DIRECT N-BODY SIMULATIONS WITH A RECURSIVE CENTER OF MASS REDUCTION AND REGULARIZATION

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ABSTRACT. We report on an investigation of the core collapse of an initially bound system of 1024 point masses based on a new numerical method which incorporates a recursive center of mass reduction of the N-body system and includes regularization of the two body encounters. A tree which organizes the point masses into a logarithmic hierarchy is the primary feature of the numerical algorithm. The spatial structure of the tree allows for rapid force calculation while the associated temporal structure allows for variable time steps. Simulations are calculated for several core collapse times in an effort to follow the end point evolution of the system. The point-like nature of the interactions are maintained throughout the simulations.

1. INTRODUCTION

The dynamical evolution of star clusters has been studied by a variety of numerical methods including direct integration of the gravitational N-body equations for point-like masses. Direct methods provide realistic description of the system without any simplifying assumptions about the evolution. In contrast, the alternative methods of simulation including the fluid dynamical approach, the Fokker-Planck approximation, Monte Carlo models, and simple analytic models require certain approximations which fail for "small N" systems in which discreteness effects dominate. In particular, the nature of the end point evolution of an initially spherically symmetric system of N point-like masses is an important subject in stellar dynamics. Astrophysical systems such as open clusters (N = 1000) and Globular clusters (N = 1,000,000) are the principal motivation for the study of idealized point-like N-body models (see Lightman and Shapiro 1978). We present results of a numerical experiment in which a 1024 body system is evolved past core collapse utilizing a new method for the direct integration of the gravitational N-body equations. The results of this single experiment are compared to the results obtained by the alternative methods.

2. NUMERICAL METHOD

The new method for the direct numerical integration of the N-body equations is based on a coordinate transformation in which masses are grouped in clusters recursively and are thereby organized in a tree-like structure. Each node in the tree is associated with the center of mass and momentum of the members of that cluster. This analytic transformation generates a new set of N-body equations which describe the dynamics of the nodes of the tree instead of the

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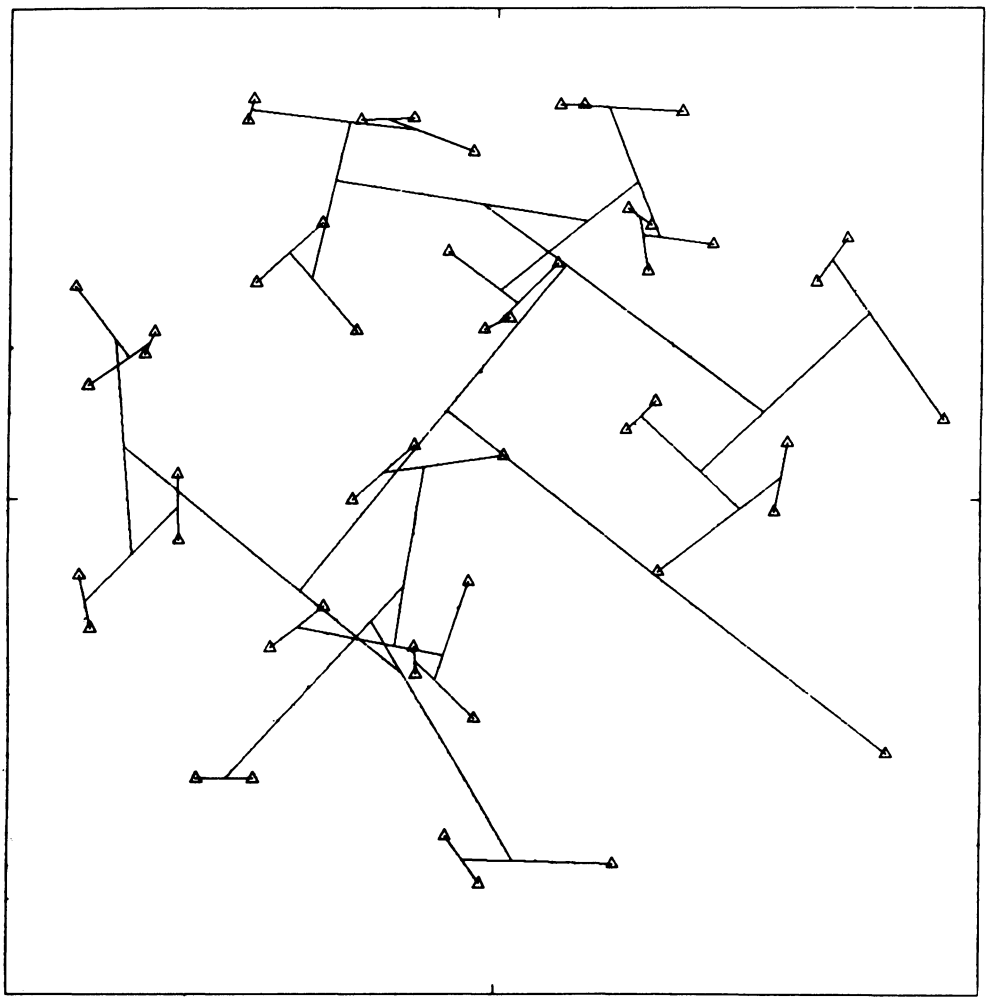

