

A DYNAMICAL ORIGIN FOR EARLY MASS SEGREGATION IN YOUNG STAR CLUSTERS

STEPHEN L. W. McMILLAN AND ENRICO VESPERINI

Department of Physics, Drexel University, Philadelphia, PA; steve@physics.drexel.edu, vesperin@physics.drexel.edu

AND

SIMON F. PORTEGIES ZWART

Astronomical Institute “Anton Pannekoek” and Section Computational Science, University of Amsterdam, Kruislaan 403,
 Amsterdam, Netherlands; spz@science.uva.nl

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ABSTRACT

Some young star clusters show a degree of mass segregation that is inconsistent with the effects of standard two-body relaxation from an initially unsegregated system without substructure, in virial equilibrium, and it is unclear whether current cluster formation models can account for this degree of initial segregation in clusters of significant mass. In this Letter we demonstrate that mergers of small clumps that are initially mass segregated, or in which mass segregation can be produced by two-body relaxation before they merge, generically lead to larger systems that inherit the progenitor clumps’ segregation. We conclude that clusters formed in this way are naturally mass segregated, accounting for the anomalous observations and suggesting that this process of prompt mass segregation due to initial clumping should be taken into account in models of cluster formation and dynamics.

Subject headings: globular clusters: general — methods: n -body simulations —

open clusters and associations: general — stars: formation — stellar dynamics

Online material: color figures

1. INTRODUCTION

A population of massive stars of mass m_h embedded in a cluster of stars with mean mass $\langle m \rangle$ will sink toward the cluster center on a timescale $t_{\text{seg}} \sim (\langle m \rangle / m_h) t_r$, where t_r is the cluster half-mass relaxation timescale (Binney & Tremaine 1987, hereafter BT87). This well-known process of mass segregation is a consequence of energy equipartition, whereby two-body relaxation causes more massive stars to slow down, and hence move inward in the cluster potential. Strong observational evidence for this mechanism has been found in many old globular clusters (Sosin & King 1997; Pasquali et al. 2004), consistent with the fact that these systems have relaxation times significantly less than a Hubble time.

Interestingly, a number of studies also show significant mass segregation in clusters having actual ages, as measured by the evolutionary state of their stars, substantially less than the time needed to produce the observed segregation by standard two-body relaxation (Hillenbrand 1997; Hillenbrand & Hartmann 1998; Fischer et al. 1998; de Grijs et al. 2002; Sirianni et al. 2002; Gouliermis et al. 2004; Stolte et al. 2006). Numerical simulations indicate that dynamical evolution from initially unsegregated systems cannot account for the degree of mass segregation observed in these clusters (e.g., Bonnell & Davies 1998).

The obvious explanation is that these clusters were born mass segregated, and recent observational and theoretical studies do indeed suggest that massive stars form preferentially in the centers of star-forming regions (Elmegreen & Krakowski 2001; Klessen 2001; Bonnell et al. 2001; Stanke et al. 2006; Bonnell & Bate 2006). The mechanism invoked to explain this primordial mass segregation relies mainly on the higher accretion rate for stars in the centers of young clusters. However, the efficiency of this mechanism is still a matter of debate (Klein & McKee 2005; Bonnell & Bate 2006), and more generally, the processes of massive star formation and feedback remain poorly understood (Krumholz et al. 2005). Simulations of clus-

ter formation have so far been confined to systems containing less than $\sim 10^3 M_\odot$ in stars; it is not currently known how the above findings scale to larger clusters.

In this Letter we report initial results of a numerical study exploring dynamical routes to mass segregation during the early stages of cluster formation. We imagine that stars form in small clumps, which subsequently merge to form larger systems (Bonnell et al. 2003; Elmegreen 2006, and references therein). We assume that the clumps are significantly mass segregated at formation, or that they have short enough relaxation times that mass segregation can occur within the merger timescale. In either case, the final clusters inherit the segregation of their progenitor clumps, providing a natural explanation for the larger systems, which are mass segregated yet physically young.

