The Great Collapse

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CHAPTER 3 Rapid Mass Segregation in Collapsing Clusters

We introduce a new method to measure and quantify mass segregation which we then use to explore the mechanism driving rapid mass segregation. The method is based on measuring how statistically likely n number of high mass particles are expected to be closer to one another than a random set of n particles drawn from the same system. This method, which we call the nearest neighbor method, is shown to provide similar results for simple star systems, a better measure of mass segregation in complex systems, while providing a significant speedup over the previous, minimum spanning tree, method.

We apply our new method to measure the mass segregation in simulations of cold, collapsing star clusters. Two, dynamical, hypotheses have been put forward to explain the mechanism causing the rapid mass segregation in collapsing clusters; we have designed and implemented an experiment to distinguish between. We find that the rapid mass segregation of star clusters is primarily driven by the very high density of the cluster toward the end of the collapse and is not the result of multiple sub-clusters forming and mass segregating during the collapse.

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In Preperation

3.1 Introduction

Mass segregation describes the phenomenon wherein a given system massive astronomical objects are statistically more likely to be found near other massive objects than objects of arbitrary mass. This will be the working definition of mass segregation throughout this paper.

Several mechanisms, e.g. dynamical friction (Chandrasekhar 1943), can account for mass segregation in general, understanding the mass segregation observed specifically in young star clusters, i.e. in the Trapezium of Orion, places a time constraint on the mechanism. Because these clusters are young the mass segregation must happen much faster than expected or the system must have formed in such a way that the most massive stars were born close together, so called premodial mass segregation. Determining the mechanism for such rapid mass segregation could have significant implications for where in a cluster stars form, which additionally could provide an indication on the formation mechanism of massive stars.

Bonnell and Davies (1998) suggested that a dynamical mechanism could not satisfy the time constraint of rapid mass segregation. However, Allison et al. (2009a) found that for clusters which were initially subvirial and initially had substructure dynamical mass segregation can satisfy the time constraint from young clusters. Olczak et al. (2011) and Caputo et al. (2014) showed that even subvirial cluster without initial substructure (distributed in a homogeneous sphere in the latter case) could produce mass segregation on a very short time scale as well, suggesting that the initial virial temperature may be the more relevant metric for rapid mass segregation driven by dynamics.

Allison et al. (2009a) suggested that subvirial collapsing clusters mass segregate more quickly than might be expected due to the dense core formed as a result of the collapse (see Caputo et al. 2014, for a detailed study of the effect of the virial temperature on collapsing clusters). McMillan et al. (2012) claimed that this rapid mass segregation happens not around the time of the "high density bounce", but rather during the entire collapse. Using the simulation data from Caputo et al. (2014) with nearly 500 simulations of collapsing systems we investigate the phenomenon of rapid mass segregation.

3.2 Method

In order to examine the effect of mass segregation on collapsing star cluster we must consider how to measure the degree of mass segregation. Allison et al. (2009b) presented a method for measuring mass segregation by using a minimum spanning tree. The minimum spanning tree (MST) is a method to connect a number of points, or vertices, in a space by the shortest path without any

loops. The MST determines the length of this path. (We used Kruskal's method (Kruskal 1956) when reimplementing their method.) Earlier methods tended to be dependent on models of the density profile or mass function and on the number of mass bins among other parameters (see Gouliermis et al. 2004). Additionally, these methods assumed the mass segregation would be found in and around the cluster's center, the definition of which was not always clear.

3.2.1 Minimum Spanning Tree Method

To determine the mass segregation the n number of most massive particles are selected and the MST length of those particles is found, $\ell_{massive}$. Next, n number of particles are selected at random from the cluster and the MST length for these particles is found, ℓ_{random}. This step of finding the MST length for random sets is repeated some number of times, Allison et al. (2009b) suggest that 50 times is adequate but that hundreds produce smoother trends. They then find the average of the MST length for all of the random sets and determine the ratio of these two lengths:

$$\Lambda_{MST} = \frac{\langle \ell_{random} \rangle}{\ell_{massive}} \pm \frac{\sigma_{random}}{\ell_{massive}}. \tag{3.1}$$

Where σ_{random} is the standard deviation of the measurements of the randomly selected sets. If Λ_{MST} is around 1 it suggests that the separation between the n most massive particles is similar to the separation between the particles in the system in general, i.e. there is no mass segregation. If Λ_{MST} is significantly > 1 it suggest that separation between the n most massive particles is much smaller than the separation between the particles in the system in general, i.e. the system is mass segregated. Finally, if Λ_{MST} is significantly < 1 it suggest that separation between the n most massive particles is much larger than the separation between the particles in the system in general, i.e. inverse mass segregation.

