A Very Fast and Angular Momentum Conserving Tree Code

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Abstract

There are many methods used to compute the classical gravitational field in astrophysical simulation codes. With the exception of the typically impractical method of direct computation, none ensure conservation of angular momentum to machine precision. Under uniform time-stepping, the Cartesian fast multipole method of Dehnen (also known as the very fast tree code) conserves linear momentum to machine precision. We show that it is possible to modify this method in a way that conserves both angular and linear momenta.

Key words: binaries: close – galaxies: general – gravitation – methods: numerical

1. Introduction

Angular momentum plays an important role in a plethora of astrophysical phenomena. These phenomena include, but are not limited to, the formation of galactic disks, the accretion of matter in interacting binary star systems, the formation of proto-stars and proto-planetary disks, the dynamics of planetary orbits, and rapidly rotating neutron stars and black holes. Considering the limit that Newtonian gravity provides an accurate description of the gravitational field of any isolated astrophysical system, we expect the total angular momentum change due to the gravitational interaction to be zero.

Classical self-gravitating astrophysical simulation codes compute the gravitational field in a variety of ways. Grid-based hydrodynamics codes (e.g., Fryxell et al. 2000; D’Souza et al. 2006; Stone et al. 2008; Almgren et al. 2010; Dupuy & Liu 2012) solve the discretized Poisson’s equation for the gravitational potential using iterative techniques, Fourier transforms, or a combination of the two. N-body codes and smoothed particle hydrodynamics (SPH) codes (e.g., Hernquist & Katz 1989; Springel 2005; Vanaverbeke et al. 2009; Lorén-Aguilar et al. 2010; Yokota & Barba 2012) may use the tree code of Barnes & Hut (1986), particle-mesh methods (Bagla 2002), or fast multipole methods (FMM; Warren & Salmon 1995; Greengard & Rokhlin 1997; Dehnen 2000; Dehnen & Read 2011). Some of the gravity solvers in the aforementioned codes conserve linear momentum, but none ensure conservation of angular momentum.

Due to the symmetry of the equations for the multipole interactions, the method of Dehnen (2000, hereafter “D2000”) naturally conserves linear momentum between any pair of particles. We have developed a modification to D2000 that preserves this property, while simultaneously conserving angular momentum between any pair of interacting multipoles. This kind of conservation is not of the same quality as the conservation of linear momentum. It introduces artificial torques; however, the added torques are within the error bound of the original scheme. In Section 2, we describe our modification to D2000. In Section 3, we provide a numerical test of the method. In Section 4, we make the case for using this technique to model double white dwarfs (DWDs), as well as discuss some of the method’s shortcomings. In the Appendix, we provide a more general derivation of the method that applies to higher orders.

2. Method

The algorithm presented by D2000 decomposes the set of particles into an oct-tree structure, with each cell in the oct-tree containing a predetermined maximum number of particles, \( n_{\text{crit}} \). The code presented in this paper was run with \( n_{\text{crit}} = 25 \). Two cells, cell “A” and cell “B,” are considered “well separated” if they satisfy the “opening criterion,”

\[
|Z_A - Z_B| > \frac{1}{\theta} (R_{A,\text{max}} + R_{B,\text{max}}),
\]

where \( Z_A \) and \( Z_B \) are the respective centers of mass of cells A and B, \( R_{A,\text{max}} \) and \( R_{B,\text{max}} \) are the maximum distances from a particle within the cells to the centers of mass of their respective cells, and \( \theta \) is an adjustable parameter called the “opening angle,” where \( 0 < \theta \leq 1 \). Forces within a cell are computed using multipole interactions and Taylor expansions for all cells that are well separated from it, while the force contributions from any remaining nearby particles are computed directly (note that Dehnen 2014 has recently developed a more complex selection criteria that uses an error estimate to select interaction pairs in a manner that maximizes execution speed for a given error. The development we present here is also applicable to that method). Here, we will present only what is necessary to describe the modifications we have made. Refer to D2000 for the full description of the original method.