2. METHOD AND INITIAL CONDITIONS

Our study is based on direct N -body simulations using the STARLAB¹ package (Portegies Zwart et al. 2001), accelerated by GRAPE-6 special-purpose hardware (Makino et al. 2003).

For all simulations presented here, we have adopted initial conditions in which the cluster consists of N_c clumps, with centers uniformly distributed within a sphere of radius R_{cluster} . The system of clumps is not in virial equilibrium, as the clump centers are initially at rest. Our simulations have $N_c = 2$ and 4, and explore the evolution of systems having two specific values of the “clumping ratio” $\mathcal{R}_c \equiv r_h / R_{\text{cluster}}$, where r_h is the half-mass radius of an individual clump. The two sets of runs have: (1) $\mathcal{R}_c = 0.037$, corresponding to clumps that are relatively close to one another (note that the 90% Lagrangian radius for a clump is $\sim 5r_h$); and (2) $\mathcal{R}_c = 0.013$, representing denser, more widely separated clumps. Hereafter, we refer to these choices as “moderately clumped” and “strongly clumped,” respectively.

¹ See <http://www.manybody.org>.

TABLE 1
INITIAL CONDITIONS OF ALL SIMULATIONS

N (1)	N_c (2)	Mass Segregation (3)	Clumping (4)	N_1/N_2 (5)	Figure(s) (6)
10,000	1	NOMS	...	18, 72	1
20,000	2	MS	Strong	18, 72	1
40,000	2	MS	Strong	18, 72	1
40,000	4	MS	Moderate	18	2, 3
			Strong	...	2, 3
40,000	4	NOMS	Moderate	18	3
			Strong	...	3, 4
40,000	4	NOMS	Strong	Kroupa MF	3
40,000	1	NOMS	...	18	4 (model S)

NOTES.—Columns list: (1) total number of particles in the run, (2) number of clumps, (3) whether or not the clumps are mass segregated, (4) degree of clumping, (5) ratio of light to heavy particles, and (6) the relevant figure(s) in the text.

Individual clumps are modeled as systems of $N = 10^4$ particles in virial equilibrium, with Plummer density profiles. We present here the results of simulations with clumps comprising just two components: N_1 light particles of mass m_1 and N_2 heavy particles of mass m_2 , with $m_2/m_1 = 20$. Our simulations have $N_1/N_2 = 18$, corresponding to $m_2/\langle m \rangle = 10$ and a heavy mass fraction of 53%, or $N_1/N_2 = 72$, with $m_2/\langle m \rangle \approx 16$ and a heavy mass fraction of 22%. While a two-component mass function is obviously not representative of the IMF of a real cluster, this simplification allows us to focus on the essential elements of mass segregation dynamics, in systems containing enough massive particles to produce statistically significant results. We note that the total mass in the massive component is unrealistically high in the former case, but it yields substantially better statistics and does not affect our overall conclusions.

Table 1 summarizes the two sets of simulations described in § 3. In the first (hereafter called the MS runs), we assume that the clumps are already mass segregated at the time of formation, targeting the preservation of initial mass segregation during the merging process. In the second set (the NOMS runs), the individual clumps are initially unsegregated, that is, both components are distributed with the same half-mass radius, but the clumps' relaxation times are short enough that mass segregation can occur before merger. The NOMS simulations explore the evolution of dynamical mass segregation before and during the merger.

Initial mass segregation in the MS runs is achieved by first letting a representative (NOMS) clump evolve in isolation for long enough for mass segregation to occur by normal two-body relaxation. We monitor the time evolution of the “segregation factor” $f_{\text{seg}} \equiv R_h/R_h(\text{heavy})$, where R_h and $R_h(\text{heavy})$ are the half-mass radii of the entire cluster and of the heavy component, respectively, and stop our calculation (after $\sim 5t_{\text{seg}}$) when f_{seg} reaches an approximate steady state (see Fig. 1). This mass-segregated system is then used as a template for all clumps in our simulations. We emphasize that this procedure is just a convenient means of generating a self-consistent system as an initial condition for an MS clump; our results are insensitive to the precise means by which the initial mass segregation comes about.

