2.1 Merger Trees

We use a new algorithm to generate merger trees that describe the formation paths of randomly selected dark matter halos. This is an improvement over the "block model" used previously (Cole et al. 1994; Heyl et al. 1995; Baugh et al. 1996a; Baugh et al. 1996b). The new algorithm is directly based on the analytic expression for halo merger rates derived by Lacey & Cole (1993). At each branch in the tree, a halo splits into two progenitors, but unlike the "block model," the mass ratio of the progenitors can take any value. Below we briefly describe this new algorithm and also how a population of merger trees is set up and utilised to provide a framework for modelling the processes of galaxy formation.

2.1.1 A New Algorithm

Our starting point for generating a merger tree to describe the history of mergers experienced by an individual dark matter halo is equation (2.15) of Lacey & Cole (1993):

$$\begin{aligned} f_{12}(M_1,M_2)dM_1 &= \frac{1}{\sqrt{2\pi}}\frac{(\delta_{c1}-\delta_{c2})}{(\sigma_1^2-\sigma_2^2)^{3/2}} \\ &\times \exp\left(-\frac{(\delta_{c1}-\delta_{c2})^2}{2(\sigma_1^2-\sigma_2^2)^2}\right)\frac{d\sigma_1^2}{dM_1}dM_1 \quad (2.1) \end{aligned}$$

This equation, derived from the extension of the Press-Schechter theory proposed by Bond et al. (1991) and Bower (1991), gives the fraction of mass, $f_{12}(M_1,M_2)dM_1$, in halos of mass M_2, at time t_2, which at an earlier time, t_1, was in halos of mass in the range M_1 to M_1+dM_1. Here, the quantities σ_1 and σ_2 are the linear theory rms density fluctuations in spheres of mass M_1 and M_2. The δ_{c1} and δ_{c2} are the critical threshold densities for collapse at times t_1 and t_2 respectively. For a critical density ($\Omega=10$ universe, we adopt $\delta_c=1.686(1+z)$, while for low Ω_0, open and flat, models we adopt the appropriate expressions in the appendices of Lacey & Cole (1993) and Eke, Cole & Frenk (1996) respectively. Equation (2.1) can be used to estimate the immediate merger history of a halo which at time t_2 has mass M_2. Taking the limit of equation (2.1) as $t_1\to t_2$, we obtain an expression for the mass fraction of the halo of mass M_2 which was in halos of mass M_1 at the slightly earlier time t_1,

$$\left.\frac{df_{12}}{dt_1}\right|_{t_1=t_2} dM_1dt_1 = \frac{1}{\sqrt{2\pi}}\frac{1}{(\sigma_1^2-\sigma_2^2)^{3/2}}\frac{d\delta_{c1}}{dt_1}\frac{d\sigma_1^2}{dM_1}dM_1dt_1. \quad (2.2)$$

Thus the mean number of objects of mass M_1 that the halo of mass M_2 "fragments into" when one takes a step dt_1 back in time is given by

$$\frac{dN}{dM_1} = \frac{df_{12}}{dt_1}\frac{M_2}{M_1}dt_1. \quad (2.3)$$

This expression gives the abundance of fragments as a function of the fragment mass, M_1. It is this simple expression that our algorithm utilizes in order to build a binary merger tree.

The quantities that must be specified in order to define the merger tree are the density fluctuation power spectrum, which gives the function $\sigma(M)$, and the cosmological parameters, Ω_0 and Λ_0, which enter through the dependence of $\delta_c(t)$ on the cosmological model. There is also one numerical parameter, the mass resolution, $M_{\rm res}$, that needs to be set. Having specified these parameters one can compute the two quantities,

$$P = \int_{M_{\rm res}}^{M_2/2} \frac{dN}{dM_1}dM_1, \quad (2.4)$$

which is the mean number of fragments with masses, M_1, in the range $M_{\rm res}<M_1<M_2/2$, and

$$F = \int_0^{M_{\rm res}} \frac{dN}{dM_1}\frac{M_1}{M_2}dM_1, \quad (2.5)$$

which is the fraction of mass in fragments with mass below the resolution limit. Note that both these quantities are proportional to the timestep dt, through the dependence in equation (2.3).

Once these quantities have been defined the algorithm we use to generate the merger trees is very simple. First, choose a timestep, dt, such that $P \ll 1$, to ensure that multiple fragmentation is unlikely. Next, generate a random number, R, in the interval 0 to 1. If $R>P$, then the main halo does not fragment at this timestep. However the original mass is reduced to account for mass accreted in the form of halos with masses below the resolution limit, to produce a new halo of mass $M_2(1-F)$. If, however, $R<P$, then a random value of M_1 in the range $M_{\rm res}<M_1<M_2/2$ is generated, consistent with the distribution given by equation (2.3), to produce two new halos with masses M_1 and $M_2(1-F)-M_1$. The same operation is repeated recursively on the fragments and a merger tree is built up.

The main advantage of this new algorithm over the "Block Model", which we used previously (Cole et al. 1994; Heyl et al. 1995; Baugh et al. 1996a; Baugh et al. 1996b), is that the there is no quantization of the halo masses. The algorithm also enables the merger process to be followed with high time resolution, as timesteps are not imposed on the tree but rather are controlled directly by the frequency of mergers. It is similar in spirit to the method used by Kauffmann et al (1993), but has several advantages, including that it does not require the storage of large tables of progenitor distributions. A detailed investigation of the behaviour of this algorithm and a comparison of its results with N-body simulations will be presented in a future paper (Lacey & Cole in preparation).

2.1.2 Utilizing the Merger Trees

Although the merger trees described above have very high time resolution the nature of the galaxy formation rules that we implement below require placing the merger tree onto a predefined grid of timesteps. The original binary merger tree is used to find which halos exist at each timestep and to identify which of them merge together between timesteps. As a consequence, mergers that are actually rapid, consecutive binary mergers in the original tree will appear as simultaneous, multiple mergers in the discretized tree. The loss of information involved is not significant since in reality, mergers are not instantaneous events and our discrete timesteps are typically much smaller than the dynamical timescales of the merging halos. The appropriate grid of $N_{\rm steps}$ timesteps depends on the problem being studied and can, for example,