Let \( \mathbf{R} = \mathbf{Z}_B - \mathbf{Z}_A \). Within cell A there are \( N_A \) particles located at positions \( \mathbf{X}_1, \mathbf{X}_2, \ldots, \mathbf{X}_{N_A} \) and with masses \( \mu_{A1}, \mu_{A2}, \ldots, \mu_{AN_A} \); similarly, within cell B there are \( N_B \) bodies located at positions \( \mathbf{Y}_1, \mathbf{Y}_2, \ldots, \mathbf{Y}_{N_B} \) with masses \( \mu_{B1}, \mu_{B2}, \ldots, \mu_{BN_B} \). Let \( \mathbf{x}_a = \mathbf{X}_a - \mathbf{Z}_A \) and \( \mathbf{y}_b = \mathbf{Y}_b - \mathbf{Z}_B \). The monopole, dipole, and quadrupole moments are

\[
M := \sum_{\mathbf{X}_a \in \text{cell}} \mu_{a},
\]

\[
M_i := \sum_{\mathbf{X}_a \in \text{cell}} \mu_a x_{a,i},
\]

and

\[
M_{ij} := \sum_{\mathbf{X}_a \in \text{cell}} \mu_a x_{a,i} y_{a,j}.
\]
Gradients of the Green’s function for the gravitational potential, \( \nabla^2 g(R) = -\nabla \frac{1}{R^3} \), are
\[
D_i := -\frac{1}{R},
\]
\[
D_i := \frac{R_i}{R^3},
\]
\[
D_{ij} := -\frac{3R_iR_j - \delta_{ij} R^2}{R^5},
\]
and
\[
D_{ijk} := 15R_iR_jR_k - 3(\delta_{ij}R_k + \delta_{ik}R_j + \delta_{jk}R_i)R^2
\]
The approximated potential generated by the particles in cell \( B \) at a position \( x := x_i \hat{e}_i \) in cell \( A \) is then
\[
\Phi_{B \rightarrow A}(X) \approx \left( M_B D_i - M_B D_j + \frac{1}{2} M_{Bij} D_{ij} \right)
+ x_i \left( M_B D_i - M_B D_j + \frac{1}{2} M_{Bij} D_{ij} \right)
+ \frac{1}{2} x_i x_j (M_B D_{ij} - M_B D_{ij}) + \frac{1}{6} x_i x_j x_k M_B D_{ijk}.
\]
The Cartesian FMM described by Equations (2)–(9) is the same as in D2000, except that: (1) we have opted to express the quadrupole moments in the extensive form, and (2) we have added terms that involve the dipole moment. These terms drop out in the case that cell coordinate centers coincide with cell centers of mass. As in D2000, we have dropped the octupole moment from Equation (9). For a given interaction, this term is constant in space and, hence, does not contribute to the force calculation.

Using Equation (9), the gravitational acceleration caused by the particles in cell \( B \) at a point \( X \) within cell \( A \) can be expressed as
\[
ge_{B \rightarrow A}(X) = -\left[ \left( M_B D_i - M_B D_j + \frac{1}{2} M_{Bij} D_{ij} \right)
+ x_i \left( M_B D_i - M_B D_j + \frac{1}{2} M_{Bij} D_{ij} \right)
+ \frac{1}{2} x_i x_j (M_B D_{ij} - M_B D_{ij}) + \frac{1}{6} x_i x_j x_k M_B D_{ijk} \right] \hat{e}_i.
\]
Similarly, the gravitational acceleration caused by the particles in cell \( A \) at a point \( Y \) within cell \( B \) can be expressed as
\[
ge_{A \rightarrow B}(Y) = -\left[ \left( -M_A D_i - M_A D_j - \frac{1}{2} M_{Aij} D_{ij} \right)
+ y_i \left( M_A D_i - M_A D_j - \frac{1}{2} M_{Aij} D_{ij} \right)
+ \frac{1}{2} y_i y_j (M_A D_{ij} - M_A D_{ij}) - \frac{1}{6} y_i y_j y_k M_A D_{ijk} \right] \hat{e}_i.
\]
Using Equations (2)–(4), (10), and (11), we can express the force between two unit masses as
\[
ge_{-+-} = \mp(D_i + (x_j - y_j) D_{ij} + (x_j - y_j) (x_k - y_k) D_{ijk}) \hat{e}_i.
\]
Although the computed force is an approximation of the force on an individual particle, Equation (12) shows that the sum of the forces between any two particles is exactly zero. This implies that the sum of linear momentum changes due to gravitation over all of the masses in pairs of interacting cells is zero. Therefore, the change over the entire computational domain is zero.