Figure 1. Two dimensional example of a tree generated by a recursive center of mass reduction. Triangles are mass points. Intersections of lines mark the center of mass of all mass points which are members of that node. The tree is arranged to match the clustering of the mass points.

particles. The system of equations is completely equivalent to the original N-body equations. Figure 1 illustrates the tree structure for a two dimensional example. Every possible tree generates a correct set of equations, but only those trees which are arranged to mimic the clustering of the particles lead to a numerically tractable scheme. The equation of each node of the tree is in the form of a perturbed two body problem, and therefore amenable to Kustaanheimo-Stiefel (KS) regularization (Kustaanheimo, 1964 and Stiefel, 1965). This leads to a numerical scheme which handles binaries in a natural manner. The properties of the integration scheme are summarized as follows; (1) rapid force calculation with tree structure, (2) rapid numerical integration with individual time steps for nodes, (3) regularization of all two body encounters, (4) accurate integration of "small N" subsystems such as binary binary collisions.

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Several numerical experiments have been calculated in order to test the veracity of the code. These include strongly interacting triple systems in which tens of close encounters and binary/single exchanges occur before ultimate disassociation of the system. Such resonant "small N" systems are the most difficult to integrate since the harmonic oscillator of the KS regularization for each node is strongly perturbed and therefore small time steps are required. Such interactions are rare and of short duration in "large N" systems.

