

# Cellular Automata Models of Kinetically and Thermodynamically Controlled Reactions

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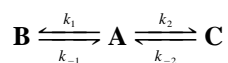
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**ABSTRACT:** Cellular automata simulations of the competition between kinetically controlled and thermodynamically controlled products of a reaction are described. The simulations are based on a stochastic first-order cellular automata model described previously [20] and demonstrate an alternative to the traditional approach to such problems that relies on solution of a set of coupled differential rate equations. Unlike the traditional approach, the cellular automata models are applicable to finite numbers of elements and yield statistical information on the fluctuations to be expected in such finite cases. The usual deterministic solutions appear as limiting cases involving either very large numbers of reacting ingredients or a large number of trials for smaller sets of ingredients. © 2000 John Wiley & Sons, Inc. *Int J Chem Kinet* 32: 529–534, 2000

## INTRODUCTION

The concept of kinetic versus thermodynamic control of reactions is a major consideration in organic synthesis [1,2] and is an important factor in many industrial processes [3]. Among the examples of reactions for which such competition is important one finds such reaction classes as Diels-Alder reactions, sulfonations, isomerizations, and addition reactions [2]. The situation is usually exemplified by a model of two competing reversible first-order reactions,



where A is the starting reactant and B and C are products. If  $k_1 \gg k_2$ , B will be initially formed at a greater rate than C, and B will be the kinetically favored product. If also  $K_c = k_2/k_{-2} \gg K_B = k_1/k_{-1}$ , species C will be favored thermodynamically. In the sulfonation of naphthalene, for instance, 1-naphthalenesulfonate is the kinetically favored product and 2-naphthalenesulfonate is the thermodynamically favored product [2].

In the traditional approach to this problem solutions are sought for the associated set of coupled differential rate equations,

$$d[A]/dt = -k_1[A] + k_{-1}[B] - k_2[A] + k_{-2}[C]$$

$$d[B]/dt = k_1[A] - k_{-1}[B]$$

$$d[C]/dt = k_2[A] - k_{-2}[C].$$

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Analytical forms for the solutions can be found, al-

though they are typically complicated functions of the rate constants and the initial conditions [4,5]. Using the common assumptions that  $[A] = [A]_0$  and  $[B]_0 = [C]_0 = 0$ , Brown et al. [6] have illustrated the temporal variations in the A, B, and C species concentrations in a kinetic/thermodynamic system for a number of conditions defined by differing values of the constants  $k_1$ ,  $k_{-1}$ ,  $k_2$ , and  $k_{-2}$ . (It should be noted that the solutions obtained in this way are *deterministic* solutions, strictly valid only for the limiting condition in which exceedingly large numbers of ingredients are involved.)

Alternatively, a *stochastic* approach to this problem assuming Markovian dynamics can be used [7]. This approach is theoretically sound and provides information on the fluctuations expected for finite systems, although the resulting stochastic master equation itself is often computationally intractable for complex systems. Gillespie has examined this approach and shown that Monte Carlo procedures can be employed to simulate numerically the stochastic time evolutions of chemical systems [8,9]. The value of this approach has been well demonstrated in some recent sophisticated studies [10,11].

Computer models based on cellular automata [12–16] provide an alternative and conceptually simpler approach to kinetic phenomena, while retaining some of the underlying characteristics of the Monte Carlo method [17]. First proposed five decades ago by Ulam [18] and von Neumann [19], cellular automata models forego employment and solution of the coupled rate equations or the stochastic master equation, replacing these equations by “rules” that govern the motions of the ingredients and the transitions between their states. In principle, the rules can be deterministic or probabilistic, although the probabilistic rules are most relevant in the present context. The cellular automata models yield “solutions” that apply to finite ensembles of reactants and also yield information on the statistical fluctuations to be expected from such finite systems. Systems evolve according to the user-specified rules and in the course of their evolutions display patterns of behavior (“emergent properties”) that can, if the rules are suitably chosen, be related to relevant physical and chemical phenomena. In the cellular automata models, the deterministic solutions appear as limiting cases for very large numbers of ingredients (or very large numbers of trials for smaller systems). Elsewhere we have presented cellular automata models for first-order chemical kinetics and shown that they can accurately simulate classic first-order phenomena such as exponential decay, series reactions, rate-limiting steps, the steady-state approximation, first-order equilibrium, and competing reactions [20].

