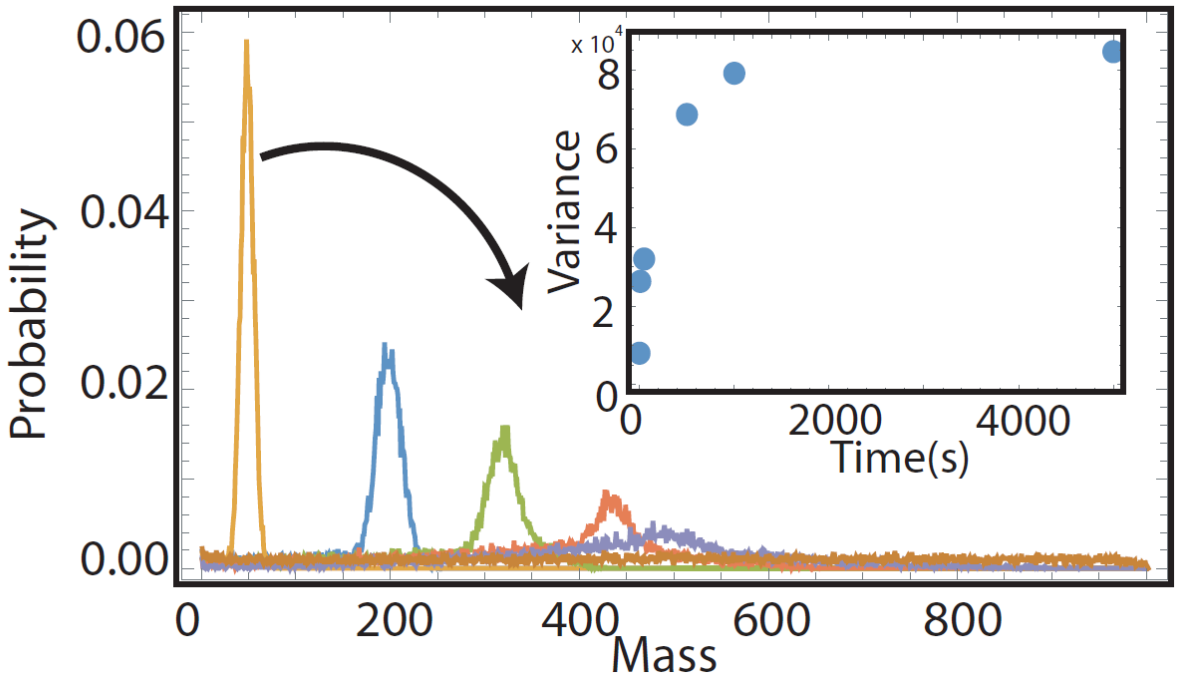

Figure S1 (Related to Figure 2): Assembly dynamics of two microtubules assembled from a common limiting pool of tubulin. To simulate the growth of dynamic microtubules, processes of rescues and catastrophes (Fygenson, 1994; Gardner et al., 2013) were included, along with the processes of growth and decay in the stochastic simulation. Microtubule filaments were assigned a state which determined whether the filament was undergoing rescues (no disassembly allowed) or catastrophe (no assembly allowed). In the initial growth phase (orange), the distribution of individual microtubule lengths starts off as a peaked distribution whose mean increases, until the total length reaches a steady state (black arrow). The growth phase is followed by the slow phase of monomers swapping which leads to anti-correlated fluctuations in the lengths of the two individual microtubules, which leads to an increase in the width of the filament length distributions. The final, steady state distribution (brown) is flat. (Inset) Plot of variance of the length distribution of a single microtubule versus the time of the simulation. The variance initially increases linearly with time, indicative of diffusive dynamics, and later it saturates. The parameters used for simulations were $k'_+ = 0.5\, N_{free}\ s^{-1}$, $k_- = 10\ s^{-1}$, $N = 1000$ and $N_{free} = N - l_1 - l_2$ is the amount of free monomer in solution. l_1 and l_2 are the lengths of the two microtubule filaments. Rates of rescue and catastrophe were the same for both the filaments, each equal to $0.5\ s^{-1}$. Time was varied from $0 - 5000\ s$.

