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A particle-based hybrid code for planet formation

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ABSTRACT

We introduce a new particle-based hybrid code for planetary accretion. The code uses an *N*-body routine for interactions with planetary embryos while it can handle a large number of planetesimals using a super-particle approximation, in which a large number of small planetesimals are represented by a small number of tracers. Tracer–tracer interactions are handled by a statistical routine which uses the phase-averaged stirring and collision rates. We compare hybrid simulations with analytic predictions and pure *N*-body simulations for various problems in detail and find good agreements for all cases. The computational load on the portion of the statistical routine is comparable to or less than that for the *N*-body routine. The present code includes an option of hit-and-run bouncing but not fragmentation, which remains for future work.

1. Introduction

Terrestrial planets and cores of giant planets are generally considered to have formed through accretion of many small bodies called planetesimals. To simulate accretion processes of planets, two methods, which are complementary to each other, have been applied.

The first one is *N*-body simulations in which orbits of all bodies are numerically integrated and gravitational accelerations due to other bodies are calculated in every time step (e.g., Kokubo and Ida, 1996; Chambers and Wetherill, 1998; Richardson et al., 2000; Morishima et al., 2010). *N*-body simulations are accurate and can automatically handle any complicated phenomena, such as resonant interactions and spatially non-uniform distributions of planetesimals. Gravity calculations are accelerated by such as tree-methods (Richardson et al., 2000) or special hardwares (Kokubo and Ida, 1996; Grimm and Stadel, 2014), and a large time step can be used with sophisticated integrators, such as Mixed Variable Symplectic (MVS) or Wisdom–Holman integrators (Duncan et al., 1998; Chambers, 1999). Even with these novel techniques, *N*-body simulations are computationally intense and the number of particles or the number of time steps in a simulation is severely limited.

The second approach is statistical calculations in which planetesimals are placed in two dimensional (distance and mass) Eulerian grids, and the time evolutions of the number and the mean velocity of an ensemble of planetesimals in each grid are calculated using the phase-averaged collision and stirring rates (e.g., Greenberg et al., 1978; Wetherill and Stewart, 1989, 1993; Inaba et al., 2001; Morbidelli et al., 2009; Kobayashi et al., 2010). While this approach does not directly follow orbits of individual particles, it can handle many particles, even numerous collisional fragments. Largest bodies, called planetary embryos, are handled in a different manner than small bodies, taking into account their orbital isolation. The mutual orbital separation between neighboring embryos is usually assumed to be 10 mutual Hill radii.

The last assumption is not always guaranteed, particularly in the late stage of planetary accretion (e.g., Chambers and Wetherill, 1998). To handle orbital evolution of embryos more accurately, Eulerian hybrid codes[1] have been developed (Spaute et al., 1991; Weidenschilling et al., 1997; Bromley and Kenyon, 2006; Glaschke et al., 2014), in which small planetesimals are still handled by the Eulerian approach whereas orbital evolutions of largest embryos are individually followed by such as *N*-body integrations. Gravitational and collisional interactions between embryos and small planetesimals are handled using analytic prescriptions. Glaschke et al. (2014) took into account radial diffusion of planetesimals due to gravitational scattering of embryos and their code can approximately handle gap opening around embryos' orbits.

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[1] The term "hybrid" means a combination of two different approaches/schemes. While this term might be used as a combination of Eulerian grids and Lagrangian embryos by the authors, we use the term for a combination of statistical calculations and *N*-body calculations.

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A Lagrangian hybrid method has also been introduced by Levison et al. (2012) (LDT12 hereafter). In their LIPAD code, a large number of planetesimals are represented by a small number of Lagrangian tracers. This type of approach is called a super-particle approximation and is also employed in modeling of debris disks (Kral et al., 2013; Nesvold et al., 2013) and planetesimal formation (Johansen et al., 2007; Rein et al., 2010). Orbits of individual tracers are directly followed by numerical integrations, and interactions between planetesimals (stirring and collisions) in tracers are handled by a statistical routine. Embryos are represented by single particles and the accelerations of any bodies due to gravity of embryos are handled in the *N*-body routine. Lagrangian hybrid methods have several advantages than Eulerian hybrid methods. For example, Lagrangian methods can accurately handle spatial inhomogeneity in a planetesimal disk (e.g., gap opening by embryos), planetesimal-driven migration, resonant interactions between embryos and small planetesimals, and eccentric ringlets. A drawback of Lagrangian methods would be computational cost as orbits of all tracers need to be directly integrated. Therefore, it is desirable that Lagrangian hybrid methods can handle various problems accurately even with a moderately small number of tracers.

In this paper, we develop a new Lagrangian hybrid code for planet formation. While we follow the basic concept of particle classes introduced by LDT12, recipes used in our code are different from those used in the LIPAD code in many places. The largest difference appears in the methods to handle viscous stirring and dynamical friction. The LIPAD code solves pair-wise interactions while our method gives the accelerations of tracers using the phase-averaged stirring and dynamical friction rates. While the LIPAD code conducts a series of three body integrations in the stirring routine (in the shear dominant regime) and in the routine of sub-embryo migration during a simulation, our code avoids them by using unique routines. The complete list of comparison with the LIPAD code turns out to be rather long and is given in Appendix G.