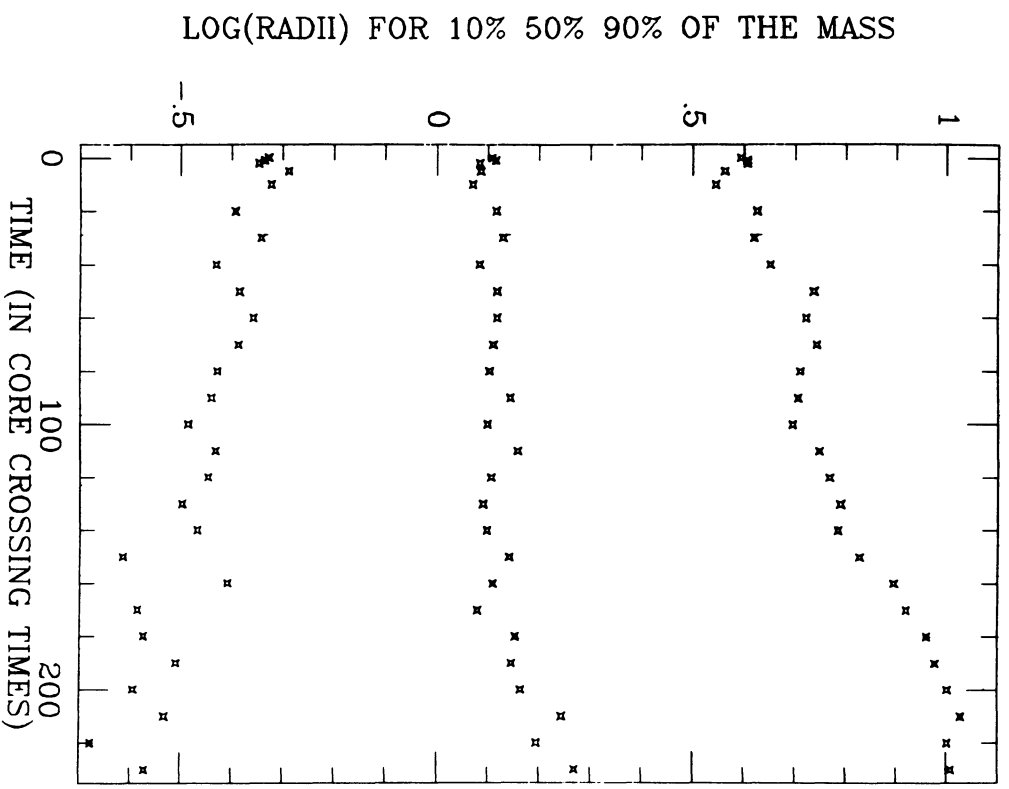

Figure 2. Display of the radii containing 10%, 50%, and 90% of the particles of an approximately spherically symmetric 250 body problem. The initial condition is a Plummer model.

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Also the code was tested for a sample "large N" problem which has been independently calculated with alternative methods. A Plummer model with 250 equal masses was simulated for several hundred crossing times and compared to previous experiments (Aarseth, Henon, Wielen 1974). The results shown in figure 2 are in excellent agreement with previous efforts and clearly show the expected core contraction, halo expansion, and formation of a hard binary during the late stages.

3. CORE COLLAPSE EXPERIMENT

A single numerical experiment with 1024 point-like masses was evolved for ~120 initial crossing times. The initial distribution was a two component Plummer model in which the heavy particles are three times the mass of the light particles and the ratio of the total mass in heavies to the total mass in lights is 0.3. The velocities and spatial coordinates of each component (931 lights and 93 heavies) are generated according to the algorithm in Aarseth, Henon, and Wielen (1974) for a single component Plummer model. The initial core radii and velocity dispersion are the same for the heavy and light components as expected just after violent relaxation. This configuration corresponds to the analytic model E of Lightman and Fall (1978) and was selected to facilitate a direct comparison. The mass equipartition parameter Γ as defined by Lightman and Fall is equal to 3.5 for the initial condition, therefore since $\Gamma > 1$ the system is unstable to mass segregation as would be expected for any realistic stellar system. The criterion for mass segregation instability as noted here is essentially the same as that derived by Spitzer (1969). The left panel of figure 3 is a display of the initial condition in projection. The region shown is ten Plummer radii across and clearly indicates the approximate spherical symmetry and central concentration. The numerical model is scaled such that in one unit of time a typical particle of the initial Plummer distribution will travel one Plummer core radius. The right panel of figure 3 is a display of the system after 100 units of time (initial crossing times). The linear scale is the same as for the left panel clearly indicating the increased central density of the system following core collapse.

