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Stochastic Simulation of Imperfect Mixing in Free Radical Polymerization

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Summary: A modified algorithm for the stochastic simulation of chemical reactions subject to mass transfer limitation (imperfect mixing) is presented. This algorithm takes into account the mixing by diffusion of the reacting species between two consecutive reactions. The method is used to simulate the effect of mass transfer limitation in free-radical polymerization. Since this is a stiff reaction network, a hybrid stochastic-deterministic approach is considered. The hybrid stochastic algorithm under imperfect mixing (HSSA-IM) is applied to the bulk polymerization of methyl methacrylate up to high conversions. The accuracy of the algorithm relies on the precise determination of diffusion coefficients during the reaction.

Keywords: hybrid stochastic simulation; imperfect mixing; kinetic monte carlo simulation; radical polymerization; stochastic simulation algorithm; trommsdorff effect

Introduction

The Stochastic Simulation Algorithm (SSA), was introduced by Gillespie[1] as an alternative to the Reaction-Rate Equation (RRE) for the solution of the Chemical Master Equation (CME). In the thermodynamic limit of a system, that is, for a system composed of an extremely large number of molecules, the results obtained using both SSA and RRE approaches are identical.[2] However, chemical reacting systems involving infrequent chemical reactions or chemical species in limited amounts are better represented by the stochastic description of the CME than by the corresponding deterministic formalism.[3,4] One main disadvantage of the original SSA formulation is that it is a very inefficient method for simulating stiff chemical reactions. Stiffness is observed when at least one reaction pathway is orders of magnitude more frequent than the others. Several approaches,[5,6] including the hybrid stochastic method,[7,8] have been proposed to overcome stiffness using stochastic algorithms. In radical polymerization processes, many different reactions take place simultaneously, some of them very frequently (such as propagation), but some other infrequently (such as initiator decomposition), and in addition, radical species are usually present in very low concentrations. These features of radical polymerization motivates the simulation of the process using efficient stochastic methods in order to obtain a better representation of the system and to get a deeper understanding of the polymerization process. A common feature of both stochastic and deterministic methods is the assumption of perfectly mixed reaction volumes. In this context, it is not sufficient that a system is homogeneous (that is, the local concentrations are the same for the whole volume), but also the probability of finding one given single molecule at any position in the system must be uniform. This means that a single molecule has the same probability of reacting with every other molecule present in the system; however, this is not possible in real systems because of mass transfer limitations.[9,10] In the first part of this work an example of hybrid stochastic simulation

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(HSSA) for radical polymerization is presented. This algorithm is used to simulate the effect of the perfectly mixed volume on the conversion and molecular weight distribution of a free radical batch solution polymerization. Next, a novel method is proposed for the simulation of a reacting system under imperfectly mixed (IM) conditions as an improvement of the usual stochastic simulation algorithms which assume perfect mixing in the whole system. As an example, a HSSA incorporating the algorithm for imperfectly mixed conditions (HSSA-IM) is used to simulate the radical polymerization of methyl methacrylate up to high conversions. This new stochastic simulation algorithm can be used to simulate homogeneous systems with mass transfer limitations, as well as heterogeneous systems.

Hybrid Stochastic Simulation Algorithm

The stochastic simulation algorithm (SSA) of chemical reacting systems, also known as kinetic Monte Carlo (kMC) algorithm, is a numerical method used to solve the Chemical Master Equation which describes precisely the dynamic behavior of the system.[1] For a detailed description of the SSA method, the reader is referred to the original work of Gillespie[1,3] or to his recent review paper.[2] The reactions in the system can be classified as slow or fast reactions depending on the value of the propensity of the reaction and on the number of reacting species present in the system.[5] When fast and slow reactions are simultaneously present in the system (stiffness), the original SSA formulation becomes very inefficient and alternative algorithms should be used instead (tau-leaping SSA, hybrid stochastic simulation, etc.)[2,5–8] In the hybrid stochastic approach for simulating stiff systems (HSSA), the SSA is only applied to infrequent events (slow reactions) or to events involving changes in the number of elements (molecules) in limited amount, while the frequent events (fast reactions) not involving changes in the state of limited-number elements are simulated using a "faster" solution which can be the deterministic solution of their corresponding ordinary differential rate equations. As an illustrative example, a simple case of free-radical solution polymerization is considered, which was previously simulated by Lu and coworkers[11] using the original SSA formulation. Only three reactions are considered: Initiator decomposition, propagation and termination by combination. It is possible to model any other reaction such as photochemical initiation, redox initiation, thermal initiation, termination by disproportionation, chain transfer to monomer, to solvent, to polymer or to any other chain transfer agent, and so on. The reaction scheme considered is presented in equation 1 to 3.