3.2.2 Nearest Neighbor Method

We have developed a new method which we have dubbed the Nearest Neighbor (NN) method. The method is similar to the MST method in that it calculates a length for the n most massive particles and then the length is measured again for some number of randomly selected groups each with n particles as well. The difference is that in place of calculating the minimum spanning tree we calculate the average distance to the nearest neighbor for each set. Other than the distance measurement the remainder of the algorithm is the same, Λ_{NN} is calculated just as it was for Λ_{MST}:

$$\Lambda_{NN} = \frac{\langle \ell_{random} \rangle}{\ell_{massive}} \pm \frac{\sigma_{random}}{\ell_{massive}}, \tag{3.2}$$

and the interpretation of the results is the same as well.

As we will show, the advantages of the NN method over the MST method include better detection of mass segregation in clusters with complex structure as well as a dramatic reduction in computation time.

3.3 Comparing Results

3.3.1 Measurements of the Mass Segregation

Simple Mass Distribution

In order to compare the MST method to the NN method we have constructed an artificial data set of a star cluster; the cluster is constructed such that there are 16K (i.e. 2^{14}) particles arranged in a plummer sphere with a Salpeter mass function (Salpeter 1955), with masses from 1 to 50 $M_{\odot}$, which are assigned randomly to the particles in the cluster. The inner 160 particles ($\approx$ 1 per cent of the cluster) are then reassigned masses based on a Salpeter mass function with masses from 50 to 100 $M_{\odot}$. This produces a cluster in which the 160 most massive particles are mass segregated, in a core, from the remainder of the cluster, however there should be no significant mass segregation outside of the core.

In Figure 3.1 we plot the mass segregation ratio for the artificial cluster described above out to the 200 most massive particles. The red line is produced by the NN method (this paper), whereas the blue line is produced by the MST method, in both cases 50 random sets were used in order to calculate $\langle \ell_{random} \rangle$. The two methods give nearly identical results. The region shaded in red is the $\pm 1\sigma$ level of error from the NN method, we chose not to show the error from the MST method because the two of them were so similar that showing both resulted in confusion in the plot. The horizontal, solid green line indicated a mass segregation ratio of 1, i.e. no mass segregation, and the vertical, dotted green line is placed at 160 particles, the number of mass segregated particles (by construction).

Both methods indicate the presence of mass segregation of the 160 most massive particles.

Using the NN method we plot, in Figure 3.2, the mass segregation ratio for the artificial data set described above; each line represents the data from using a different number of random sets, from 1 to 100, to calculate $\langle \ell_{random} \rangle$. We plot the data for sets from 1 to 100, though we only show every other value in the legend so as to make it (nearly) readable. Using the NN method we are able to do this out to 512 particles due to its increased speed, however after several months the MST version of the same plot is not finished running.

Figure 3.2 demonstrates how using more random sets reduces the noise in

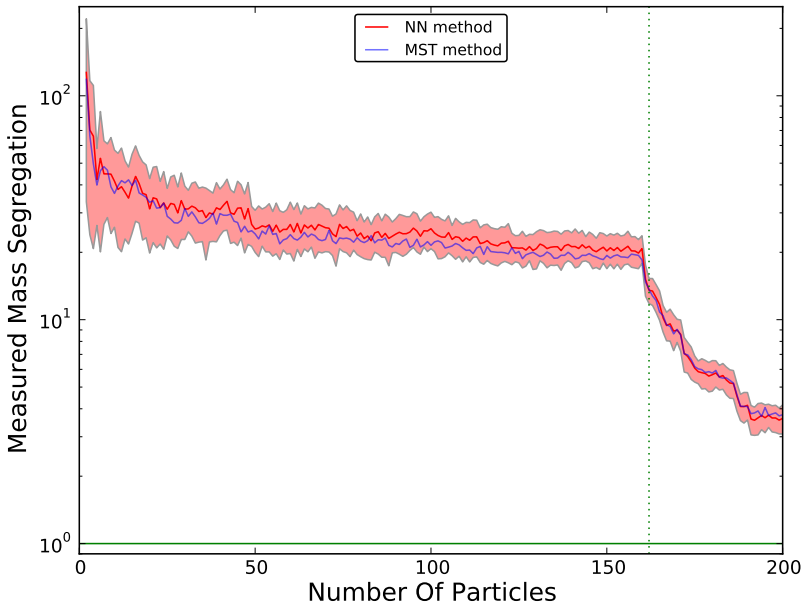


Figure 3.1: Results from the NN (red line) and MST (blue line) methods on an artificial data set in which the 160 most massive particles are mass segregated in the center of the system, see text for more details. The red shaded area represents the ± 1 σ error level of the NN method. The horizontal, solid green line indicates a mass segregation ratio of 1, i.e. no mass segregation; the vertical, dotted green line indicates 160 particles, the number of particles which are mass segregated in the data set.