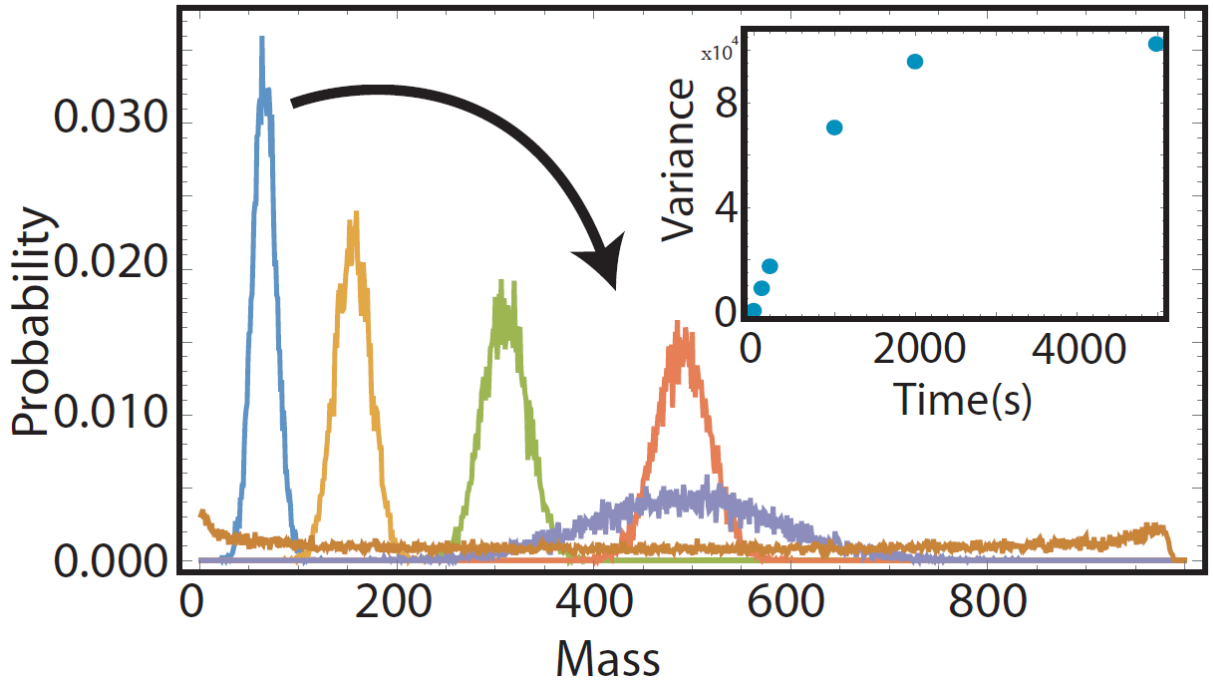

Figure S2 (Related to Figure 2): Assembly dynamics of two three-dimensional structures assembled from a common limited pool of subunits. To simulate the growth of a model 3D structure, stochastic simulations were done with the assembly and disassembly rates proportional to the radius of the growing structure (Berg and Purcell, 1977), while the assembly rate diminishes as the free monomer pool is depleted, i.e., the rates are: $k'_+ M^{\frac{1}{3}}(N-M)$ and $k_- M^{\frac{1}{3}}$, respectively, where M is the mass of the structure and is proportional to its volume, k'_+ and k_- are rate constants. In the simulation, we consider the assembly of two identical structures with these dynamics and measure the mass fluctuations of one. In the initial growth phase (blue to orange), the mass distribution for one structure starts off peaked with a mean that increase with time (black arrow), until the sum of the masses of the two structures reaches a steady state. The growth phase is followed by the slow phase of monomers swapping which leads to anti-correlated fluctuations, which are seen in the individual trajectories. These fluctuations lead to an increase in the width of the mass distributions while the mean stays unchanged. (Inset) Plot of the variance of the mass distribution against the time of simulation. The variance initially increases linearly with time, indicative of a diffusive regime, and later saturates. The parameters used for simulations were $k'_+ = 0.5\, N_{free}\, m^{-1}\, s^{-1}$, $k_- = 10\, m^{-1}\, s^{-1}$, $N = 1000$ and $N_{free} = N - M_1 - M_2$ is the amount of free mass in solution and M_1 and M_2 are the masses of the two structures. Time was varied from $0 - 5000\ s$.