Initiator decomposition :

$$I \xrightarrow{fk_d} 2R_1^\bullet \tag{1}$$

$$\text{Propagation}: \quad R_i^\bullet + M \xrightarrow{k_p} R_{i+1}^\bullet \tag{2}$$

$$\text{Termination}: \quad R_i^\bullet + R_j^\bullet \xrightarrow{k_t} P_{i+j} \tag{3}$$

k_d is the rate coefficient of initiator decomposition (s^{-1}), f is the efficiency of initiation, k_p is the rate coefficient of radical propagation (L/mol · s) and k_t is the rate coefficient of radical termination by combination (L/mol · s).

The CME formulation for the number of initiator molecules and radicals in a system of volume V is:

$$\frac{dP(n_I)}{dt} = -fk_d P(n_I) \tag{4}$$

$$\begin{aligned}\frac{dP(n_R)}{dt} &= 2fk_d I N_A V[P(n_R-2) - P(n_R)] \\ &\quad + \frac{k_t}{N_A V}\left[(n_R+2)(n_R+1)P(n_R+2)\right. \\ &\quad \left. - n_R(n_R-1)P(n_R)\right]\end{aligned} \tag{5}$$

where $P(n_I)$ is the probability of finding n_I molecules of initiator in the system, $P(n_R)$ is the probability of finding n_R radicals in the system and N_A is Avogadro's number. Although not presented explicitly, these are also functions of the time t and the initial conditions.

The corresponding Reaction-Rate Equations for this system are the following:

$$\frac{d[I]}{dt} = -fk_d[I] \tag{6}$$

$$\frac{d[R]}{dt} = 2fk_d[I] - k_t[R]^2 \tag{7}$$

where $[I]$ is the concentration of initator molecules and $[R]$ is the total concentration of radicals in the system.

Two of these reactions (initiation and termination) are designated as slow reactions because they involve changes in the state of low-number species (radicals), and therefore, they must be simulated using the SSA. Only for the propagation events, the total number of radicals in the system remains constant (equation 2). When there is an excess of monomer molecules, the monomer propagation can be safely simulated using the deterministic solution. As the monomer is consumed, the number of monomer molecules decreases to a critical value, after which the propagation reaction must be simulated using the SSA. A typical condition used to determine the transition from deterministic to SSA, is when the change in the number of monomer molecules at each time step is above 10% of the total number of monomer molecules currently available.[5] In excess of monomer, many propagation reactions take place between two consecutive stochastic events (initiation or termination). The reaction rate equation for monomer propagation is expressed by equation 8.

$$\frac{d[M]}{dt} = -k_p[R] \cdot [M] \tag{8}$$

$[M]$ is the concentration of monomer in the system at time t. Given that between two stochastic events there is no change in the total number of radicals in the system, equation 8 can be solved considering $[R]$ constant:

$$\ln\frac{[M]_{t_0+\Delta t}}{[M]_{t_0}} = -k_p[R]_{t_0}\Delta t \tag{9}$$

where Δt is the time elapsed between the two consecutive stochastic events and t_0 is the time at which the first stochastic event occurs. Therefore, the change in monomer concentration due to propagation between two stochastic events can be expressed by:[12]

$$\Delta[M] = [M]_{t_0}\left(e^{-k_p[R]_{t_0}\Delta t} - 1\right) \tag{10}$$

Once the amount of monomer consumed by propagation is determined, it is randomly distributed among the existing growing radicals. The simulation continues until all the radicals and initiator molecules in the system are exhausted. If the number of monomer molecules is below the 10% condition given above, the simulation method of the propagation reaction is switched from deterministic to stochastic. Similar results are obtained between a normal SSA and this HSSA, but the HSSA runs much faster.