the measurement, of course this comes at the expense of more computing time needed. Also note how the values for the mass segregation drop off after the 160^{th} particle, after which there is no mass segregation. The value decays to around 2 for 512. This decay, instead of a fast drop, is the result of the first 160 most massive particles having an effect on the mass segregation ratio of the remainder of the particles; for example, when calculating the mass segregation ratio for the first 161^{st} particles the result is dominated by the first 160, mass segregated, particles, and at the 320^{th} particle the first half of the particles are mass segregated so the mass segregation ratio will show values greater than 1 even though there is no mass segregation at that value. For this reason it is important that these methods be used with a regular interval of particles, calculating the mass segregation ratio out to only one particle value, i.e. only calculating the mass segregation ratio for the first X-number of particles while not doing so for the particles before it may result in results which cannot be interperted correctly.

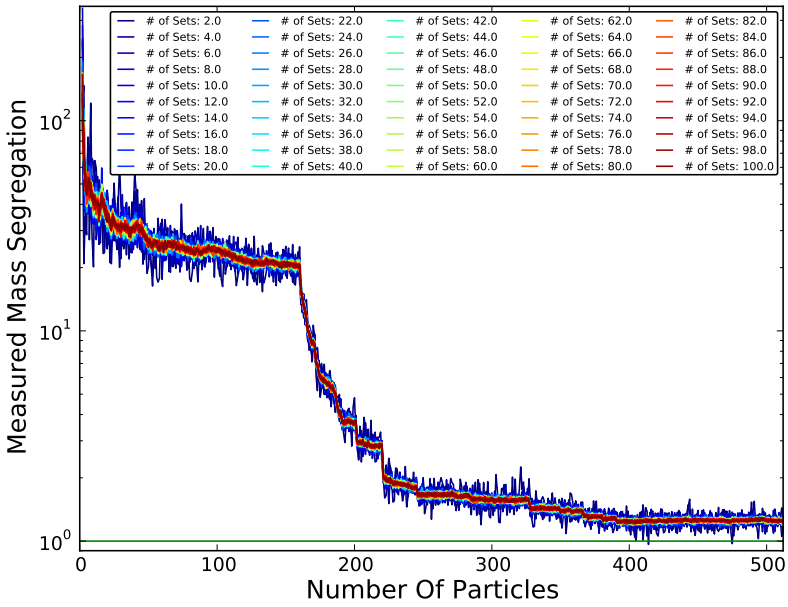


Figure 3.2: The mass segregation ratio, using the NN method, out to 512 particles for the same data as in Figure 3.1. Calculated with different number of random sets, up to 100, as indicated in the legend. For the sake of readability only the even number of sets are labeled in the legend, however all number of sets, from 1 to 100 are plotted.

What is the benefit then of this new method if the results are essentially the same?

Complex Mass Distribution

We produced another artificial system to test the difference between the NN and MST methods. For this test case we created a system just as we did above with all of the most massive particles located in the center, but this time with the nine separate cluster each with $^1/_9{}^{th}$ the number of particles (both massive and non-massive). We then place all nine identical, mass segregated systems into a single volume. Of the nine systems one is placed in the center and the remaining eight are placed equally around a sphere such that the radius of each system does not overlap with the radius of any other systems.

Each subsystem has 1,820 particles with 18 massive particles in their center, resulting in a total of 16,380 particles and 162 massive particles. Figure 3.3 is a plot of the mass segregation measure of this system out to the 200 most massive particles using 50 random sets to calculate ℓ_{random}. The solid red line