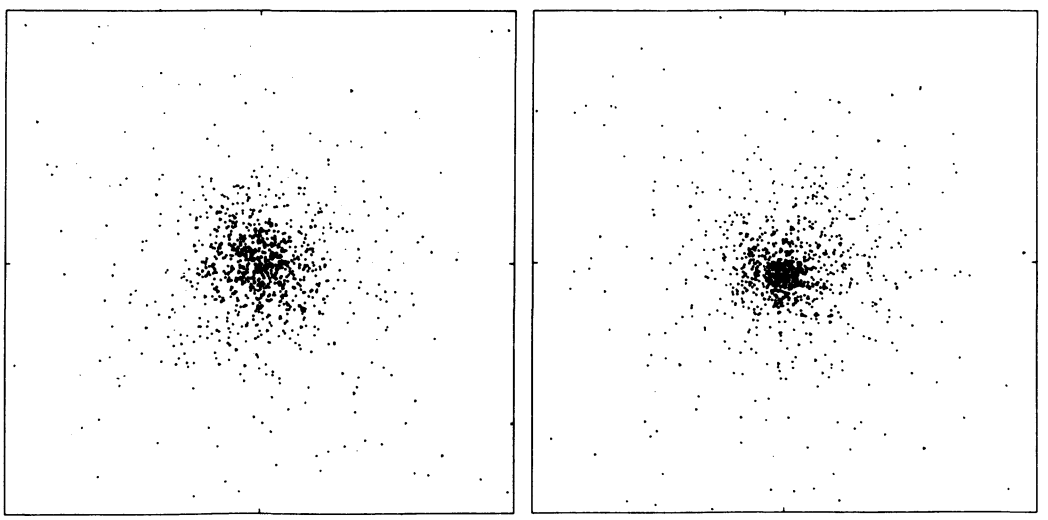

Figure 3. Two dimensional projection of a 1024 body Plummer model with two mass components: initial configuration (left panel) and after 100 initial crossing times (right panel). The linear scale across each panel is ten initial Plummer core radii.

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The evolution of the numerical system follows closely the stages of development of the model of Lightman and Fall (1978) outlined as follows. During the conductive regime the heavy particles transfer energy to the light particles and thereby cool with a subsequent decrease in central velocity dispersion and a decrease in core radius since approximate virial equilibrium is maintained. The process continues for about 30 crossing times when thermal equilibrium is reached between the heavy and light components. Even though the two components are strongly gravitationally interacting, the simple scheme of a slow approach to thermal equilibrium of two separate components each in virial equilibrium is accurate. During this period the evolution of the lighter component is slow since the relaxation time is much longer than for the heavy component. From 30 to 60 crossing times the heavy component evolves with a slowly contracting core nearly in thermal equilibrium with the lights. During this period the heavy component evaporates mass into an intermediate halo thereby decreasing the mass of the inner core composed predominately of heavies. Eventually the heavy component becomes sufficiently compact and therefore self gravitating that it undergoes core collapse with an associated increase in central velocity dispersion and a further decrease in core mass. This runaway core collapse is similar to single component core collapse (see figure 2) since the heavy component is now thermally decoupled from the light component. This last phase is rapid, occurring in less than ten initial crossing times and corresponds to the singular event which terminates the analytic model. In the numerical experiment this phase ends with the formation of a single dominate hard binary which halts and reverses the core contraction. Figure 4 tracks the evolving central density of the heavy component. Unfortunately there is no unique model independent indicator of