Effect of Imperfect Mixing on Radical Polymerization

In a real reactor the assumption of perfect mixing is no longer valid. Since the volume of the system has practically no effect on the results obtained with usual deterministic methods, they are not suitable for simulating imperfectly mixed reactors (although some attempts have been made considering many small interconnected reactors[9] or using models based on partial differential equations[10]). On the other hand, it is possible to simulate the effect of imperfect mixing in a real solution polymerization reactor simply by using different volumes in the stochastic algorithm. The effect of the size of the perfectly mixed volume on the final conversion and on the number average chain length for a polymerization reaction example described by Lu et al.,[11] are presented in Figure 1. The volume sizes considered correspond to spherical systems with diameters between 25 nm and 1.5 μm, which are similar to those observed in particles obtained by microemulsion, miniemulsion or emulsion

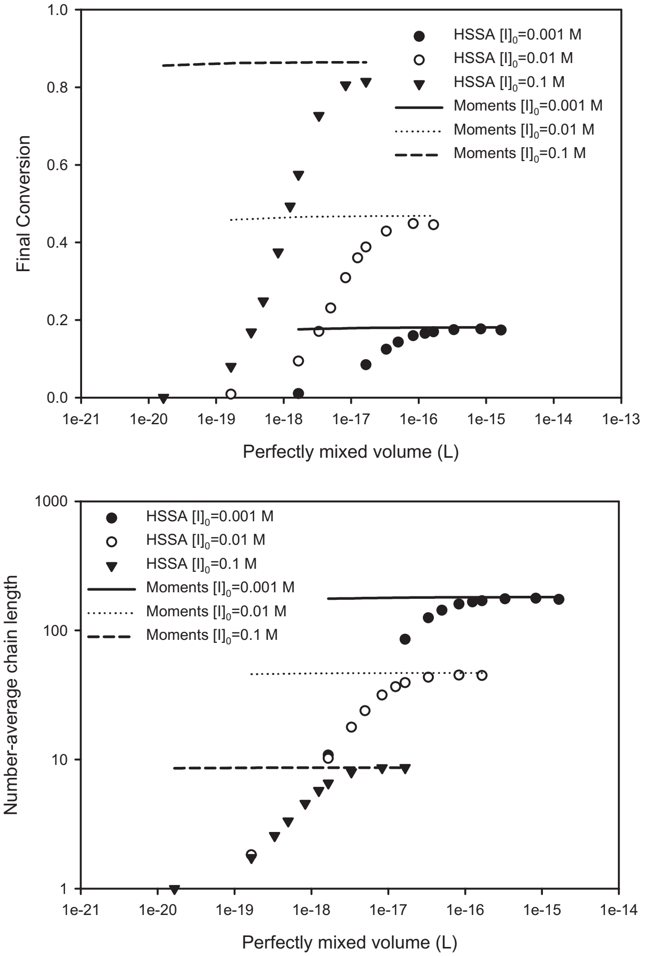

Figure 1.

Effect of the perfectly mixed volume on final monomer conversion (left) and on the number-average chain length (right) for different initial initiator concentrations. Data points: Hybrid stochastic simulation. Lines: Deterministic simulation (method of moments). $[M]_0 = 1$ M; $k_p = 100$ L/mol · s; $k_t = 10^7$ L/mol · s; $k_d = 10^{-4}$ s^{-1}; $f = 1$.

polymerization, indicating that these effects are also significant for heterophase polymerizations. These results are compared with the corresponding deterministic solution for the same system volume, obtained using the method of moments. In this case, the volume of the system (V) was used to calculate the minimum possible concentration of any species in the system:

$$C_{\min} = \frac{1}{N_A V} \tag{11}$$

The deterministic simulation is stopped when the concentration of initiator in the system drops below C_{min}. A very slight effect of the volume size on conversion and average chain length is observed (Figure 1).