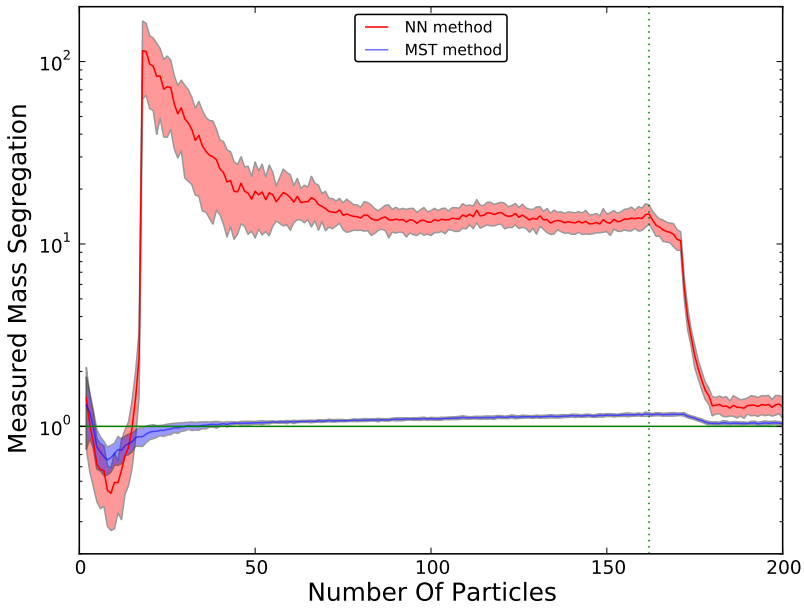


Figure 3.3: Results from the NN (red line) and MST (blue line) methods on an artificial data set in which the 162 most massive particles are mass segregated in the center of nine sub-clusters arranged in a non-overlapping way, see text for more details. The red and blue shaded area represents the ± 1 σ error level of the NN and MST methods respectively. The horizontal, solid green line indicates a mass segregation ratio of 1, i.e. no mass segregation; the vertical, dotted green line indicates 162 particles, the number of particles which are mass segregated in the data set.

is the measurement from the NN method, with a $\pm 1\sigma$ error shown by the red shaded area; the blue line is the measurement from the MST method, a $\pm 1\sigma$ error is shown by the blue shaded area. The solid, horizontal green line is plotted at 1.0, i.e. no measured mass segregation, and the vertical dashed line marks the 162 most massive particle, i.e. the end of the designed mass segregation.

The system is mass segregated, but in small sub-clusters. For the first nine most massive particles (the single most massive particle from each of the sub-clusters) both the NN and MST method show inverted mass segregation, the most massive particles are more separated from each other than randomly selected particles are seperated. This is because the length of the NN and length of the MST for the nine most massive particles is measuring the separation between the sub-clusters, but when measuring the respective length for the random sets of particles if any two particles are selected from the same sub-clump then the length for the random set will be significantly shorter than the length

for the most massive particles. However, after the ninth most massive particles the two methods diverge in their respective measurement of the mass segregation. The MST method remains, and always will remain, dominated by the separation between the sub-clusters, whereas with the NN method the measured length for the most massive particles is a measure of the distance between those particles and not the sub-clusters.

The MST method is unable to identify mass segregated sub-clusters that are spread over the total system volume, but the NN method can make good measurements of simple systems while also adjusting to more complex systems. While not fool-proof, there are cases that both the NN and MST methods would be poor at accurately measuring mass segregation, we have shown that the NN method is more graceful at adapting to different mass distributions.

More importantly, we have shown that the NN method is able to measure mass segregation of sub-clusters, a required step if we are to distinguish between the two proposed mechanisms of dynamical rapid mass segregation.

But wait there is more, the NN method is also much faster.

3.3.2 Speed

The MST method was a considerable improvement over previous methods which either did not quantify the degree of mass segregation and/or were model dependent. However, to quantify mass segregation using this method when provided with an unknown system one must preform the method on a regular interval for every number of most massive particles up to the final degree of mass segregation one desires to test. That is, if one wished to know if a given a system of 10^4 particles was 10 per cent mass segregated the method would have to preformed 1000 times; constructing the MST for the 2 most massive particles, then 3, 4, . . . , 1000 particles, each time constructing 50 other MSTs for the random sets.

The MST method has a runtime complexity of $O(E\log E)$ where E is the number of edges, i.e. the number of connections between points. Since we assume all points can connect to all other points we have a complete graph which has $n(n-1)/2$ edges. So to highest order the complexity is $O(n^2\log(n^2))$. However, before we calculate the MST length we must also calculate the length of all the edges which has a complexity of $O(n^2)$; so in total our expected runtime complexity is $O(n^2 + n^2\log(n^2))$.

The Nearest Neighbor Method requires the calculation of all of the distances between all particles, the exact same calculation as determining the length of all the edges, which has a runtime complexity of $O(n^2)$[1]. This means the

[1]This is for the naive implementation, using a more sophisticated approach, such as a k-d tree has a complexity of $O(\log(n)[n+1])$.

Nearest Neighbor method should be roughly $2\log(n)+1$ times faster than the MST method for each iteration.

In the case we want to know the the mass segregation out to 10 per cent of a cluster with 10^4 particles the NN method would be faster by a factor of $\sum_{2}^{1000} 2\log(n)+1$, which is a whopping 6,100 times faster than the MST method. In Figure 3.4 we plot the number of particles, n, used for the NN and MST method versus the time it takes for each iteration, the solid lines, and the cumulative time, the dashed lines. The red lines are for the NN method and the blue lines for the MST method. We show that for $n > 11$ particles the total cumulative time for the NN method is shorter than the time needed for a *single step* with the MST method. Moreover, the cumulative time using the MST method for $n = 200$ particles is a factor 1000 times longer than the NN method. The savings in runtime we obtain from the NN method over the MST method is so large it allows us to explore portions of the parameter space that were not avalible before; e.g. in trying to run the simulations to produce Figure 3.2 the NN method took ≈ 8 hours (iterating from 2 to 512 particles and from 1 to 100 random sets), at the time of writing the MST method had been running for *3 months* and at that point was only to particle 344.