The same result does not generally hold for the sum of the torques generated between pairs of cells. Referring to the more general derivation of the method in the Appendix, we write Equation (34) to expansion order \( P = 3 \) and find the sum of all torques to be
\[
\tau_{AB} = \frac{1}{2} \epsilon_{lmp} (M_{A\mu}k M_B - M_A M_{B\mu}k) D_{ijk} \hat{e}_q,
\]
where we define the octupole moments,
\[
M_{ijk} := \sum_{x_i \in \text{cell}} \mu_{x_i} x_{ij} x_{ik} x_{jk}.
\]
For many evolution methods employing the FMM, such as SPH or \( N \)-body, the net torque found in Equation (13) (or the equivalent expression for a higher expansion order) is the sole source of angular momentum non-conservation. Eliminating this efficiency would, therefore, guarantee angular momentum conservation to machine precision.

We seek a correction to the Cartesian FMM of D2000 that: (1) balances the net torque found in Equation (13), (2) produces an equal and opposite force on each cell, and (3) is within the error bounds of the computed force. One possible solution satisfying these requirements uses the corrective force
\[
F_c = -\frac{1}{2} (M_{A\mu}k M_B - M_A M_{B\mu}k) D_{ijk} \hat{e}_i,
\]
where \( D_{ijk} \) is the fourth derivative of the Green’s function. Proof that \( F_c \) cancels the torque imbalance is found in the Appendix. The correction for cell \( A \) is
\[
ge_{C,A \rightarrow -}(X) = -\frac{1}{M_A} F_c,
\]
and the correction for cell \( B \) is
\[
ge_{C,- \rightarrow B}(Y) = -\frac{1}{M_B} F_c.
\]
The corrective accelerations, \( g_{C,A \rightarrow -} \) and \( g_{C,- \rightarrow B} \), are added to \( g_{A \rightarrow -} \) and \( g_{- \rightarrow A} \), respectively, to obtain the total acceleration. This correction produces an extra acceleration that is constant over each cell. The torque produced is equal in magnitude but opposite in direction to the torque imbalance found in Equation (13). The sum of the corrective forces on one cell is equal and opposite to that on the other cell, preserving the force balance of the original method. Because it uses a higher order Green’s function derivative, the corrective force is within the error bounds of the original method.

Another possible solution is to replace \( D_{ijkl} \) in Equation (15) with the non-symmetric tensor,
\[
D'_{ijkl} := \frac{15(\delta_{ik} R_j R_l + \delta_{jl} R_k R_i + \delta_{kl} R_j R_i)}{R^7}
- \frac{3(\delta_{ik} \delta_{jl} + \delta_{il} \delta_{jk} + \delta_{jk} \delta_{il})}{R^5},
\]
yielding the alternative force correction,
\[
F'_c = -\frac{1}{2} (M_{A\mu}k M_B - M_A M_{B\mu}k) D'_{ijk} \hat{e}_i.
\]
Note that \( D'_{ijkl} \) is simply \( D_{ijkl} \) with any terms that do not contribute to Equation (13) removed. As shown below in
Section 3, Equation (19) yields a faster implementation for a given opening angle while slightly increasing the solution error.

It is important to note that the quality of torque conservation in our modified FMM is not the same as the quality of force conservation. As shown by Equation (12), the force between any two individual particles sums to zero. An analogous relation does not hold for the torques. The torques satisfy the less strict requirement that the sum of torques between all of the masses in two interacting cells is zero. The correction also introduces unphysical torques between particles in the same cell; however, these corrections are within the error bounds of the original scheme.

3. Numerical Test

To test our new method, we have implemented a minimalistic version of the method of D2000, with options to use the corrections described by Equations (15) or (19). This code is written in C++ for serial execution on a single processing core. The version of the code used in this paper is available through the Zenodo repository, https://doi.org/10.5281/zenodo.571523. Note that the code is intended only to illustrate our method and is not intended for production purposes.