For the stochastic method, both the final monomer conversion and the final number-average chain length increase with the volume of the system and tend towards a limiting value corresponding to the final monomer conversion obtained with the deterministic method. The change in polymerization kinetics observed by decreasing the volume of the system is caused by the confinement of pairs of radicals (“cage” effect).[13–15] If the volume is further decreased, a zero monomer conversion condition is reached because in this case, the most probable fate of a radical pair generated by initiator decomposition is its subsequent recombination. By decreasing even further the volume (reaching almost the same volume scale of the polymer molecules $\sim 10^{-21}$ L) it is no longer possible to assume perfect mixing because the system becomes inherently heterogeneous. In this case, more elaborated multiscale simulation methods are required.[16] Similar systematic reductions in monomer conversion by decreasing the system volume has been recently observed by Chaffey-Millar et al.[17] for the Monte Carlo simulation of RAFT polymerization of star polymers. They ascribed this effect to deterioration in the accuracy of the method when the number of simulated molecules is reduced, and recommended the use of larger simulation volumes. However, we consider that although the variability of the results may increase for smaller systems, this does not explain the behavior observed in Figure 1. On the contrary, the lower conversions and average chain lengths are in very good agreement with the confined space effect for pairs of radicals observed by Zetterlund and Okubo[14,15] using modified Smith-Ewart equations for controlled/living radical polymerization in dispersed systems below a certain critical particle size. In the following section, a modified SSA method for the simulation of chemical reaction networks under mass transfer limitation is proposed based on the diffusion of the reacting molecules.

Stochastic Simulation Algorithm for Imperfectly Mixed Systems

In the original SSA formulation, the time at which the next stochastic event occurs (τ) can be calculated using the following equation:[1]

$$\tau = -\frac{\ln(\xi)}{\sum_i a_i} \tag{12}$$

where ξ is a uniformly distributed random number between 0 and 1, and a_i is the propensity function of the i-th stochastic event (in s^{-1}). In general, the propensity function can be expressed as:

$$a_i = c_i f(n_1, n_2, \ldots,) \tag{13}$$

where c_i is a reaction probability, and $f(n_1, n_2, \ldots)$ is a function of the number of molecules in the system which depends on the order of the reaction. For the general case of a bimolecular reaction between the molecules A and B, $c_i \equiv k_i/N_A V$, where k_i is the rate coefficient of the i-th reaction. The propensity function is then given by:

$$a_i = \frac{k_i n_A n_B}{N_A V} \tag{14}$$

and can also be expressed as a function the molar concentrations (C):

$$a_i = k_i C_A C_B N_A V \tag{15}$$

Proceeding similarly with other types of reactions, it can be found that in general:

$$a_i = N_A V k_i f_i(C) \tag{16}$$

The type of event taking place at time τ is determined randomly, where the probability P of choosing an i-th event is:

$$P(i) = \frac{a_i}{\sum_j a_j} \tag{17}$$

In the modified SSA for imperfectly mixed systems, the type of reaction must be determined first. From equation 16 and 17, we obtain the probability for the i-th reaction being the next event:

$$P(i) = \frac{k_i f_i(C)}{\sum_j k_j f_j(C)} \tag{18}$$

Notice that it is not necessary to know the volume of the system in order to determine the next event. Once the next reaction has been identified, we need to determine the time at which the next reaction takes place and the perfectly mixed volume for the particular reaction at the particular time.

Stickler[18] proposed the use of Einstein's equation of Brownian motion for the determination of effective reaction volumes in diffusion-controlled reactions. Considering the diffusion of a single molecule from any given initial position at any initial time, it is possible to calculate the mean square displacement in space ($\langle x^2 \rangle$) using Einstein's equation:

$$\langle x^2 \rangle = 6D\Delta t \tag{19}$$

where D is the diffusion coefficient of the molecule and Δt is the time elapsed after the initial time. Equation 19 describes the diameter of a sphere inside which the probability of finding the diffusing molecule is 50%. Therefore, we can estimate the diffusion volume for the particular molecule as twice the volume of the sphere described by equation 19:

$$V_{dif} = \frac{8\pi}{3}(6D)^{3/2}\Delta t^{3/2} \tag{20}$$

An estimate of the perfectly mixed volume (V_{pm}) is then given by the diffusion volume of the fastest molecule involved in the next reaction, considering that $\Delta t = \tau$:

$$V_{pm} = \frac{8\pi}{3}[6\tau \max(D)]^{3/2} \tag{21}$$

Using equation 12 and 16, the next reaction time for the perfectly mixed volume is:

$$\tau = -\frac{1}{N_A V_{pm}} \frac{\ln(\xi)}{\sum\limits_i k_i f_i(C)} \tag{22}$$