However, Figure 3.2 is a very artificial examination of the method rather than a useful science tool. Where this speedup becomes needed is to do science when the number of particles in a system is very large. Allison et al. (2009b) tested their method on systems on 1000-body clusters, measuring the mass segregation ratio of up to 10 per cent of the cluster size (i.e. up to 100 particles). The MST method works well enough at those numbers, but simulations are becoming ever larger (even simulations with $N = 10^{10}$ are becoming possible see e.g. Bédorf et al. (2014), though Portegies Zwart and Boekholt (2014) provides an interesting counter-example). Testing mass segregation for up to 10 per cent of systems with $N = 10^4$ become very tedious with the MST method and simply unobtainable for $N = 10^5$.

We find that for the NN method using 50 random sets the cumulative time, in seconds, grows as power law with the form $\approx 0.03n^{1.23}$ (see the red dotted line in Figure 3.4); whereas, the cumulative time for the MST method, again using 50 random sets, grows as $\approx 0.001n^{3.1}$ (see the blue dotted line in Figure 3.4). Assuming these holds for very large values it implies that calculating the mass segregation for 10 per cent of a 10^6-body system, that is calculating the mass segregation out to 10^5 particles, would take about 12 hours with our NN method, and much longer than a career time for the MST method. The NN method makes exploring mass segregation much more practical for nearly any size system, and obtainable even for large systems.

The NN method will always have a speedup over the MST method which is not something that can be compensated for by improving the MST algrithum

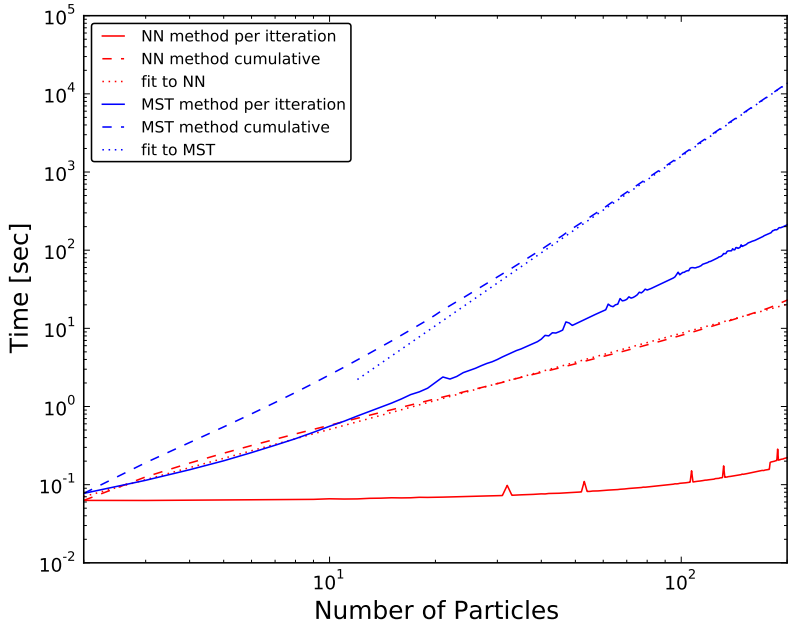


Figure 3.4: The solid lines show the per iteration time in seconds, the dashed lines show the cumulative time, and the dotted lines show the fit to the cumulative time. The red lines are for the NN method (this paper) and the blue lines are for the MST method. The fit to the NN method (red, dotted line) is of the form $0.03\ n^{1.23}$ and is in good agreement with the cumulative time for the NN method. The fit to the MST method (blue, dotted line) is of the form $0.001\ n^{3.1}$ and is in good agreement with the cumulative time for the MST method after $n \approx 30$. We used 50 sets of data to calculate $\langle \ell_{random} \rangle$.

or moving the two methods to other archatectures, e.g. graphics processing units, because the NN method is a required part of the MST method. While preforming the MST method one must find all of the

3.4 Results and Discussion

3.4.1 Simulation Methods

We have simulated systems with 15,210 particles initially spatially distributed in a homogeneous sphere. The masses of the particles are drawn from a Salpeter mass function in N-body units with a physical equivalent of 0.3 to 100 $M_{\odot}$. The systems examined below, unless otherwise noted, are produced cold, i.e. with a virial fraction of 0.0. They are then simulated for 10 N-body times in the AMUSE environment (Pelupessy et al. 2013) using the fourth-order Hermite

code ph4 (McMillan in prep.). For more details about the simulation setup see Section 2 in Caputo et al. (2014).