In Section 2, we explain our method. In Section 3, we show various tests of the new hybrid code and compare them with analytic estimates and pure *N*-body simulations. The computational speed and limitations of our code are discussed in Section 4. The summary is given in Section 5. For the sake of clarity, specific derivations are deferred to appendices.

2. Method

2.1. Particle classes

The particle classes in our hybrid code are the same as those introduced by LDT12. The code has three classes of particles: tracers, sub-embryos, and full-embryos (Fig. 1). In the present paper, we do not consider fragmentation of planetesimals and dust-tracers are not introduced. A tracer represents a large number of equal-mass planetesimals on roughly the same orbits. The mass of a planetesimal and the number of planetesimals in the tracer i (i for the index of the tracer) are defined to be m_i and k_i. Therefore, the tracer mass is given by $k_i m_i$. Through collisional growth, m_i increases and k_i decreases while $k_i m_i$ remains close to its original value. We allow mass exchanges between tracers through collisions so the tracer mass, $k_i m_i$, is not necessarily fixed but has the upper and lower limits, $m_{t,\max}$ and $m_{t,\min}$ ($m_{t,\min} < k_i m_i < m_{t,\max}$). We employ $m_{t,\max} = 2.0 m_{t0}$ and $m_{t,\min} = 0.1 m_{t0}$ in this paper, where m_{t0} is the minimum mass of a sub-embryo. The mass m_{t0} is usually the initial mass of a tracer, which is the same for all tracers at the beginning of a simulation. If $k_i = 1$ and $m_i \geqslant m_{t0}$, the tracer is promoted to a sub-embryo. If $m_i \geqslant f_f m_{t0}$, the sub-embryo is further promoted to a full-embryo, where we employ the numerical factor f_f of 100, as recommended by LDT12. The number k_i is an integer in our model.

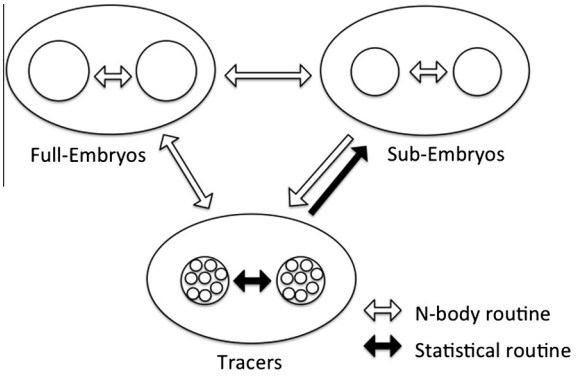

Fig. 1. Schematic illustration of our hybrid code. Accelerations due to gravity of embryos are handled by the *N*-body routine. Tracer–tracer interactions and back reaction of tracers on sub-embryos including collision are handled by the statistical routine.

Orbits of any types of particles are directly integrated. We use a Mixed Variable Symplectic integrator known as SyMBA (Duncan et al., 1998), which can handle close encounters between particles. This integrator is also used by LDT12. The collisional and gravitational interactions between full-embryos with tracers are directly handled in every time step of orbital integrations, as is the case of pure *N*-body simulations. On the other hand, tracer–tracer interactions are handled in a statistical routine which is described in subsequent sections in great detail. While the time step for the orbital integration δt is $\sim 10^{-2}$ of the orbital period, the time step Δt for the statistical routine can be taken to be much larger as long as Δt is sufficiently smaller than the stirring and collisional timescales. In this paper, we employ $\Delta t = 30\delta t$ for all test simulations. We confirmed that almost the same outcome is obtained even with a smaller Δt for all the test simulations.

In interactions between a tracer and a full-embryo in the *N*-body routine, the tracer is assumed to be a single particle with the mass equivalent to the total mass of planetesimals in the tracer. This is not a problem as long as the embryo is sufficiently massive compared with tracers. However, if the embryo mass is similar to tracer masses as is the case immediately after its promotion, and if embryo–tracer interactions are handled by the direct *N*-body routine, the embryo suffers artificially strong kicks from tracers. To avoid this issue, sub-embryos are introduced. Accelerations of sub-embryos due to gravitational interactions with tracers are handled by the statistical routine whereas accelerations of tracers due to gravitational interactions with sub-embryos are handled by the direct *N*-body routine (Fig. 1). Collisions of planetesimals in tracers with sub-embryos are also handled in the statistical routine to avoid artificially large mass jumps in sub-embryos, contrary to LDT12 (see Appendix G for more discussion).

2.2. Neighbor search for calculating surface number densities

Our statistical routine uses the surface number density of nearby tracers. We first describe how we determine the surface number density for tracer–tracer interactions. The surface number density of tracers for interactions between a sub-embryo and tracers is derived in a similar way, but slightly modified so that close and distant encounters are treated differently (Section 2.5).

Consider a target tracer i, surrounded by nearby interloping tracers. The cylindrical co-ordinate system (r, θ, z) is introduced and we consider a curved region, called the region i, located at