For our test problem, we have chosen a binary star system for which the net torque imbalance can be relatively high. As can be seen in Equation (13), the torque imbalance grows with the difference between octopole moments of the stellar components of a binary. Therefore, the larger and less centrally condensed a star is compared to its companion, the larger the net torque imbalance. One such system is a high mass ratio DWD with the larger, less massive star filling its Roche lobe. A system like this, if stable to mass transfer, is a potential progenitor of an AM Canum Venaticorum (AM CVn) type cataclysmic variable binary star (Marsh et al. 2004; Kilic et al. 2016). Our test problem is an approximation of such a system. The accretor has a mass of 1M⊙ and the donor a mass of 0.2M⊙, with the donor’s volume equal to the volume of its Roche lobe. Each component is taken to be a spherical Lane–Emden polytrope. In realistic systems, the donor will be tidally distorted; however, the spherical approximation is sufficient to demonstrate the usefulness of our method. The donor has a polytropic index of 3 and the accretor has a polytropic index of 3, approximating the cold white dwarf equation of state in the low and high mass limits, respectively. The test problem consists of 10⁶ equal mass particles, chosen by sampling the density distribution computed from integrating the Lane–Emden equation for each component.

Our test was executed on a single core of a 2.8 GHz E5-2680v2 Intel Xeon Processor on the QB2 cluster of the Louisiana Optical Network Initiative (LONI). The code was compiled using the GNU C++ compiler version 4.9.0. The gravitational solution was generated, using opening angle θ = 0.2, 0.3, ..., 1.0, for the original uncorrected D2000 method, the torque corrected method (using Equation (15)), and the torque corrected and optimized method (using Equation (19)). We refer to these three methods, respectively, as the “UC”, “TC”, and “TCO” variants.

The net force and torque balances were computed using the formula

$$\epsilon_n = \frac{|g_n - g_{\text{PP},n}|}{|g_{\text{PP},n}|},$$

(21)

over all particles, where g_{\text{PP},n} is the exact, directly computed force on the nth particle. The relative torque error is similarly defined using

$$\epsilon_n = \frac{|X \times g_n - X \times g_{\text{PP},n}|}{|X \times g_{\text{PP},n}|},$$

(22)

where, here, X is the distance to the coordinate origin. We plot these errors in Figures 1(b) and (d). Both the force and torque errors are virtually identical between the UC and TC variants. The torque correction in the TC variant does not result in a force or torque error higher than in the original scheme of the UC variant. Both errors are higher for the TCO variant; therefore, for a given error, the TCO variant requires a smaller θ than the TC variant, resulting in more interactions to compute.

4. Discussion

The method of Dehnen (2000) conserves linear momentum to machine precision, but not angular momentum. We have presented two modifications to this method that each enable it to also conserve angular momentum to machine precision. This extra feature comes at computational expense, requiring approximately twice the compute time.

Whether or not the extra computational effort is worth the benefit of conserving angular momentum to machine precision will depend on the particular astrophysical system under investigation. One example of such a system would be a DWD at the onset of stable mass transfer. Past simulations of interacting DWDs have found angular momentum is artificially either added or removed from the system as the simulation proceeds.

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progresses. Motl et al. (2002) found a normalized gain rate of \(10^{-3}/\text{orbit}\) for polytropic binaries of mass ratios 1.0 and 0.8436. Dan et al. (2011) found a normalized violation rate using SPH to simulate 84 orbits of an interacting 0.8 \(M_\odot\) accretor and 0.2 \(M_\odot\) donor. These loss rates are sufficient that over many hundreds or more orbits, the violation of angular momentum conservation may cause systems that should be stable to become unstable (or vice versa). One possible way to avoid this problem is to increase the resolution to the point that the artificial angular momentum gain or loss rate is small compared to changes in the orbital and spin angular momenta of the system. However, it is difficult to determine what resolution is needed a priori. Increased resolution also comes at significant computational cost. The method described in this paper provides a remedy without increasing resolution.