In analyzing the mass segregation of the simulations we primarily make use of the NN method outlined above. To calculate the density of the cluster core we use the code hop (Eisenstein and Hut 1998) with 50 nearest neighbors.

3.4.2 Mass Segregation

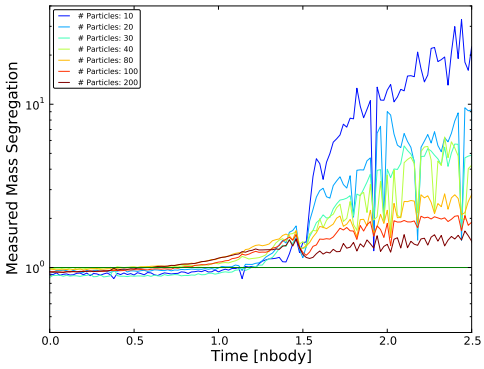
McMillan et al. (2012) suggested that rapid mass segregation happens as a result of a collapsing system forming sub-cluster which due to their small size mass segregate on their, fast, dynamical timescale; whereas, Allison et al. (2009a) had proposed rapid mass segregations is due to the short-lived, but very dense state that happens as the cluster's collapse reaches a maximum. In order to distinguish between these two scenarios, or uncover a different mechanism, we have designed an experiment to disentangle these cases.

The experiment works in the following way: first, we run a simulation of a collapsing cluster and plot the mass segregation ratio as a function of time. Second, we take a snapshots from that simulation at 0.9, 1.25, 1.5, 1.75, and 2.1 N-body time units (or Henon time units Heggie and Mathieu 1986) and randomly swap the masses (it is important to note that we do not produce new or different masses, we simply rearrange the masses). Finally, we continue running the simulations from that point with the swapped masses, and when each one finishes we again measure the mass segregation ratio as a function of time for the new simulation.

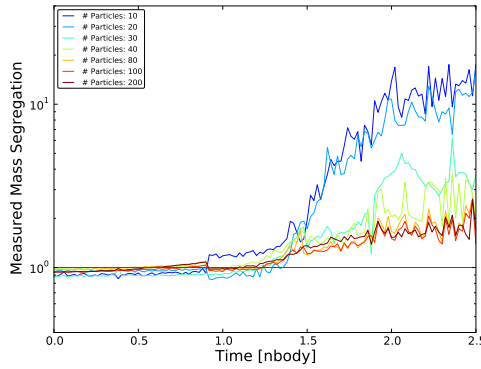
By swapping the masses we are able to remove all of the effect of dynamical mass segregation up to that point and determine what amount of dynamical mass segregation is effecting the cluster after that point. We have plotted the results of this experiment in Figure 3.5.

In Figure 3.5a we plot the "natural" evolution of the cluster, with no mass swapping going on. The horizontal green line, which is common to all six subfigures, is plot at a mass segregation ratio of 1, which is exactly non-segregated. The other lines mark the mass segregation ratio for different number of particles, n, from 3 to 193 particles in steps of 10, as shown in the legend.

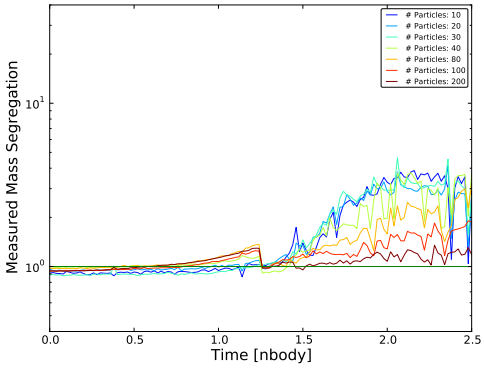
We note that the mass segregation is highest for the fewest number of particles; this is expected since when we measure the mass segregation for 3 particles it is the the 3 most massive particles and for 13 it is the 13 most massive, so it follows that the most massive particles would be the most mass segregated. Caputo et al. (2014) examined these type of collapsing clusters in detail and found that at for an initially cold system, such as in this case, the deepest moment of collapse, the moment with the highest density, happens at 1.46 N-body times, which is visible with a local peak in the mass segregation at the same time in Figure 3.5. Also note the gradual rise in the mass segregation



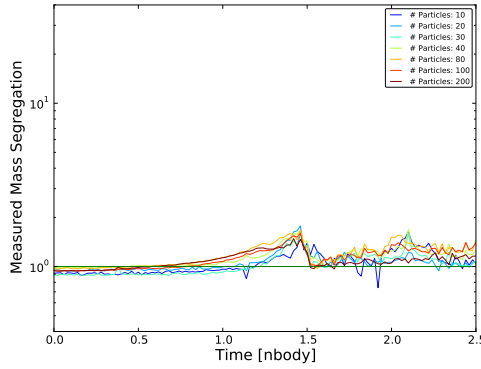
(a) No masses switched.