Applications of the first-order model to atomic and molecular excited-state phenomena have also been presented [21,22]. In this report we examine the application of the first-order model to the phenomena of kinetic and thermodynamic reaction control in order to demonstrate the capabilities of this approach for kinetic problems.

## MODEL

The first-order cellular automaton model has been described earlier in some detail [20], and here only a brief résumé of its essential features will be given. Simulations take place on a grid of  $n \times m = N$  cells, each cell of which acts as an independent agent. Due to the nature of a first-order model, no movement rules are necessary. Each species is identified on the grid by a different color, and probabilistic transition rules are defined for transitions between the species, here A (blue), B (green), and C (red). During each iteration, representing a time step for the system, every ingredient is interrogated by the program and given the possibility of undergoing a transition to another species, the probability of such a transition being set in the operating rules. Because of the probabilistic nature of the rules, each trial run is in effect an independent “experiment.” As the system consisting of the  $N$  ingredients evolves under the rules, an inventory is kept of the numbers of each species.

In order to compare the results of our cellular automata models with the results of the traditional approach utilizing differential rate equations, we have selected for examination two examples (cases 3 and 6) from the study of Brown et al. [6]. For the transition probabilities  $P_i(i,j)$  between the species we have used the rate constants employed for each case by Brown et al. The transition probabilities can thus be represented by the transition probability matrix.

$$P_i = \begin{pmatrix} - & k_1 & k_2 \\ k_{-1} & - & 0 \\ k_{-2} & 0 & - \end{pmatrix}$$

The rate constants employed for the two examples, which we shall call Case I and Case II, are shown in Table I. Since Brown et al. arbitrarily defined their rate constants in units of  $\text{sec}^{-1}$ , each iteration in the present model corresponds to one second. Note that species B and C do not interconvert directly, but do so only through the intermediate species, A.

All trials were conducted using a  $100 \times 100 = 10,000$  cell grid. Concentrations are expressed as the number of cells of a given species divided by 10,000.

**Table I** Rate and Equilibrium Constants Employed in the Experiments

Constant	Case I	Case II
$k_1$	0.01	0.01
$k_{-1}$	0.02	0.009
$k_2$	0.001	0.001
$k_{-2}$	0.0005	0.0001
$K_B$	0.5	1.11
$K_C$	2.0	10.0

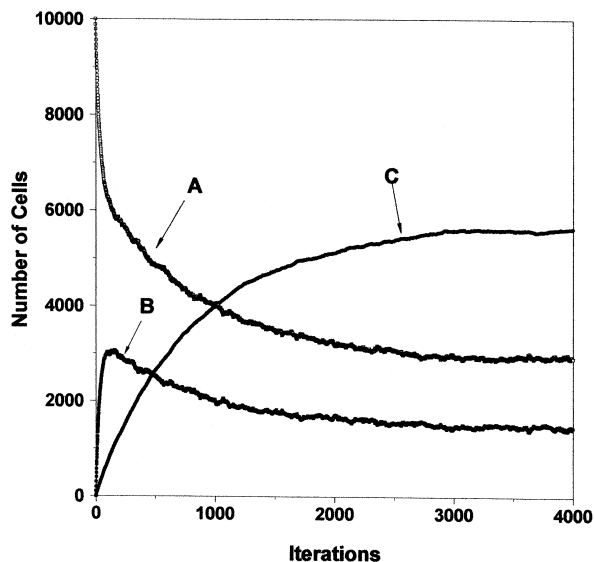
Statistical analyses were carried out using the StatMost 3.5 analysis program [23]. Deterministic analyses were carried out using *Mathematica*<sup>®</sup> [24,25].