Combining equation 21 and 22, the next reaction time can be calculated as:

$$\tau = \left[-\frac{3}{8\pi N_{Av}(6\max(D))^{3/2}} \frac{\ln(\xi)}{\sum\limits_i k_i f_i(C)} \right]^{2/5} \tag{23}$$

and the perfectly mixed volume, after some algebra, is found to be:

$$\begin{aligned} V_{pm} &= \left(1536\pi^2\right)^{1/5} \left[-\frac{\max(D)}{N_A} \frac{\ln(\xi)}{\sum\limits_i k_i f_i(C)} \right]^{3/5} \\ &\approx 6.857 \left[-\frac{\max(D)}{N_A} \frac{\ln(\xi)}{\sum\limits_i k_i f_i(C)} \right]^{3/5} \end{aligned} \tag{24}$$

For this perfectly mixed volume, the number of molecules for each species is given by:

$$n_k = \mathrm{int}(C_k V_{pm} N_A) \tag{25}$$

There are different ways to define the integer function (*int*) used in equation 25. Some common ways include rounding to the nearest integer, rounding to the next integer, or truncating the number. The method used to discretize the system may systematically overestimate or underestimate the actual number of molecules in the system. In order to reduce this effect, we suggest performing a Monte Carlo discretization, as follows:

$$n_k = \begin{cases} ceil(C_k V_{pm} N_A), & \zeta < C_k V_{pm} N_A - floor(C_k V_{pm} N_A) \\ floor(C_k V_{pm} N_A), & \zeta > C_k V_{pm} N_A - floor(C_k V_{pm} N_A) \end{cases} \tag{26}$$

where ζ is a uniform random number between 0 and 1, and *ceil* and *floor* are discretizing functions giving as a result the closest integers greater than or less than the number evaluated, respectively. Although this method will increase the computational effort, the biasing due to discretization will be reduced. An additional condition that must be checked after discretization is that the number of molecules of the fastest species for the selected next reaction should always be greater or equal than one, because this is the molecule around which the perfectly mixed volume is considered.

Using the number of molecules actually present in the perfectly mixed volume, it is now possible to calculate the actual propensity function of the next reaction (equation 14). If the calculated propensity function is zero, the time is updated but no reaction takes place. If the actual propensity function is greater than zero, the event takes place, the time and the concentration of the species are updated, and the simulation continues. Care must be taken when updating the concentrations, because the reactions take place every time for different volumes:

$$C_{k,new} = C_{k,old} + \frac{\nu_{k,i}}{N_A V_{pm}} \tag{27}$$

where $\nu_{k,i}$ is the stoichoimetric coefficient for the i-th reaction and k-th component.

It should be noticed that the accuracy of this algorithm relies on the use of an adequate model for the estimation of diffusion coefficients in the reacting mixture.

The proposed algorithm for simulating chemical systems under imperfectly mixed conditions is presented graphically in Figure 2.