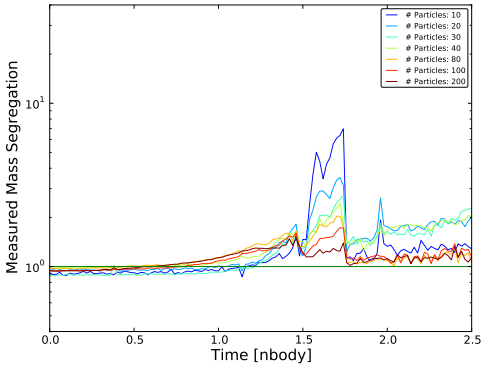
(b) Masses randomly switched at 0.9 N-body times.



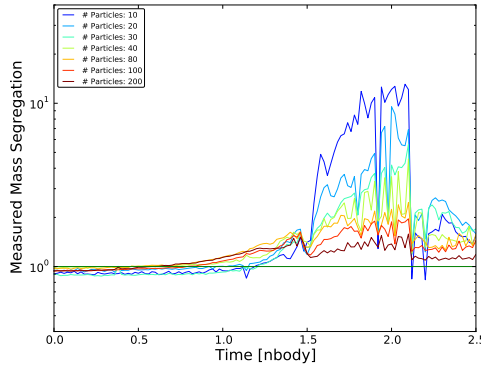
(c) Masses randomly switched at 1.25 N-body times.



(d) Masses randomly switched at 1.5 N-body times.



(e) Masses randomly switched at 1.75 N-body times.



(f) Masses randomly switched at 2.1 N-body times.

Figure 3.5: Mass segregation as a function of time for different number of particles as show in the legend. (a) shows the evolution of the mass segregation as it would normally occur, i.e. without switching mass. (b)–(f) show the evolution of the mass segregation with the masses being randomly switch at 0.9, 1.25, 1.5, 1.75, and 2.1 N-body times, respectively.

starting around 0.6 N-body times for most particle sets. This rise maybe the result of sub-clusters forming and then mass segregating or it maybe the result of an increase in density as the density of the whole cluster increases. Finally, we note that with the exception of the set of three particles the none of the other sets even rise to a mass segregation ratio of two before or during the collapse.

Figures 3.5b–3.5f show the simulations where we have randomly swapped the masses at different times: 0.9, 1.25, 1.5, 1.75, and 2.10 N-body times respectively. In Figure 3.5d we swap the masses just as the cluster is at the deepest part of its collapse; and the other plots are spaced at 0.25 and 0.6 N-body times before and after that time. The swap can be seen in each plot by the sudden drop in the mass segregation ratio at the designated time.

Peculiarly the mass swap shown in Figure 3.5b actually produces an increase in the mass segregation of the three most massive particles. While this is not the intended effect of the swapping the masses, it is a natural outcome when randomly reassigning the masses to sometime put the more massive particles close together; this can be seen as similar to primordial mass segregation (the effects of which we do not explore here).

We observe the general trend that the when the mass is swapped before the deepest moment of the collapse, 1.46 N-body times, after the collapse the mass is always highly segregated compared to when the mass is swapped at or after the collapse which leads to no or at a minimum much reduced mass segregation. This leads us to conclude that the whatever the mechanism is that is driving the future mass segregation it is happening before or at the moment of deepest collapse, i.e. 1.46 N-body time.

In order to distinguish between the two mechanisms suggested above we must carefully examine Figures 3.5b and 3.5c. In Figure 3.5b we are just able to see the steady rising of the mass segregation that we mentioned above started around 0.6 N-body times, then we swap the masses and the segregation ratio gets reset to unity. It then starts to slowly rise again with most of the particle sets reaching the same degree of mass segregation at the local maxima around 1.5 N-body times, though decidedly without the strong drop off following that peak as seen in Figure 3.5a.

Figure 3.5c again shows the rise from around 0.6 N-body times, and since the simulation runs longer without the mass being swapped it reaches a higher level of segregation before it is rushed back to unity with the masses being swapped at 1.25 N-body times. Just a before the segregation ratio rises again, but the particle sets do not tend to reach the same degree of mass segregation as before.