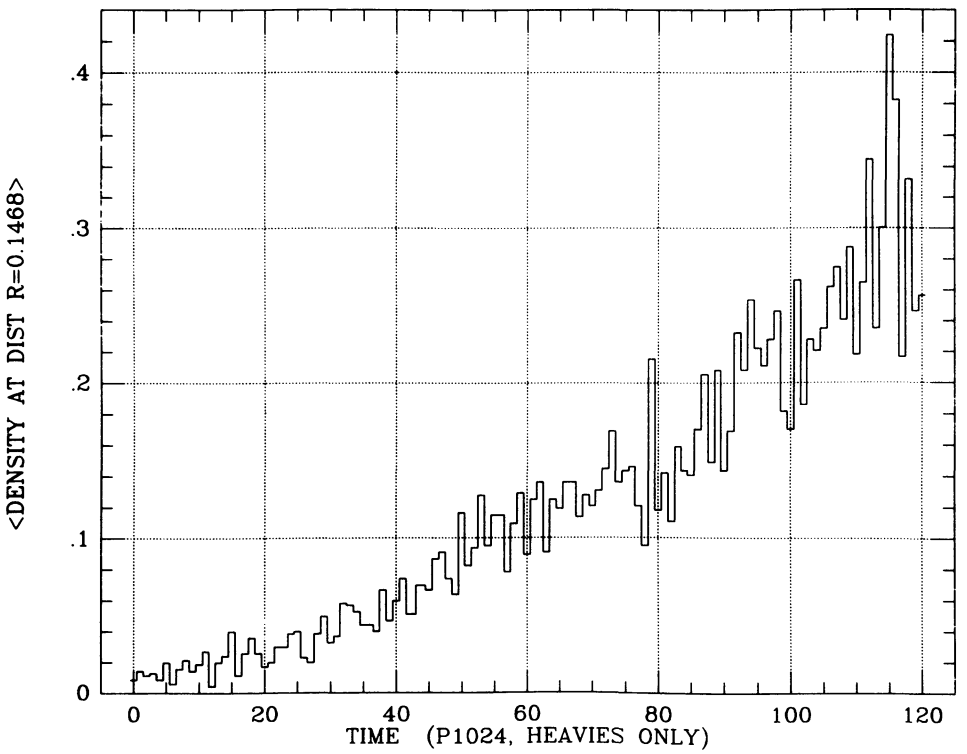

Figure 4. Central density of the heavy mass component as a function of time determined by counting all pairs of heavy point masses with separations less than ~.15.

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core collapse, but any function of the distribution which depends on the relative rather than absolute coordinates is numerically suitable. In figure 4 the central density is computed by counting all pairs of heavies with separations less than ~.15. Any other function of relative coordinates such as potential energy would be desirable, in contrast to model fitting a spherical profile with an assumed point of symmetry. Any core parameter is likely to be ill defined after the formation of hard binaries (after time 60 in this example).

The best indicator of the onset of core collapse is the formation of hard binaries which then dominate the immediate post-collapse phase. Figure 5 is a display of the binding energy of the hardest binary and the sum of the five hardest binaries. The endpoint core collapse is clearly indicated by the rapid growth in the hardness of one or perhaps two binaries. The process is highly stochastic since the identity of the dominate binary is not the same throughout the post collapse evolution. Episodes of hardening and softening of the binaries are correlated with rapid fluctuations of the velocity dispersion of a core of ~30 predominately heavy point masses.

The experiment required about one hour of CPU time per crossing time on a VAX11/780 with a floating point accelerator. Approximately half of the time is required for the post collapse phase. The clear advantage of a direct simulation is the possibility of investigating the post-collapse phase without the encumbrance of special assumptions.