Throughout, our adopted time unit is the dynamical timescale (Heggie & Mathieu 1986) of one of the initial unsegregated clumps used to generate the initial models. Using the scalings from BT87 we find that, in these units, the clump relaxation timescale is $t_r \sim 0.1N/\ln N \sim 100$ (for $N = 10^4$); the free-fall time for the clump system is $t_{\text{ff}} \sim 0.7\mathcal{R}_c^{-3/2} \sim 90(450)$ for $\mathcal{R}_c = 0.037(0.013)$.

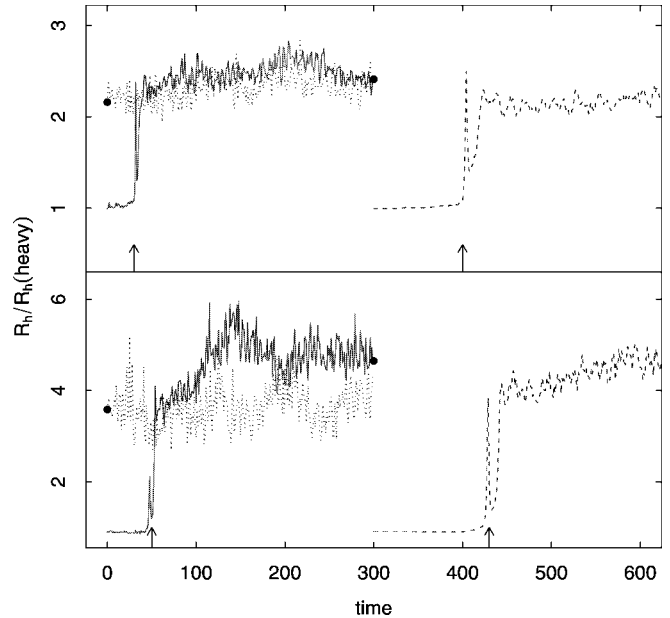


FIG. 1.—Time evolution of the segregation factor $f_{\text{seg}} = R_h/R_h(\text{heavy})$, measured relative to the system center of mass, for the hierarchical merger simulations described in § 3.1. The upper panel shows results for $N_1/N_2 = 18$, the lower panel for a smaller fraction of heavy particles ($N_1/N_2 = 72$). Dotted lines show the variation of f_{seg} for the initial clumps used in the merging simulations, when evolved in isolation. The dots at left represent the initial conditions for individual mass-segregated clumps. Solid lines show the time evolution of f_{seg} when two such clumps merge. Dashed lines refer to the second merger simulation, in which two copies of the first merger product are allowed to coalesce. The dot at the end of each solid line indicates the state of the clumps at the start of the second merger calculation. Vertical arrows mark the times when the mergers occur. [See the electronic edition of the *Journal* for a color version of this figure.]

3. RESULTS

3.1. Systems with Initial Mass Segregation (MS Runs)

The goal of the MS runs is to establish a connection between the mass segregation of the original clumps and that of the cluster resulting from the merger. Our first sets of simulations describe a “hierarchical” merger scenario, in which two identical, initially mass-segregated clumps are placed at a separation of 10 times their half-mass radius with zero relative velocity and allowed to merge. Subsequently, two copies of the merged system are again placed at a separation of 10 half-mass radii with zero relative velocity and merged. Figure 1 shows the time evolution of f_{seg} during these runs. The upper and lower panels in the figure correspond to different choices of the mass fraction of heavy stars: $N_1/N_2 = 18$ and 72, respectively. Both choices show qualitatively similar results. The effective merger time, defined as the time when the system is approaching dynamical equilibrium and has a single well-defined center, is marked by a vertical arrow. In each case, it is on the order of the free-fall time of the clump system.