While there are minor differences between the mass segregation in these simulations up to the collapse, they are more similar than not after another N-body time, particularly when compared to the other cases (3.5d–3.5f). The fact that the systems show such similarities after we had removed the effect of early

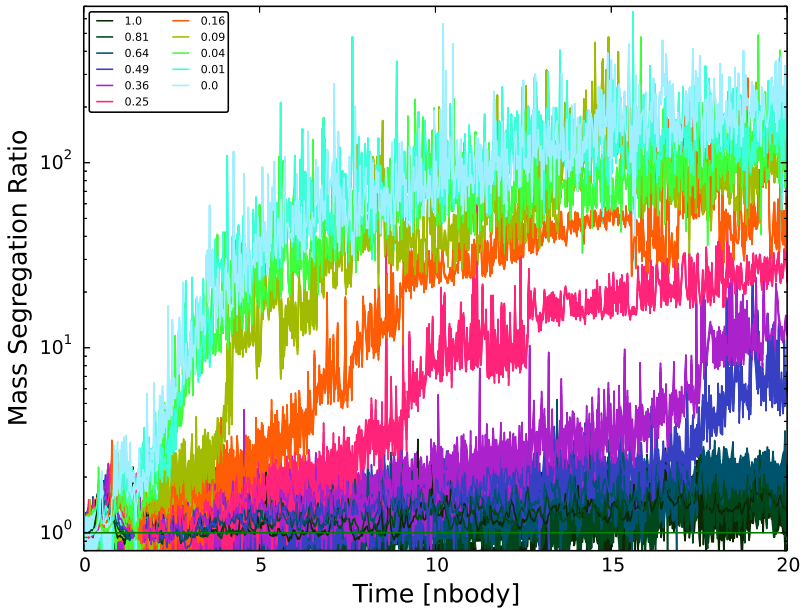


Figure 3.6: The mass segregation ratio as a function of time for several FoVs as indicated in the legend.

segregation (possibly from sub-clusters segregating) suggest that the dominate mechanism leading to this rapid mass segregation is due to the short duration of very high density at the moment of deepest collapse.

3.4.3 Effect of the Initial FoV on Mass Segregation

Caputo et al. (2014) defined FoV to be $2Q$ where Q is the more traditionally defined virial ratio, $Q \equiv |T/V|$ where T and V are the kinetic and potential energies, respectively. For example, since a system in virial equilibrium has a Q value of 0.5, its FoV would be 1.0. Caputo et al. (2014) showed that many cluster parameters are directly impacted, and in some cases even dominantly controlled, by the initial FoV. In Figure 3.6 we show the significance on the initial FoV on the evolution of the mass segregation of a cluster.

Figure 3.6 is a plot of time versus the mass segregation ratio for initial FoVs ranging from 0.0 to 1.0. Lower initial FoVs, initially colder systems, are toward the left of the plot because they seem to segregate more quickly than initially warmer systems. Caputo et al. (2014) found that the most likely initial FoV for a cluster was between 0.36 and 0.49, which corresponds to the purple and blue curves in the plot, and that R136 most likely formed with an initial FoV

of 0.25 which corresponds to the pink curve.

The effect of increasing initial FoV seems to be two fold: first, the time at which the mass begins to segregate is delayed with an increase in FoV, and second, the degree of mass segregation tends to decrease as FoV increases. The second of these effects are explained by observations in Caputo et al. (2014). We note that the depth of the collapse is a function of FoV, namely $R_{min} \approx Q + N^{-1/3}$ where R_{min} is the minimum radius reached during the collapse, Q is as defined above FoV$/2$, and N is the number of particles, which for these simulations is constant. That we find a correlation between a deeper collapse, i.e. smaller FoV, and the more mass segregated the system becomes seems natural.

3.5 Conclusion

We have introduced a new method to measure and quantify mass segregation. This method is based on determining the ratio of the average nearest neighbor distance of the most massive particles with respect to the average the nearest neighbor distance of several sets of randomly chosen particles. This method is very similar in principle and results to the MST method developed by Allison et al. (2009b), however we show that this new method is dramatically faster, providing an ≈1000 times speedup over the MST method for 200 particles. With such a speedup we are able to do science that was unaccessible using the previous method, such as measuring the mass segregation ratio of 10 per cent of simulations with $10^4 - 10^6$ particles. We estimate that our new method would require nearly 12 hours to measure the mass segregation, out to 10 per cent, of a 10^6 particle system, the old method would require more than a career's worth of time (using current hardware, not hardware from 20 years from now).

We then applied this method to simulations of a collapsing cluster to better understand the mechanism which drives rapid mass segregation. We perform an experiment to disentangle whether the rapid mass segregation is a result of sub-clusters mass segregating or the result of the very high density near the deepest part of the collapse. The experimental technique was to randomly swap the masses of particles at and near the critical moment of deepest collapse, thus allowing us to nullify any earlier mass segregation and so to isolate the degree of mass segregation that could be produced from that point forward.

The results are definitively that something prior to or at the collapse is required to drive the rapid mass segregation. By changing the time before the deepest part of the collapse we are able to show that while the sub-cluster mass segregation mechanism may play a role, the dominate drive of the rapid mass segregation is environment when the cluster is nearly at the deepest part of the collapse, likely the very high density.