## RESULTS AND DISCUSSION

### Case I

A plot of the variations in the populations of the species for Case I over a single trial run of 4000 iterations is shown in Figure 1. It is apparent from this plot that initially species B, the kinetically favored species, is formed in excess, whereas at later times species C, the thermodynamically favored species, predominates. The “noise” or slight raggedness seen in the plots of the populations is due to the relatively small number of ingredients being monitored. The crossing point at which  $[B] = [C]$  occurs for this trial at 477 iterations, which is to be compared with the value of approximately 470 s obtained by Brown et al. [6]. The maximum value of  $[B]$  occurred near 130 iterations, and our  $[B]_{\max}$  value for this single trial corresponds to a concentration of 0.301, a value different from the 0.5 value given by Brown et al. [6].

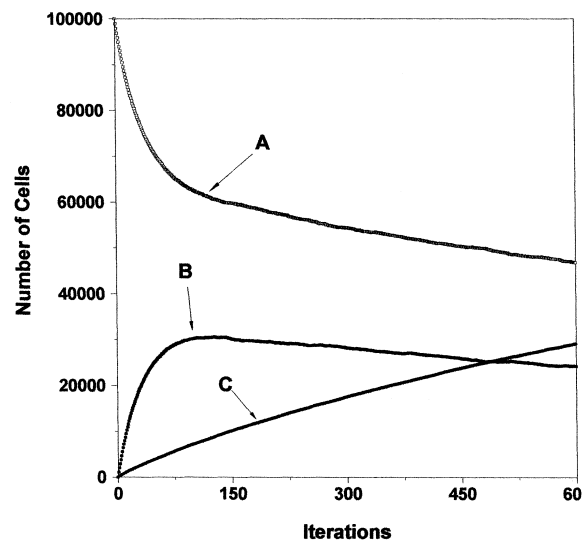
In order to obtain statistical information on the  $[B] = [C]$  crossing point and the  $[B]_{\max}$  point, a series of ten trials of 600 iterations each was run. In Figure 2 the summed data for the species concentrations from these ten trials are plotted vs. the number of iterations. Because of the tenfold increase in the number of cells monitored, these curves are seen to be significantly smoother than those from the single trial run shown in Figure 1. The crossing point for  $[B] = [C]$  was found to occur at  $492 (\pm 21, \text{standard deviation})$  iterations for the ten trials, a value fairly close to that reported for the equation-based model [6]. The maximum of the B concentration occurred at  $132 \pm 15$  iterations, and the average concentration at  $[B]_{\max}$  was  $0.309 \pm 0.003$  in this instance, a value significantly different from the 0.5 value suggested by Brown et al. [6]. Moreover, our data do not exhibit the highly peaked



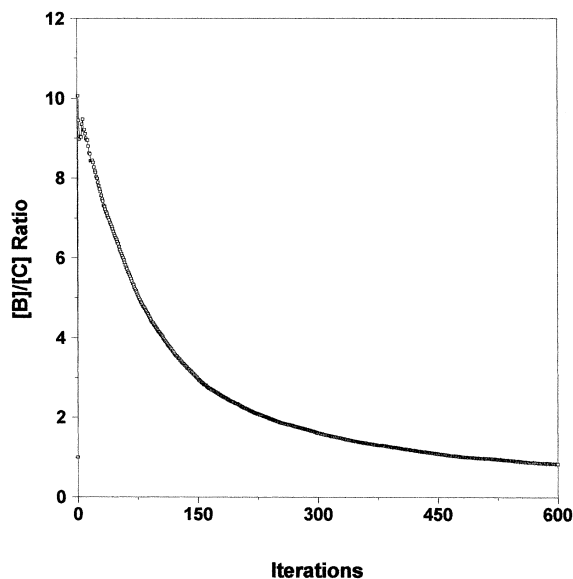
**Figure 1** Evolution of the numbers of A, B, and C ingredients for a single trial under the conditions of Case I.

behavior for the concentration of species B reported in their study. We had sufficient confidence in the cellular automaton simulations to believe that these features of the equation-based model should be reexamined, and indeed reevaluation of the deterministic solution by K. Gross in our laboratory yielded  $[B]_{\max} = 0.303$  at 131 iterations [25]. We conclude that the reported value of  $[B]_{\max} = 0.5$  [6] is incorrect.