In each panel in Figure 1, the first and second merger simulations are represented by solid and dashed lines, respectively. This figure suggests no mass segregation at the start of each merger because the individual clumps, while themselves segregated, are initially widely separated, and the Lagrangian radii are measured relative to the center of mass of the system. The dotted lines show the evolution of a single clump in isolation, indicating the value of f_{seg} before the merger and demonstrating that internal dynamics leads to negligible structural evolution within each clump on the merger timescale. In all cases, once

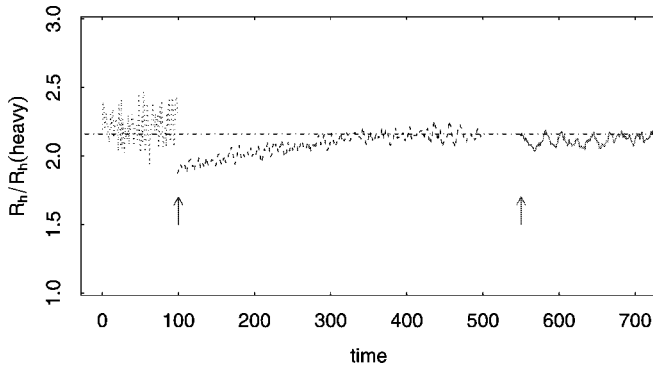


FIG. 2.—Time evolution of f_{seg} for simulations starting from four mass-segregated clumps (MS runs), for the two choices of the clumping ratio described in the text. Vertical arrows mark the effective end of the merging process (Fig. 3 shows the duration of the mergers more clearly). The factor of ~ 5 in merging times between the two sets of simulations reflects the scaling of the free-fall time presented in § 2. The dotted line at left shows a portion of the internal evolution of an isolated component clump (as in Fig. 1, upper panel), as an indicator of the state of the clumps before the merger occurs. The horizontal dot-dashed line shows the initial value of f_{seg} in the individual clumps. [See the electronic edition of the Journal for a color version of this figure.]

the merger is complete, the degree of mass segregation in the final cluster, as measured by f_{seg} , is approximately equal to that in the original clumps; mass segregation is preserved during the merging process. This is consistent with van Albada (1982) and Funato et al. (1992), who found that memory of particles' initial binding energy is not erased during violent relaxation.

Figure 2 presents the time evolution of f_{seg} for several MS simulations with $N_c = 4$. For clarity, we show the behavior of f_{seg} only after each merger is complete. In these more general cases too, the final cluster inherits the mass segregation of the component clumps. Note that, unlike f_{seg} , other bulk properties of the resultant cluster, e.g., central concentration and virial radius, do depend on the properties of the initial clumps, denser clumps tend to produce more concentrated final clusters.

3.2. Initially Unsegregated Systems (NOMS Runs)

To explore whether initial mass segregation is an essential ingredient in the scenario just described, we have repeated two of the $N_c = 4$ simulations presented in the previous section, but without initial mass segregation in the individual clumps. In these NOMS simulations, the segregation properties of the end products are controlled by the ratio $\tau = t_{\text{ff}}/t_{\text{seg}}$, representing the degree to which significant internal mass segregation can occur in a global free-fall time. For our choice of system parameters, with $t_{\text{seg}} \sim 0.1t_{\text{ff}}$, $\tau \sim 2$ for moderately clumped initial conditions, and $\tau \sim 10$ for the strongly clumped case, so significant mass segregation is expected within a merger time.

Figure 3 compares the time evolution of f_{seg} for these simulations with the corresponding MS simulations having the same initial distribution of clumps. It shows the detailed merger history of the original clumps, illustrating how mass segregation proceeds first within the clumps, then within each new merger product, culminating in the final merged cluster. In the moderately clumped case, some individual mergers occur quite rapidly, even before significant internal mass segregation has occurred. In the strongly clumped case, we clearly see internal mass segregation in the clumps before they merge. However, in both cases, the final values of f_{seg} are comparable to those found in the MS simulations.