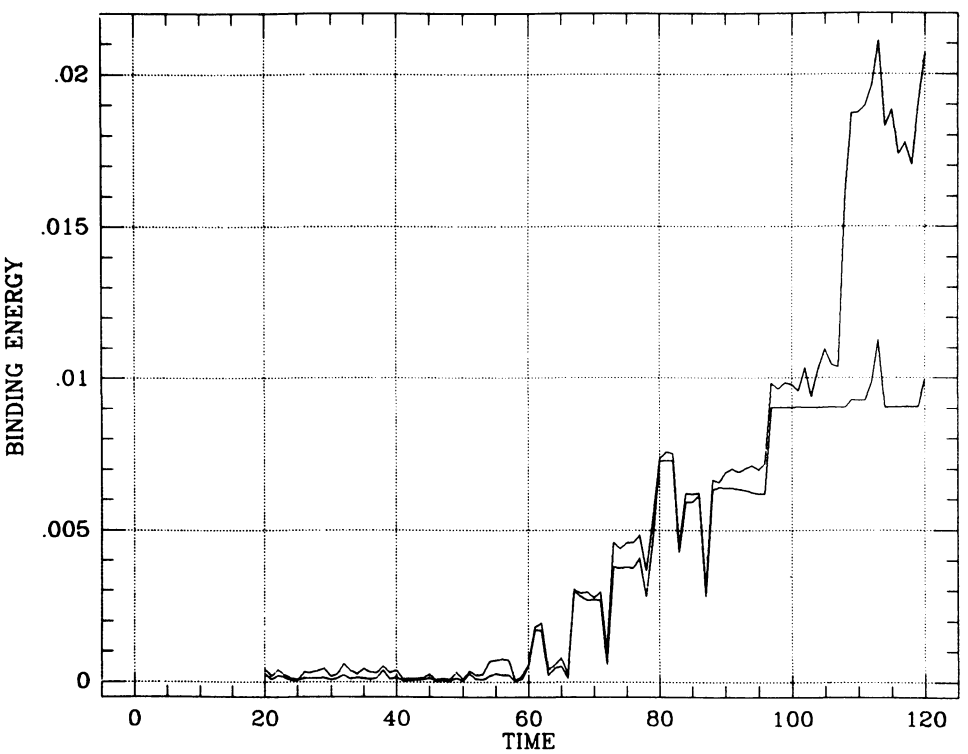

Figure 5. Binding energy of the most tightly bound binary and the sum of the five most tightly bound binaries as a function of time in units of initial crossing time.

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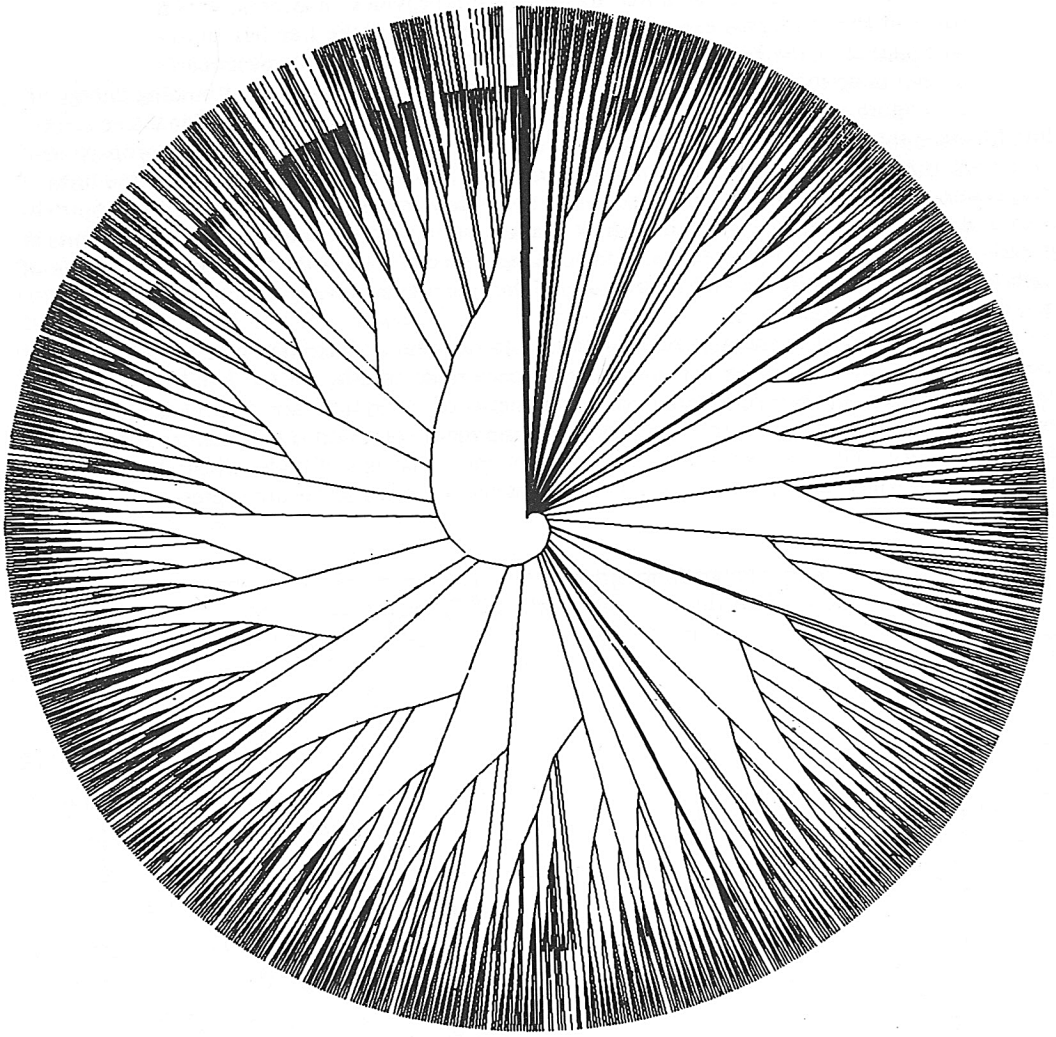