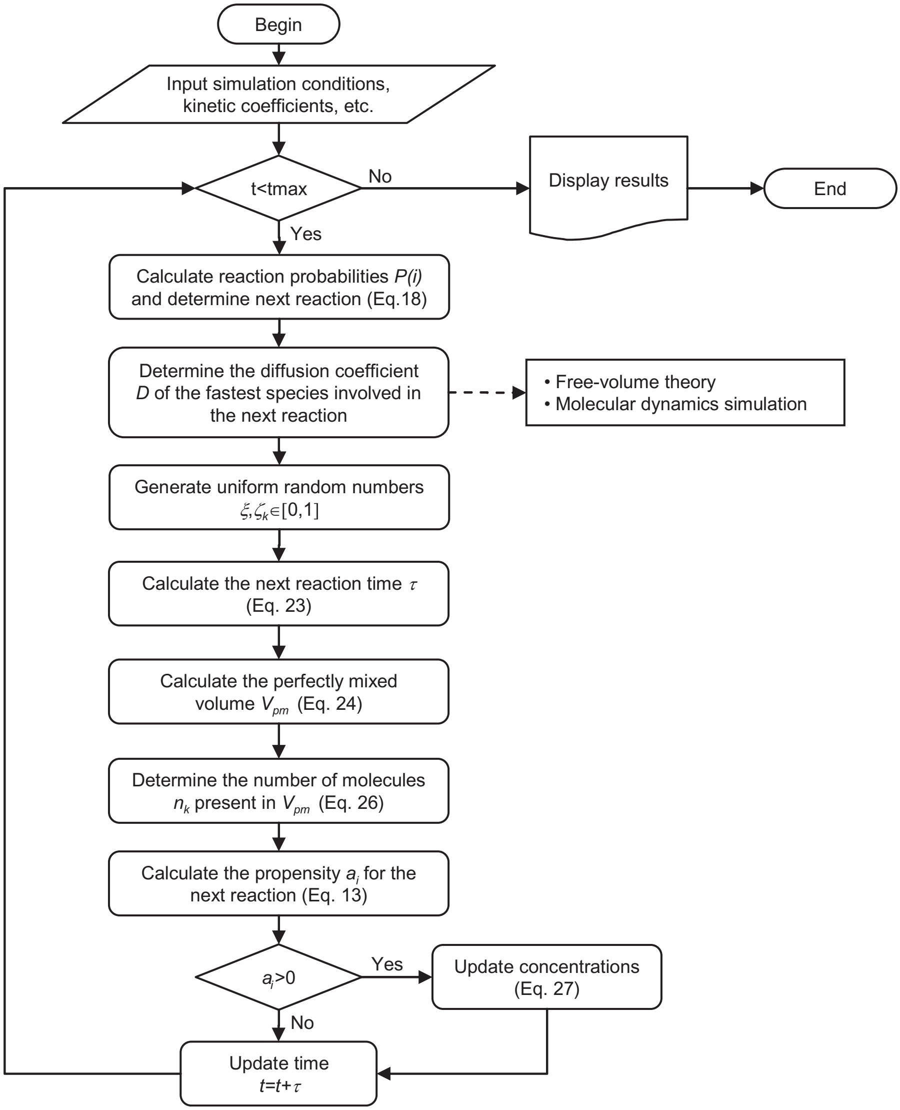

Figure 2.
Stochastic simulation algorithm for systems under imperfect mixing conditions

Bulk Radical Polymerization of Methyl Methacrylate

In this section, the algorithm for imperfectly mixed systems described above is implemented with the HSSA presented in section 2 to simulate a typical diffusion-limited polymerization reaction: the bulk radical polymerization of methyl methacrylate (MMA) up to high conversions. The reaction scheme for this example is similar to that considered before (equation 1–3), but now the termination mechanism is assumed to be disproportionation instead of combination. The polymerization conditions for the simulation, the kinetic parameters and the experimental data were taken from Tefera et al.[19] The values used were those reported as "initial", that is, without fitting any parameter to the experimental data. The diffusion coefficients were estimated using the Free-Volume theory as presented by Vrentas and Duda,[20] using the parameters reported by Faldi et al.[21] for the MMA/PMMA system. The fastest species in the reactions considered are initiator molecules and primary radicals. It is assumed that the diffusion coefficients of these molecules are the same as the diffusion coefficient of MMA. The simulation results for HSSA-IM (incorporating the algorithm for imperfect mixing) and HSSA (assuming perfect mixing), and the experimental data are presented in Figure 3. For the HSSA, a system volume of 10^{-16} L was used which gives results in agreement to the deterministic simulation.

Different conclusions can be extracted from Figure 3. In first place, it is clear that the unfitted parameters are not suitable to describe the experimental data with any of these methods. However, the HSSA-IM algorithm was able to predict the gel or Trommsdorff effect,[22] which is a sudden increase in the polymerization rate due to the segregation of the growing radicals caused by mass transfer limitations, although at a much higher conversion (about 80% vs. 30%). The experimental data also show a glass effect, that is, a limiting conversion below 100%, also caused by the diffusion limitation of monomer molecules which can no longer reach the radical chains. This effect was not predicted by the simulations using this set of parameters. Two different HSSA simulations for different initiator efficiency factors (f) are presented. The value of 0.43 is that reported in the literature.[19] Given that this efficiency