As an additional point of comparison, the dot-dashed line in

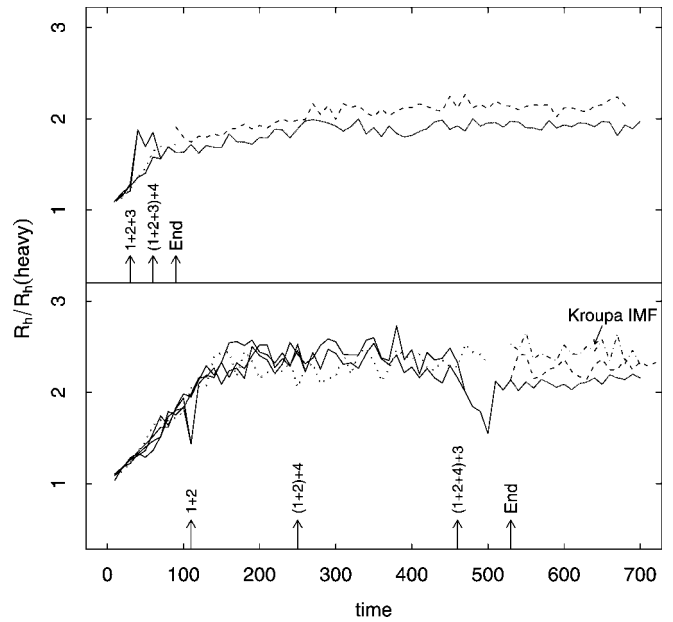


FIG. 3.—Time evolution of f_{seg} for simulations with initially mass-segregated clumps (MS runs; dashed lines), or starting with the same initial clump positions and velocities, but without initial mass segregation (NOMS runs; solid lines). The upper and lower panels show data for moderately and strongly clumped initial models, respectively. For clarity, only the final (postmerger) portions of the MS runs are shown. Vertical arrows mark various merging events between the clumps (arbitrarily numbered 1–4); the labels above each arrow indicate the clumps involved in the merger. The solid lines at each stage of the merging process show the evolution of f_{seg} for the remaining clumps in the cluster. The dotted lines show f_{seg} for an individual clump evolved in isolation. The dot-dashed line in the lower panel shows the results of a comparable NOMS simulation with a Kroupa initial mass function; in this case we plot the ratio of the half-mass radius of the whole system to the half-mass radius of stars having masses between 2.5 and $8 M_{\odot}$. [See the electronic edition of the Journal for a color version of this figure.]

Figure 3 shows the corresponding ratio for an additional simulation with the same overall parameters, but using a mass function from Kroupa et al. (1993), demonstrating that the effect persists when a realistic cluster mass distribution is used.

These simulations demonstrate an important alternative route leading to early mass segregation in young clusters, hinging on the multiscale nature of the system's early evolution: mass segregation is produced in individual small clumps and is preserved by the subsequent merging. For the MS runs, the merger time is the only timescale relevant to the process of forming a single large mass-segregated cluster, as the segregated cores merge rapidly once the clumps come into contact. However, because of the role of the additional parameter τ in the NOMS runs, the results of the NOMS and MS runs are expected to scale differently with increasing clump and/or cluster mass.

For the NOMS scenario to work, the clumps must have $\tau > 1$; for $t_{\text{ff}} \sim 1$ Myr, this implies $t_r \lesssim 10$ Myr. We note that 4 (out of 5) of the young embedded clusters listed by Baba et al. (2004) have relaxation times between 2 and 10 Myr, and the segregated clusters cited in § 1 have relaxation times ranging from ~ 6 Myr (Orion) to ~ 40 Myr (NGC 3603). The relaxation time in the final cluster is expected exceed that in a clump by a factor $\approx N_c^{1/2} (0.1/\mathcal{R}_c)^{3/2} = 8.9(43)$ for $N_c = 4$, $\mathcal{R}_c = 0.037(0.013)$. [The “ N ” in the relaxation time contributes a factor of N_c , the dynamical timescale contributes $(N_c/\mathcal{R}_c^3)^{-1/2}$, and the numerical factor 0.1 comes from an estimate of the relationship between the final half-mass radius and R_{cluster} , based on energy conservation and the virial theo-

rem.] We conclude that the above condition on t_r would be met for even a modest number of clumps or moderate clumping.