Figure 6. Unfolded display of the node tree for the 1024 body Plummer model after 100 initial crossing times. The radial position of a node is proportional to the logarithm of its mass with the center corresponding to the entire system and the outer perimeter corresponding to an individual light mass point. The order of the mass points on the outer rim is selected so that no interior lines cross. The angular position of a node or mass point indicates the radial position in the three dimensional system with the distant halo at the top right, the core at the top left, and with clockwise rotation corresponding to decreasing radial coordinate.

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The evolution of the recursive tree for the system provides an alternative description of the dynamics of the numerical experiment. Since each node of the tree has an associated dynamical equation of the KS regularized form, the system can be fully described by the properties of each node including the spatial displacement, relative velocity, and binding energy or frequency. Figure 6 is a two dimensional unfolded display of the three dimensional tree structure of the system after 100 initial crossing times. The radial position of a node is proportional to the logarithm of the mass of the node. The angular position is selected such that the lines connecting nodes to subnodes do not cross and nodes (and mass points) are organized approximately according to distance from the center of the system with the most distant components at the top right, clockwise for decreasing radial distance, reaching the core at top left. The state of each node combined with the global structure of the tree (figure 6) are a complete dynamical description of the system.

The advantage of the tree-like description of the system is illustrated in a scatter plot of the mass versus binding energy per unit mass for each node (see figure 7). Unlike a display of particle properties, all the major dynamical components of the system are clearly visible in the plot, including escapers, the formation of a two component core, and the existence of a single dominate binary. This representative scatter plot of the properties of nodes illustrates the natural way in which dynamical constructs of all spatial and mass scales are represented in the tree structure.