A plot of the ratio of the concentrations of B and C is given in Figure 3, based on the data from the ten trials. This plot clearly shows the predominance of the



**Figure 2** Evolution of the summed numbers of A, B, and C ingredients for ten trials, under the conditions of Case I.



**Figure 3** Ratio of the concentrations of species B and C for the early evolution of the cellular automaton for Case I. The curve is based on results from ten trials.

kinetically favored species B during the early stages of the “experiment” and the subsequent shift toward the thermodynamically favored species C. In the initial state of the reaction  $[B]/[C] \approx 10$ , reflecting the ratio of the forward rate constants  $k_1$  and  $k_2$ , but in the later course of the reaction the influence of the equilibrium constants  $K_B \ll K_C$  becomes a dominant feature.

Experiments showed that equilibrium conditions were achieved by about 4000 iterations for this system. In order to find the equilibrium concentrations of the three interacting species, a single run of 10,000 iterations with 10,000 cells was performed. In keeping with the finite number of active ingredients involved, the concentrations of A, B, and C continuously fluctuate, so that averages should be determined for these concentrations following achievement of equilibrium. Sta-

**Table II** System Properties Obtained for Case I

Condition	This Work	Literature Value [6]
Iteration at $[B] = [C]$	$492 \pm 21$	$\sim 470$
Concentration $[B]_{\max}$	$0.3085 \pm 0.0025$	0.5*
Iteration at $[B]_{\max}$	$132 \pm 15$	—
$[A]_{\text{eq}}$	$0.2866 \pm 0.0045$	0.29
$[B]_{\text{eq}}$	$0.1439 \pm 0.0038$	0.14
$[C]_{\text{eq}}$	$0.5695 \pm 0.0048$	0.571

\* See text.

tistical analyses were therefore carried out on the species concentrations over the final 5000 iterations of the 10,000 iteration trial. (Earlier examination showed the first-order model to be ergodic within reasonable criteria, so that the result over time for a single system should be equivalent to the average result for a great number of systems at a single time [20].) The results are shown in Table II. The deterministic solutions for the equilibrium concentrations are given by the expression [26]

$$[A]_{\text{eq}} = [A]_0 / (1 + K_B + K_C)$$

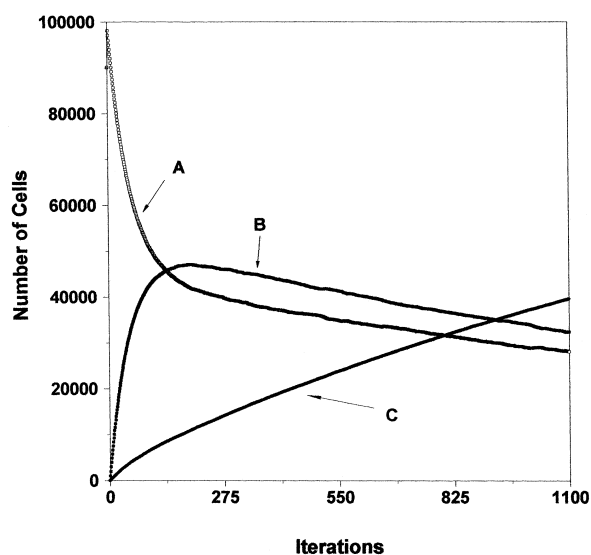
$$[B]_{\text{eq}} = K_B [A]_0 / (1 + K_B + K_C)$$

$$[C]_{\text{eq}} = K_C [A]_0 / (1 + K_B + K_C)$$

These yield the equilibrium values shown in the table. The deterministic solution for  $[C]_{\text{eq}}/[B]_{\text{eq}}$  is given by the ratio  $K_C/K_B$ , or 4.00 in the present case. The cellular automaton result was  $[C]_{\text{eq}}/[B]_{\text{eq}} = 3.96 \pm 0.11$ .