4. DYNAMICAL HISTORY OF A YOUNG SEGREGATED CLUSTER

The end products of the simulations described above are young, yet significantly mass segregated, clusters. Without knowing the actual dynamical history of such a system, one might imagine “observing” one of these simulated clusters to try to reproduce its properties and reconstruct its past dynamical evolution. The traditional way to do this is to perform N -body simulations starting from the initial conditions adopted in the vast majority of numerical studies of star cluster evolution, a spherical system with no primordial mass segregation and a Plummer (or King) density profile. We have carried out this experiment, running a simulation starting from a two-component spherical system in virial equilibrium, with 40,000 particles and a Plummer density profile. We refer to this simulation as model S.

Figure 4 (*left frame*) compares the time evolution of f_{seg} in model S with the strongly clumped NOMS run described in § 3.2. Model S is scaled so that, at the indicated times, when mass segregation is effectively complete and the degree of mass segregation is similar in each run, the two models have the same half-mass radius. We see that the clumped model achieves “complete” mass segregation much sooner (at least a factor of ~ 7 – 10 faster) than model S. Furthermore, as shown in the right frame, the density profiles at the indicated times are very similar. Since model S takes much longer than the NOMS system age to reproduce the same cluster properties, one might incorrectly conclude from this numerical study that the mass segregation found in this cluster must reflect its initial conditions. However, as we have shown, several possible dynamical histories can lead to similar final systems.

5. CONCLUSIONS

We have presented the results of simulations following the early evolution of star clusters, exploring the origin of mass segregation observed in young clusters. Our simulations started from clumpy initial conditions with and without initial mass segregation in the individual clumps, and studied the properties of the resulting merged cluster. Our main conclusions are:

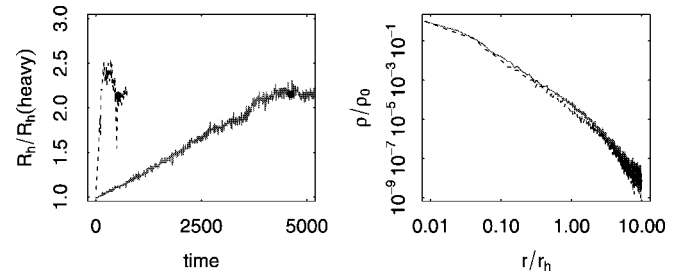


FIG. 4.—*Left:* Time evolution of f_{seg} for the two simulations discussed in § 4. The left (*dashed*) curve began from strongly clumped NOMS initial conditions with $N_c = 4$ (see the lower panel of Fig. 3); the right (*solid*) curve from a single unsegregated Plummer profile. *Right:* The density profiles of the two runs at the indicated points are almost indistinguishable. [See the electronic edition of the Journal for a color version of this figure.]

1. For clumps with initial mass segregation, the degree of mass segregation in each clump is largely preserved during the merging process.

2. For clumps without initial mass segregation, the clumps may become dynamically mass segregated before merging if their initial relaxation times are sufficiently short. If so, this mass segregation too is inherited by the resulting merged cluster.

3. For clumped initial conditions, with or without initial mass segregation, the end products of our simulations are young clusters, whose properties are inconsistent with an initially unsegregated equilibrium cluster model. Clumped and unclumped initial conditions lead to similar segregated density profiles, but the clumped systems do so much more rapidly than do the unclumped ones.

Our simulations demonstrate that there are a number of viable evolutionary paths, relying on initial mass segregation in clumpy systems or on multiscale dynamical evolution, that can lead to significant mass segregation in a physically young cluster. A systematic survey of the full parameter space of the problem is now underway.

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