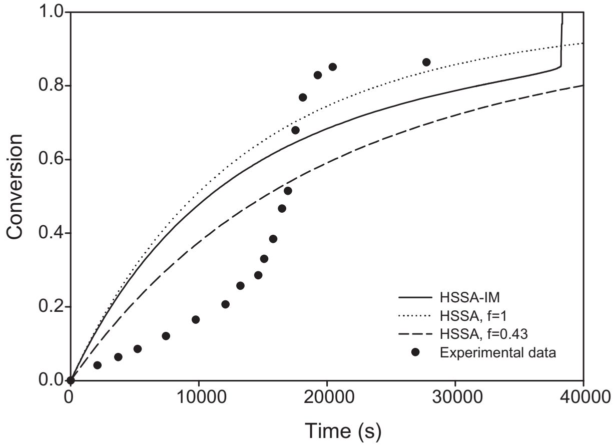

Figure 3.

Simulation of bulk polymerization of methyl methacrylate up to high conversions using unfitted parameters using 2,2′-Azodiisobutyronitrile (AIBN) as initiator. $T = 323$ K; $[I]_0 = 0.0166$ M; $[M]_0 = 9.08$ M; $k_p = 649$ L/mol · s; $k_t = 2.55 \times 10^7$ L/mol · s; $k_d = 2.08 \times 10^{-5}$ s^{-1}. Experimental data taken from Tefera et al.[19]

factor is used to incorporate the cage effect into the model, which is another example of a reaction affected by mass transfer limitations, it was not considered for the HSSA-IM. As a result, the polymerization rate using for the HSSA-IM initially follows the HSSA with $f = 1$. However, as the polymerization proceeds, the polymerization rate decreases faster than for the HSSA as a consequence of the cage effect, until the viscosity of the solution is so high that two different radicals are unable to reach each other and terminate, giving rise to the gel effect. Considering the high deviations with respect to the experimental data, a new set of kinetic parameters was used, which was previously fitted to describe the experimental results at the beginning of the polymerization (without mass transfer limitations). The conversion-time curves obtained with this new kinetic set of parameters are presented in Figure 4 for two sets of diffusion parameters, the parameters reported by Faldi et al.[21] (left), and a modified set of parameters where only some of the parameters were adjusted (right).

Using the new set of kinetic parameters, it is possible to evidence that the HSSA-IM algorithm is able to describe all the effects

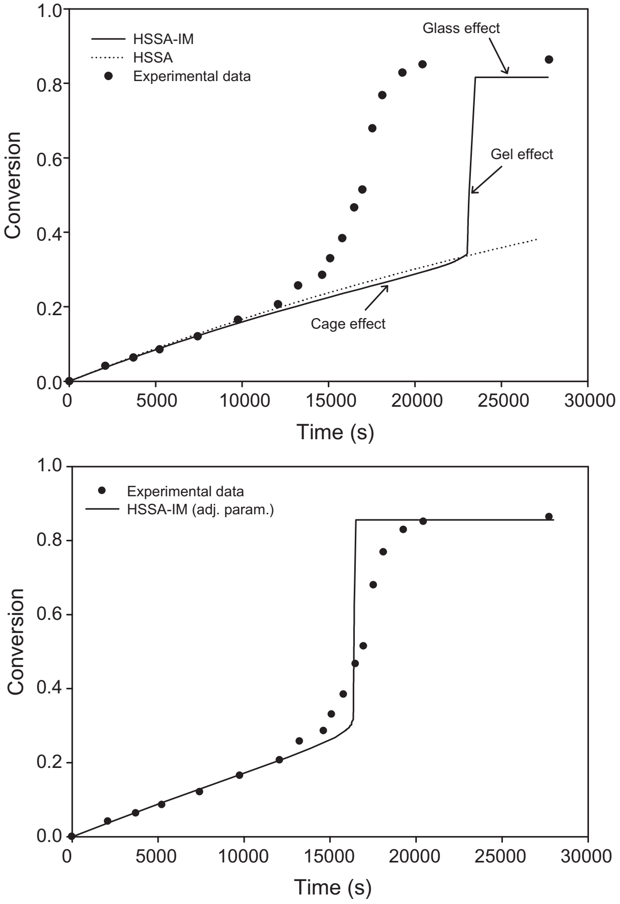

Figure 4.

