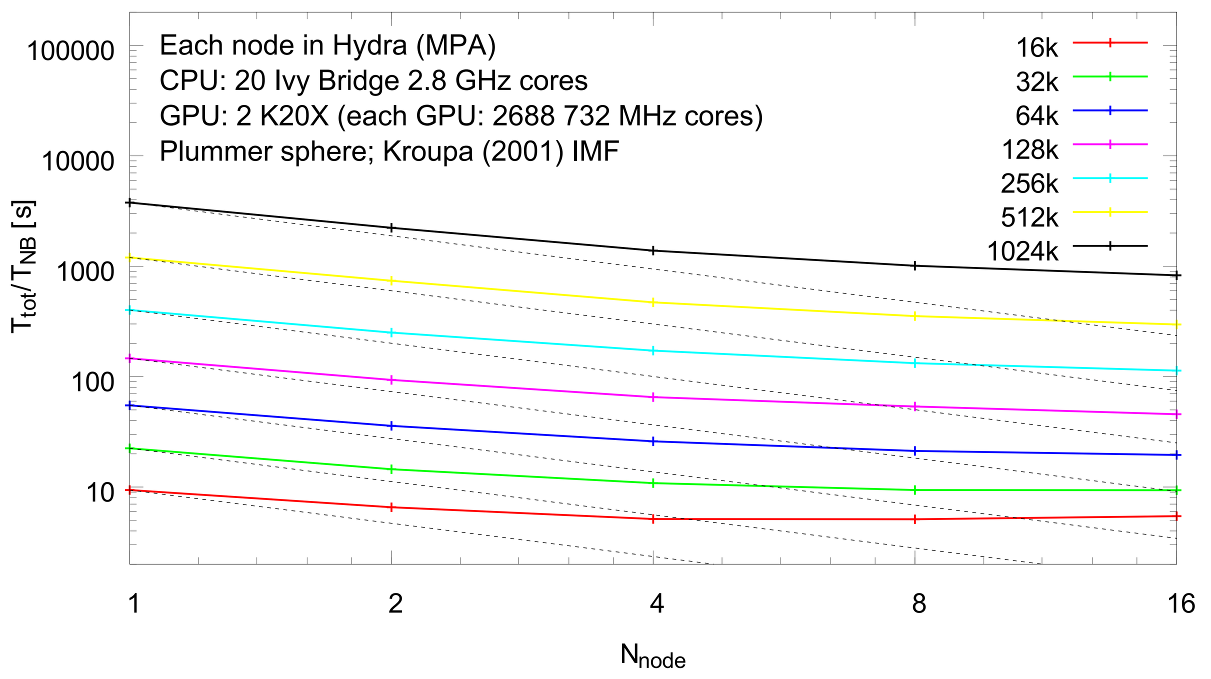
The cost of direct N-body simulation per relaxation timescale can be O($N^{10/3}$/ln(N) for a homogeneous system with 4th order Hermite scheme and individual time step based on Aarseth (1985) criterion (Makino & Hut 1988). Thus, we developed hybrid parallelized NBODY6++GPU with MPI, GPU, OpenMP and AVX/SSE to for the million-body system like globular clusters. The parallelization structure is shown below:



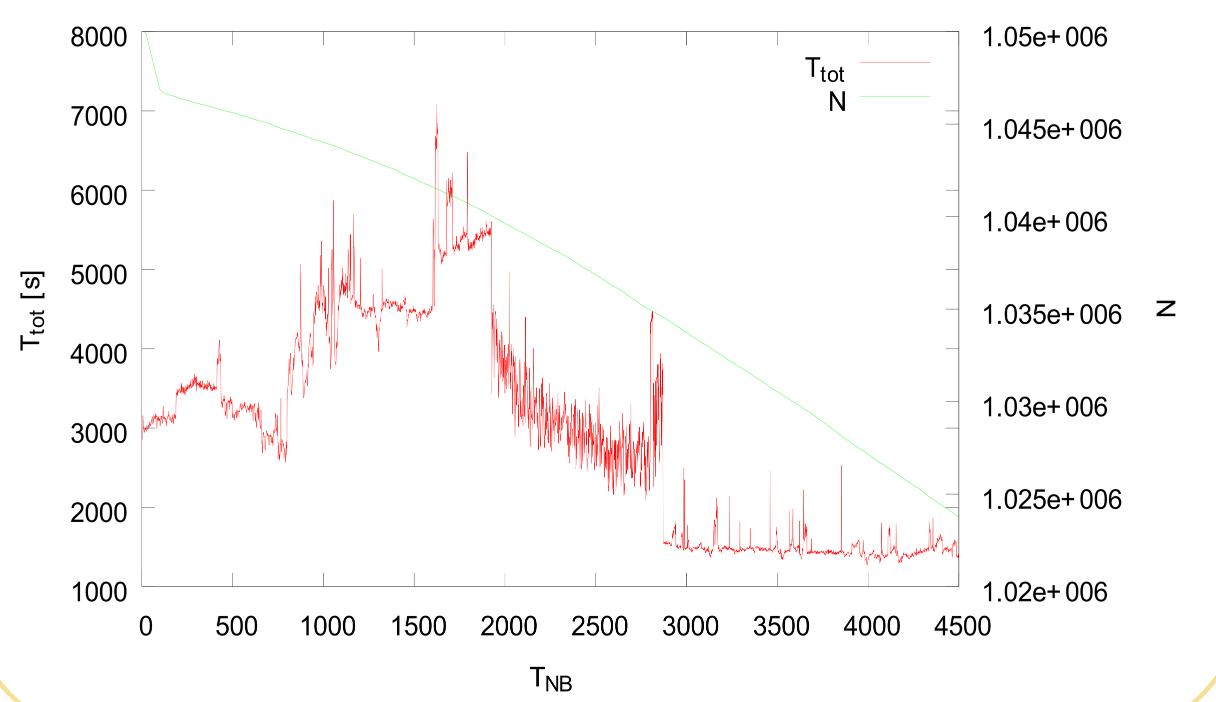
The one cycle of integration can be separated to three hierarchical time step blocks:
Regular block: Full force calculation
Irregular block: Fast neighbor force calculation (Ahmad & Cohen 1973)
Kustaanheimo & Stiefel 1965 (KS) block: Accurate treatment of close encounters and binaries

Performance

Benchmark of different particle numbers and node numbers. Plummer sphere and Kroupa (2001) IMF are used. The dashed lines show the ideal parallel limit with zero communication cost. The scaling appears poor, but the scaling with computing cores is excellent because the K20X GPU has 2688 cores which means for 16 nodes there will be 86016 computing cores for regular force and potential energy calculations. There are also 320 CPU cores fore irregular force calculation.



Computing time and number of particles evolution for a realistic globular cluster model with initially 950K single stars and 50k binaries. The time cost is large (3000-6000 s) at the early stage due to the choice of unsuitable KS regularization and time step parameters. After ~2800 N-body time unit, we optimize the parameters then the computing time reach stable stage (~1500 s).



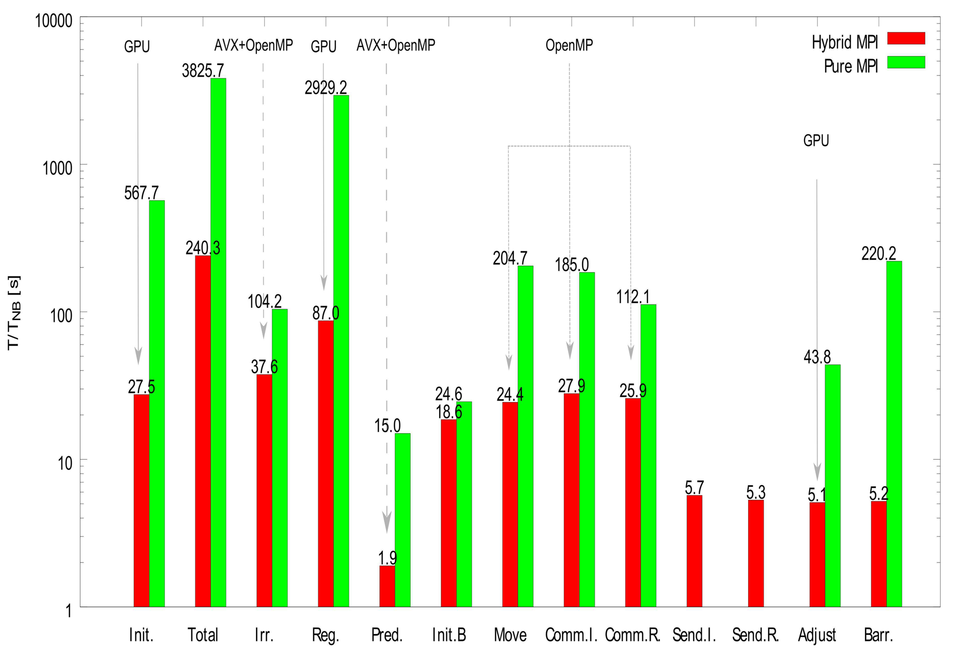
Downloads

Subversion: svn co http://silkroad.bao.ac.cn/repos/betanb6
GitHub: git clone https://github.com/lwang-astro/betanb6pp.git

Pure MPI vs. Hybrid MPI (MPI + GPU + OpenMP + AVX/SSE)

This figure compares the performance between NBODY6++ with only MPI parallelization and NBODY6++GPU with hybrid parallelization methods. The simulation includes 256k particles sampled by Plummer (1911) sphere and Kroupa, Tout & Gilmore 1993 (KTG93) initial mass function (IMF). The hybrid MPI test uses 4 nodes with 8 Intel Xeon E5-2650 (2.0 GHz) cores and one NVIDIA K20m GPU (2496 cores) per node on "Kepler" cluster at ARI, Heidelberg University. The pure MPI test uses the same configuration of CPU.