## Case II

For this study the rate constants from case 6 in the report of Brown et al. were used to form the transition probability matrix  $P_t$ . The rate constants used are given in Table I. For this case, ten trials of 1100 iterations were performed, leading to the (summed) results plotted in Figure 4. Here the  $[B] = [C]$  crossing point



**Figure 4** Evolution of the summed numbers of A, B, and C ingredients for ten trials, under the conditions of Case II.

occurred at  $916 \pm 37$  iterations, compared to the deterministic estimate of about 900 s. The model gave the position of  $[B]_{\max}$  at  $190 \pm 22$  iterations. Here, however, the model's estimate for the maximum concentration achieved for B,  $[B]_{\max} = 0.474 \pm 0.002$ , was closer to the reported deterministic estimate of 0.5 [6]. However, our reevaluation of the deterministic result for this case yielded  $[B]_{\max} = 0.468$  at 197 iterations [25]. The statistical results for case II are summarized in Table III.

A plot of  $[B]/[C]$  for this example is shown in Figure 5. Again, the initial stage reflects the dominance of the forward rate constant  $k_1$  over the rate constant  $k_2$ , whereas the later stages of the process evolve according to the relative influences of the equilibrium constants  $K_B$  and  $K_C$ . The equilibrium results for the model, given in Table III, agree reasonably well with the deterministic solutions.

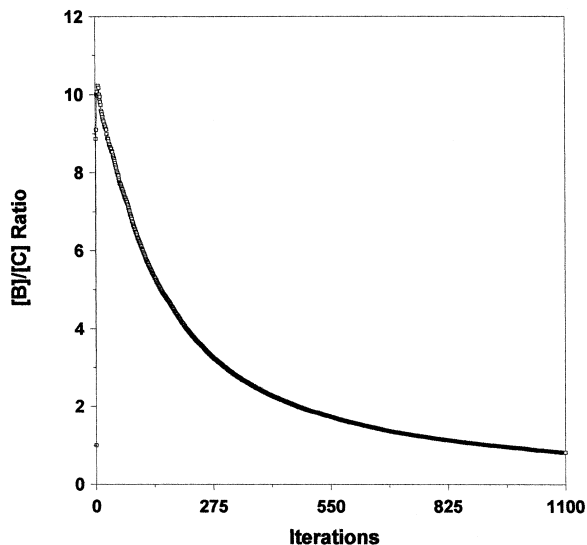
## CONCLUSIONS

The simulations presented demonstrate the efficacy of cellular automata models in describing the phenomena of kinetic and thermodynamic reaction control. Such simulations represent an alternative to, and in some cases a complement and method for verifying (or disputing), results from the traditional, differential equation-based deterministic approach [27]. We would further argue that the rule-based cellular automata approach has a strong heuristic appeal in this type of analysis, clearly revealing the influences of the rate and equilibrium constants on the progress of the observations and also the fluctuations to be expected in real, finite systems. Since advances in analytical instrumentation have pushed the limits of experimental observation to ever-lower levels, and even, increasingly, to the single-molecule level [28–30], the ability to analyze the behavior of small, finite systems should prove increasingly valuable in the future.

**Table III** System Properties Obtained for Case II

Condition	This Work	Literature Value [6]
Iteration at $[B] = [C]$	$916 \pm 37$	$\sim 900$
Concentration $[B]_{\max}$	$0.4738 \pm 0.0071$	0.5*
Iteration at $[B]_{\max}$	$190 \pm 22$	—
$[A]_{\text{eq}}$	$0.0850 \pm 0.0023$	0.082
$[B]_{\text{eq}}$	$0.0935 \pm 0.0021$	0.092
$[C]_{\text{eq}}$	$0.8215 \pm 0.0021$	0.826

\* See text.



**Figure 5** Ratio of the concentrations of species B and C for the early evolution of the cellular automation for Case II. The curve represents an average for ten trials.

This is the sixth report under Project Arch, describing applications of cellular automata to chemical phenomena. The cellular automata simulations were run using the program DING-HAO [31]. We thank Kevin Gross for carrying out the deterministic calculations.

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