We also note that preservation of linear or angular momentum holds when the time-stepping is not uniform throughout the entire domain. In practice, many SPH and N-body codes use individual time-steps for particles or groups of particles, resulting in a faster computation speed (Ahmad & Cohen 1973). In order to fully realize the benefits of the method presented here, one has to abandon individual time-stepping and the speed-up that comes with it. Another benefit of individual time-stepping is that the non-conservation of momentum is often used as a proxy for the measure of the force error. With exact conservation of momentum and angular momentum, this is no longer possible, necessitating the choice of a different proxy. One possibility is to sum the magnitudes of the highest order expansion terms over the entire domain. A higher order extension to this method is presented in the Appendix. The method is also applicable for any Green’s function that is solely a function of the scalar distance between points, such as softened gravitational potentials.

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Figure 1. Here, we shows plots of (a) the force and torque imbalance, (b) the mean relative force error, (c) the compute time, and (d) the mean relative torque error against opening angle, \(\theta\), for each of the tested FMM schemes. The original, uncorrected FMM of D2000 is referred to as “UC” (red squares), our torque corrected version is referred to as “TC” (blue circles), and our optimized torque corrected version is referred to as “TCO” (green triangles).
The total torque, $\mathbf{\tau}_{AB}$, about the coordinate origin of cell $A$ is,

$$\mathbf{\tau}_{AB} = \sum_{Y_i \in cellB} \mu_j \mathbf{R}_j \times \mathbf{g}_{j,A-B} + \sum_{X_i \in cellA} \mu_i \mathbf{x}_i \times \mathbf{g}_{i,B-A} + \sum_{Y_j \in cellB} \mu_j \mathbf{y}_j \times \mathbf{g}_{j,A-B}.$$  \hspace{1cm} (29)

The total torque can be thought of as the sum of a bulk torque, 

$$\sum_{Y_j \in cellB} \mu_j \mathbf{R}_j \times \mathbf{g}_{j,A-B} = \mathbf{e}_r \sum_{X_i \in cellA} \sum_{Y_j \in cellB} \mu_i \mu_j \sum_{m=0}^{p-1} (-1)^n n/m! \epsilon_{pkr} \mathbf{R}_p X_i x_i \cdots x_i y_j q_j \cdots y_{j,q_n}$$  

and the spin torques of each cell,

$$\sum_{X_i \in cellA} \mu_i \mathbf{x}_i \times \mathbf{g}_{i,B-A} + \sum_{Y_j \in cellB} \mu_j \mathbf{y}_j \times \mathbf{g}_{j,A-B}$$  

Using the fact that

$$R_{p,x_i,x_i \cdots x_i y_j q_j \cdots y_{j,q_n}} = m \mathbf{x}_i \mathbf{p} \mathbf{x}_i x_i \cdots x_i y_j q_j \cdots y_{j,q_n}$$  

we can express the spin torques as

$$\sum_{X_i \in cellA} \mu_i \mathbf{x}_i \times \mathbf{g}_{i,B-A} + \sum_{Y_j \in cellB} \mu_j \mathbf{y}_j \times \mathbf{g}_{j,A-B}$$  

We see that the RHSs of Equations (30) and (33) differ only in sign and the range of summation indices. The spin torques of expansion order $m$ are canceled by the bulk torque of expansion order $m + 1$. The spin torques that result from the highest expansion order do not have a bulk torque to cancel them, resulting in a net torque. Using Equations (29), (30), and (33), we can express the net torque

$$\mathbf{\tau}_{AB} = \sum_{X_i \in cellA} \mu_i \mathbf{x}_i \epsilon_{pkr} \mathbf{R}_p X_i x_i \cdots x_i y_j q_j \cdots y_{j,q_n}.$$  \hspace{1cm} (34)

If we apply a constant corrective force, $F_c$ to the particles in cell $A$, and $-F_c$ to the particles in cell $B$, the balance of force
remains unaltered. The contribution to the torque is

\[ \tau_c = \sum_{x_i \in \text{cellA}} \sum_{y_j \in \text{cellB}} \mu_i \mu_j \left\{ -e_r \epsilon_{p q k} R_k \mathcal{F}_{c,k} + e_r \epsilon_{p q k} x_i^p y_j^p \mathcal{F}_{c,k} \right\} \]  

(35)