Simulation of bulk polymerization of methyl methacrylate up to high conversions with parameters fitted for the beginning of the polymerization. $T = 323$ K; $[I]_0 = 0.0166$ M; $[M]_0 = 9.08$ M; $k_p = 299$ L/mol · s; $k_t = 2.91 \times 10^7$ L/mol · s; $k_d = 6.74 \times 10^{-6}$ s^{-1}; $f = 1$. Left: Diffusion parameters from Faldi et al.[21] Right: Adjusted diffusion parameters. Experimental data from Tefera et al.[19]

related to mass transfer limitation in free-radical polymerization: cage effect, gel effect and glass effect. On the other hand, the HSSA formulation and the deterministic methods (both assuming perfect mixing) are unable to describe these phenomena unless the kinetic parameters are forced to change during the polymerization either by using arbitrary breaking points or semi-empirical equations (based for example on the free-volume theory of diffusion).[23] It is observed in Figure 4 that using only the fitted kinetic parameters, the HSSA-IM algorithm was not able to quantitatively describe the experimental data. On the other hand, the agreement between the simulation results and the experimental data adjusting some of the parameters of the diffusion model, is certainly improved. Even better results are expected to be obtained if better models for the estimation of the diffusion coefficient of the molecules can be used, and if additional important factors are included in the algorithm, such as the segmental diffusion of the chains[24], the full molecular weight distribution of the polymer formed,[23] and the mesoscopic hydrodynamic contribution to the mixing process.[25] A very promising alternative to improve the accuracy of the stochastic algorithm for imperfect mixing is to perform multiscale simulations in which the diffusion coefficients are determined periodically for the corresponding polymerization conditions (temperature, polymer concentration, molecular weight distribution) using a lower-level Molecular Dynamics, Monte Carlo, or any other suitable simulation method.[26] The estimated values can then be used by the higher-level HSSA-IM simulation.

Conclusions

A modified stochastic algorithm was developed to simulate chemical reactions under imperfect mixing conditions. In the presence of mass transfer limitations, the perfect mixing assumption is valid only up to a certain volume, designated as the perfectly mixed volume. In particular, a hybrid stochastic simulation algorithm is used for the simulation of the stiff free-radical solution polymerization reactions under imperfectly mixed conditions (HSSA-IM). The results obtained show that imperfect mixing seriously affects the final conversion and molecular weight distribution of the polymer formed. This effect is a direct consequence of the competitive nature of radical polymerization reactions. The increased rate of termination due to radical confinement ("cage" effect) reduces the rate of propagation of radicals yielding lower final monomer conversions as well as lower molecular weight polymers. On the other hand, the characteristic perfectly mixed volume of a solution polymerization may decrease continually during the process due to the increase in the viscosity of the solution, causing isolation of the growing radicals and giving rise to the Trommsdorff or gel effect, and eventually, isolating also the monomer molecules so that the polymerization completely stops (glass effect). All these effects caused by mass transfer limitations can be described by the stochastic algorithm for imperfect mixing presented in this work. This method can be considered as the stochastic counterpart to the well-established deterministic methods used to describe diffusion-controlled polymerization reactions.[27]

Further potential applications of the HSSA-IM include pulsed-laser polymerization (PLP) and heterophase polymerization reactions. Stochastic simulation methods have already been proposed for the simulation of PLP experiments,[28] but the incorporation of mass transfer effects (imperfect mixing) into the stochastic simulation will certainly help improve the accuracy in the determination of chain-dependent propagation rate coefficients. On the other hand, diffusion and mass transfer limitation phenomena are extremely important for heterogeneous polymerization processes (such as emulsion, miniemulsion, microemulsion, suspension or dispersion polymerization) where segregation and compartmentalization have a predominant effect on polymerization kinetics. In addition, there are also certain processes which exhibit a system transition from homogeneous to heterogeneous. Perhaps, the most representative of these transitions is particle nucleation in heterophase polymerization. This transition has been very difficult to investigate experimentally especially because of its extremely fast dynamics; however, a multi-scale modeling approach involving hybrid stochastic simulation of the system under mass transfer limitations can offer new insights about this complex process.

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