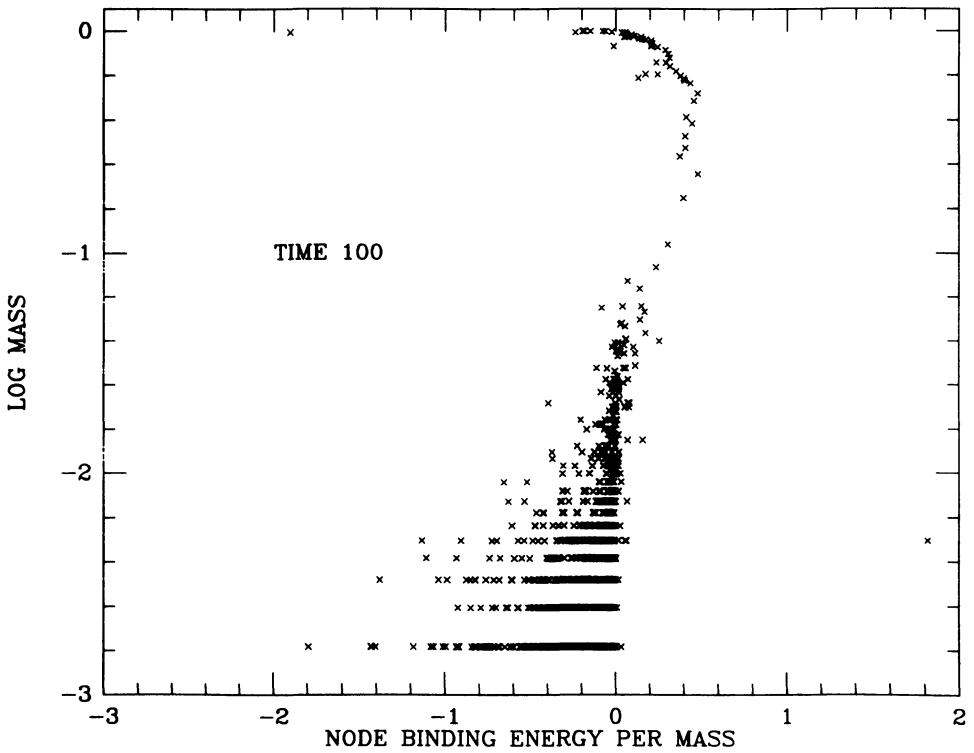

Figure 7. Scatter plot of node mass versus binding energy per unit mass after 100 crossing times. Positive (negative) binding energy corresponds to a bound (unbound) node. The most massive unbound nodes indicate escapers. The core of the system appears as the curved portion at the top of the diagram. The single dominate hard binary is in the lower right corner.

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3. SUMMARY

A recursive and regular transformation of the gravitational N-body equations is derived in the form of a hierarchical tree of nodes, each individually associated with a KS regularized two body equation or perturbed harmonic oscillator. This transformation provides both an efficient numerical method for the simulation of a large system and a new approach for diagnosing the nature of the dynamical evolution of the system under study. The specific numerical experiment, the core collapse of 1024 body point mass system is intended as a representative and idealized example of the methodology. Any direct N-body technique (also see Aarseth in this volume) has the advantage of assumption free simulation of the "small N" core of the late and post-collapse phases. The disadvantage of the direct approach is the limitation on the size of N that is practical. Alternative methods utilizing Fokker-Planck or Monte-Carlo techniques readily deal with the large N boundary associated with a small collapsing core. McMillan and Lightman (1984 and in this volume) have developed a "hybrid code" which combines the advantages of both types of methods. Clearly a variety of efficient hybrid are needed to fully explore the post-collapse evolution of large systems.

Acknowledgements

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DISCUSSION

GOODMAN: This is very clever and interesting work, but could you say something about what seems to be the hardest part of the calculation, namely how to choose the tree in the optimal manner? I should think that there are of the order of N! trees possible for N particles, and that the optimal tree for one particle pair would not be optimal for another pair.

JERNIGAN: First of all, every possible tree produces a new set of analytic equations which are correct. However, only a small fraction of the trees produce a set of numerically stable equations. One way to generate a numerically useful tree is to build the tree recursively by first connecting the closest two bodies in the system and then replacing the two bodies by a particle at their center of mass, thereby reducing a N body system to an N-1 body system. This process is recursed until the entire tree is built. This process can also be shown to require only NlogN steps, since one can also recursively add a new particle to a tree for N particles and produce a tree for N+1 particles. In the actual integrator the process is easier since one only modifies the tree at a previous step to generate the tree for the next step.

TERLEVICH: I run models of 1000 bodies (Aarseth regularized code) to compare them with open clusters (therefore they have included mass loss through stellar evolution, galactic tidal field, a power low mass function (α = 2.75)). I do not find signs of core collapse, which I attribute to the combined action of binaries and mass-loss (which occur frequently when the stars are binary components).

JERNIGAN: This is an interesting comment and indicates the large difference between open and globular clusters.

TOOMRE. Would you care to compare the speed or cost of using your algorithm, for instance on some 1000-body problem, versus whatever Aarseth's or anyone else's code would have yielded in the same circumstances?

JERNIGAN: My code requires $\sim$1 hour of VAX780 CPU time per crossing time for a 1000 body Plummer model. I have run problems for N up to 10,000 and see a $N^{1.3}$ dependence for the force calculation which is the dominant part of the computation. This is somewhat faster than the $N^{1.6}$ for the Ahmad-Cohen method that Aarseth uses. The $N^{1.3}$ dependence over the range N=100 to N=10,000 is consistent with NlogN dependence asymptotically. The particular 1000 body problem which Aarseth presented earlier today runs about 3 times slower than the problem that I have presented. However, it is not exactly the same problem, therefore a definite comparison is not possible. For large N, I would predict that my code would scale NlogN whereas the Ahmad-Cohen scheme would ultimately scale N^2. However, for any numerically realistic N the asymptotic behavior may not be relevant.