When the coordinate centers for cells A and B are coincident with the centers of mass for the respective cells, dipole moments vanish and the sum of corrective torques for the last two terms on the RHS of Equation (35) vanish. Comparing Equation (34) with the first term on the RHS of Equation (35), we find that if we set

\[ F_c = e_k \sum_{x_i \in \text{cellA}} \sum_{y_j \in \text{cellB}} \mu_i \mu_j \sum_{n=0}^{P} \frac{(-1)^n}{n!(P-n)!} \times x_i^{(p)} y_j^{(q)} \mathcal{D}_{\text{cellA}}^{(p)} \mathcal{D}_{\text{cellB}}^{(q)} \]  

the sum of the original FMM torque and the corrective torque vanishes,

\[ \tau_{AB} + \tau_c = 0. \]  

(37)

Summing over all masses in each cell, the total corrective force, \( F_c \), is

\[ F_c = e_k \sum_{x_i \in \text{cellA}} \sum_{y_j \in \text{cellB}} \mu_i \mu_j \sum_{n=0}^{P} \frac{(-1)^n}{n!(P-n)!} \times x_i^{(p)} y_j^{(q)} \mathcal{D}_{\text{cellA}}^{(p)} \mathcal{D}_{\text{cellB}}^{(q)} \]  

(38)

Here, we have defined the generalized moments for each cell,

\[ M_{A,x_i \cdots x_i} = \sum_{x_i \in \text{cellA}} \mu_i x_i^{(p)} \cdots x_i^{(p)} \]  

(39)

and

\[ M_{B,y_j \cdots y_j} = \sum_{y_j \in \text{cellB}} \mu_j y_j^{(q)} \cdots y_j^{(q)} \]  

(40)

Making the definition,

\[ D_{h_{l_1 \cdots l_n}}^{(p)} = D_{h_{l_1 \cdots l_n}} - \frac{R_k R_l}{R^2} D_{h_{l_1 \cdots l_n}} \]  

(41)

we can define an alternative corrective force,

\[ F_c' = e_k \sum_{n=0}^{P} \frac{(-1)^n}{n!(P-n)!} M_{A,x_i \cdots x_i} M_{B,y_j \cdots y_j} \times D_{h_{l_1 \cdots l_n}}^{(p)} \]  

(42)

This corrective force also results in a balanced torque. Depending on the choice of Green’s function, Equation (42) may result in fewer terms to compute.

References
Ahmad, A., & Cohen, L. 1973, JCoPh, 12, 389
Almgren, A. S., et al. 2010, ApJ, 715, 1221
Bagla, J. S. 2002, JApA, 23, 185
Barnes, J., & Hut, P. 1986, Natur, 324, 446
Dan, M., Rosswog, S., Guillou, J., & Ramirez-Ruiz, E. 2011, ApJ, 737, 89
D’Souza, M. C. R., Motl, P. M., Tohline, J. E., & Frank, J. 2006, ApJ, 643, 381
Dehnen, W. 2000, ApJL, 536, L39
Dehnen, W. 2002, JCoPh, 179, 27
Dehnen, W. 2014, ComAC, 1, 1
Dehnen, W., & Read, J. I. 2011, EPJP, 126, 55
Dupuy, T. J., & Liu, M. C. 2012, ApJS, 201, 19
Fryxell, B., et al. 2000, ApJS, 131, 273
Greengard, L., & Rokhlin, V. 1997, JCoPh, 135, 280
Hernquist, L., & Katz, N. 1989, ApJS, 70, 419
Kilic, M., Brown, R. W., Heinke, C. O., et al. 2016, MNRAS, 460, 4176
Lorén-Aguilar, P., Isern, J., & García-Berro, E. 2010, MNRAS, 406, 2749
Marsh, T. R., Nelemans, G., & Steeghs, D. 2004, MNRAS, 350, 113
Motl, P. M., Tohline, J. E., & Frank, J. 2002, ApJS, 138, 121
Springel, V. 2005, MNRAS, 364, 1105
Stone, J. M., Gardiner, T. A., Teuben, P., Hawley, J. F., & Simon, J. B. 2008, ApJS, 178, 137
Vanaverbeke, S., Keppens, R., Poedts, S., & Boffin, H. 2009, CoPhC, 180, 1164
Warren, M. S., & Salmon, J. K. 1995, CoPhC, 87, 266
Yokota, R., & Barla, L. 2012, CSE, 14, 30