We can see the GPU provides significant accelerations (33x) of regular (full) force calculation and AVX/SSE speeds up the irregular (neighbor) force calculation by factor of 3 and OpenMP reduce the data movement and communications by factor of 5-10.



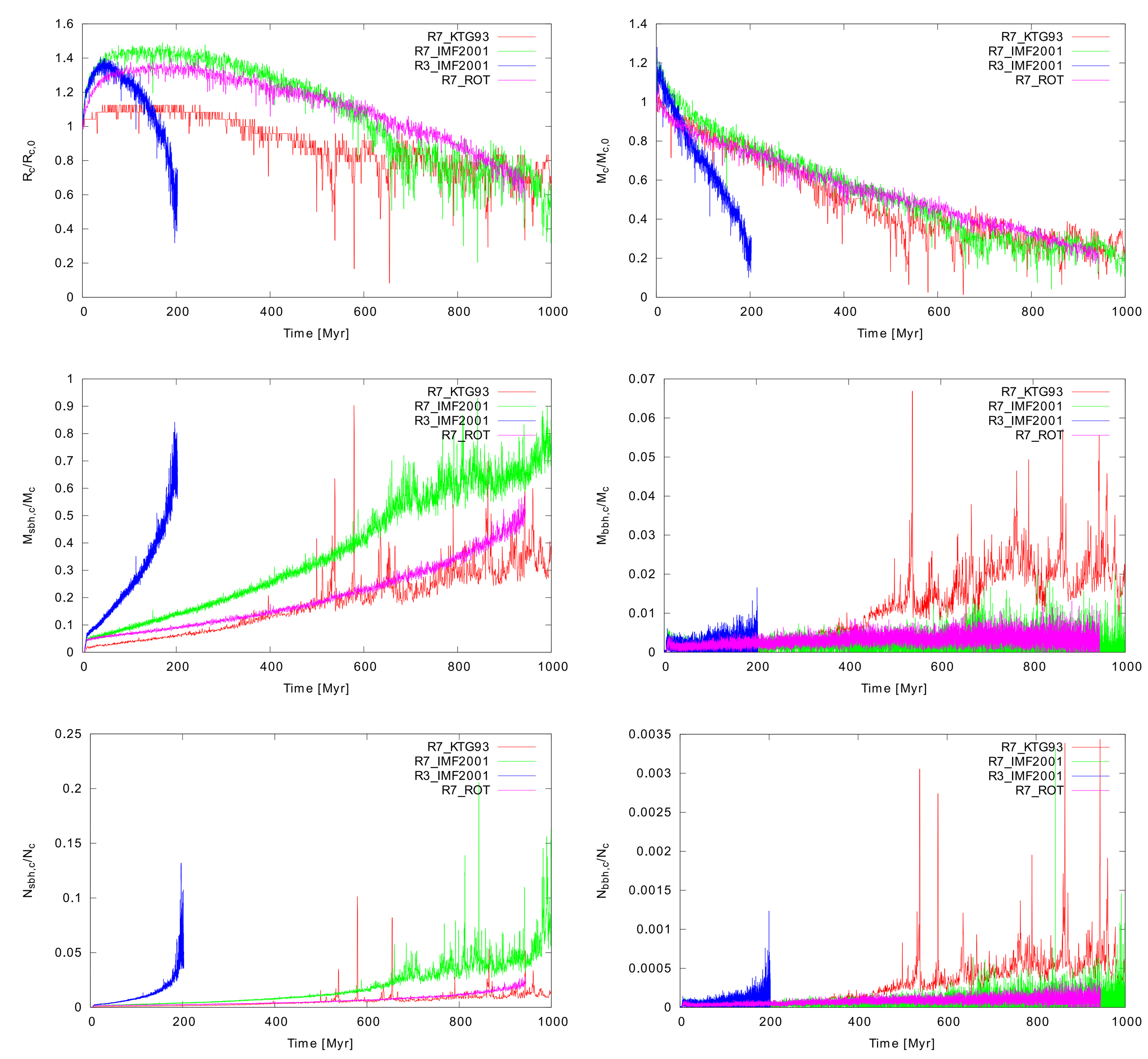
Initial models

	R7.5_KTG93	R7.5_K2001	R3_K2001	R7.5_ROT
$(\vec{r},\vec{v})$	King $W_0 = 6$			Rot. King[1]
R_h	7.5 pc		3.0 pc	8.1 pc
IMF	KTG93	Kroupa 2001		
N_{bin}/N_{tot}	5% (950,000 singles + 50,000 binaries)			
bin. semi.	logarithm uniform distribution from 0 .005 AU to 50 AU			
bin. ecc.	thermal distribution			
bin. m_1/m_2	ran. pair.[2]	$0.6(m_1/m_2)^{-0.4}$ $(m_1 \le m_2)^3$		
tidal field	point mass potential ($R_G = 7.1kpc$; $M_G = 8\times10^{10}M_\odot$)			
kick	~30 km/s[4]	265 km/s [4](Hobbs, 2005)		

1. Rotational King model with W_0=6 and w_0=0.8 (Einsel & Spurzem, 1999)
2. Random pairing from IMF
3. Distribution function based on Kouwenhoven et al. (2007)
4. Velocity dispersion of 1- dimension Maxwellian distribution

** R_h: half mass radius
** bin.: binary
** semi.: semi-major axis distribution
** ecc.: eccentricity distribution
** kick: neutron star (NS) or black hole (BH) kick velocity

Black hole inside cluster core

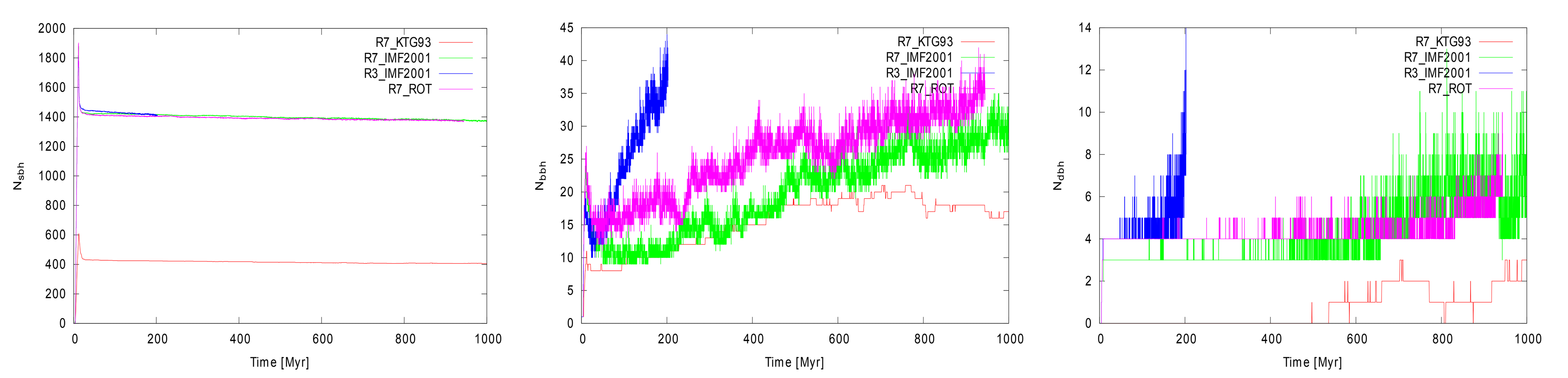


Here we present the BH and core evolution of four GC simulations. The top two panels compares the core radius (R_c) and core mass (M_c) evolution respect to their initial values. There is a clear trend that core evolution timescale depends on the concentration of clusters.

The middle panels show the ratio of BH mass inside Rc over Mc (suffix "sbh" is single BH, "bbh" is BH binary and "dbh" is BH-BH binary). The M_c will be dominated by BH within 1 Gyr for "R7" models and 200 Myr for "R3" model, although the number of BH inside core (see the bottom panels) is below 0.15 N_c, where N_c is number of stars inside core.

For models with Kroupa (2001) IMF, the core expand initially probably due to the more mass loss from massive stars compared to "R7_KTG93" model.

Black hole number



These three figures show the number evolutions of single BHs, BH binaries and double BH binaries. Due to the different IMF and kick velocity distribution, the numbers of BHs remaining in the cluster are very different for "R7_KTG93" and other three models. The number of formed BH binaries is significant larger for concentrated cluster "R3_IMF2001" before 200 Myr. The rotational cluster "R7_ROT" tends to contain more BH binaries compared to Non-rotational clusters. There are also several double BH binaries formed which may be the progenitors of gravitational waves in GCs.

Notice for "R7_KTG93" model we made a mistake that the kick velocities of BHs with progenitors core mass from 5.0 to 7.6 M_{sun} were larger than kick model from Belczynski et al. (2002). Thus, with corrected kick model, there should be more BHs remaining in cluster.