



Smith, D. A., & Wilson, R. E. (2005). Extension of cluster dynamics to cellular automata with shuffle update.

[Link to publication record in Explore Bristol Research](#)
PDF-document

University of Bristol - Explore Bristol Research

General rights

This document is made available in accordance with publisher policies. Please cite only the published version using the reference above. Full terms of use are available:
<http://www.bristol.ac.uk/pure/about/ebr-terms.html>

Take down policy

Explore Bristol Research is a digital archive and the intention is that deposited content should not be removed. However, if you believe that this version of the work breaches copyright law please contact open-access@bristol.ac.uk and include the following information in your message:

- Your contact details
- Bibliographic details for the item, including a URL
- An outline of the nature of the complaint

On receipt of your message the Open Access Team will immediately investigate your claim, make an initial judgement of the validity of the claim and, where appropriate, withdraw the item in question from public view.

Extension of Cluster Dynamics to Cellular Automata with Shuffle Update

David A. Smith¹ and R. Eddie Wilson¹

Bristol Centre for Applied Nonlinear Mathematics, Department of Engineering Mathematics, University of Bristol, Queen's Building, University Walk, Bristol BS8 1TR, United Kingdom

Abstract. The random shuffle update method for the asymmetric exclusion process (ASEP) is introduced and the cluster dynamics technique is extended in order to analyse its dynamics. A sequence of approximate models is introduced, the first element of which corresponds to the classical parallel update rule whose two-cluster dynamics is reviewed. It is then shown how the argument may be extended inductively to solve for the two-cluster probabilities for each element of the sequence of approximate models. A formal limit is then taken, and macroscopic velocities and flow rates are derived.

1 Introduction

This paper is concerned with cellular automata of Nagel-Schreckenberg type [1], with the maximum velocity parameter v_{\max} set equal to one. This type of model is sometimes referred to as the Asymmetric Exclusion Process (ASEP) [2,3]. In this well-known set-up, space is discretised into a one-dimensional array of cells each of which is either empty or occupied by exactly one agent, and each agent moves according to a pair of very simple microscopic rules:

1. If the cell immediately downstream is occupied, remain stationary. (R1)
2. If the cell downstream is unoccupied, move forward into it with probability p , $0 < p \leq 1$. (R2)

The only remaining subtlety (and the subject of this paper) concerns the precise order in which rules (R1,2) are applied.

We consider the dynamics of rules (R1,2) under the *shuffle update* scheme, which has received very little attention in the literature to date [4–6]. At each time step in this scheme, a random order is generated which contains each agent exactly once. Rules (R1,2) are then applied to each individual agent in turn, according to this order, and the system is updated incrementally as each agent takes its turn. After all agents have had their turns, a new random order is generated and the next time step begins.

The shuffle update is similar to the random sequential scheme [7] in that the occupancy of cells is updated incrementally as each agent applies its rules and consequently, the shuffle update does not require conflict resolution to preserve single-occupancy (even in multi-dimensional extensions). However, the shuffle update enjoys the modelling advantage that individual agents never receive large

	$t^* - 1$	Probability P	t^*	W
$F_1^{(1)}$	$\begin{array}{ c c c c } \hline ? & \bullet & & ? \\ \hline \end{array}$	y	$\begin{array}{ c c c c } \hline ? & \bullet & & ? \\ \hline \end{array}$	$1 - p$
$F_2^{(1)}$	$\begin{array}{ c c c c } \hline \bullet & & & ? \\ \hline \end{array}$	$(y/(1-c))(1-c-y)$	$\begin{array}{ c c c c } \hline ? & \bullet & & ? \\ \hline \end{array}$	p
$G_1^{(1),1}$	$\begin{array}{ c c c c } \hline ? & \bullet & \bullet & \\ \hline \end{array}$	$y(1-y/c)$	$\begin{array}{ c c c c } \hline & \bullet & & \bullet \\ \hline \end{array}$	p
$G_2^{(1),1}$	$\begin{array}{ c c c c } \hline \bullet & & \bullet & \\ \hline \end{array}$	$y(y/c)(y/(1-c))$	$\begin{array}{ c c c c } \hline & \bullet & & \bullet \\ \hline \end{array}$	p^2
	$\tau_0 \quad \tau_1 \quad \tau_2 \quad \tau_3$		$\sigma_0 \quad \sigma_1 \quad \sigma_2 \quad \sigma_3$	

Fig. 1. The list of all possible transitions to a $(\sigma_1, \sigma_2) = (1, 0)$ two-cluster (highlighted in bold) at time step t^* , for the truncated process of order $n = 1$. The list is identical to that for the parallel update rule. Probabilities for the window states at time step $t^* - 1$ are denoted by P ; transition probabilities are denoted by W . Cells marked by ? can be either occupied or empty, with no effect on the P or W calculation: The state probability contribution is just a factor of one, and the movement or lack of movement of an agent in this cell cannot affect the monitored (σ_1, σ_2) two-cluster. The families of left hand column states labelled by $F_i^{(n)}$, $G_i^{(n),m}$ are the building blocks of the inductive process that follows later

numbers of consecutive turns, hence the possibility of unphysical velocities is eliminated.

In this paper we give an outline of how the *two-cluster* analysis of Schreckenberg *et al* [8], which analyses (R1,2) under the parallel update scheme, can be extended to the more complicated case of the shuffle update. The argument here is more involved than [8] because under the shuffle update, it is possible for large blocks of contiguous agents to move forward in a single time step, if their turns are served in upstream order.

Due to this increase in complexity, we use a sequence of approximations to the full model. We define the *truncated process of order n* to mean that rules (R1,2) are applied under the shuffle update scheme, with the proviso that the opportunity to move is offered only to agents who are in the first n positions of a contiguous block at the beginning of the time step. Our procedure is thus to explain briefly how two-cluster dynamics works for $n = 1$ and then explain how to extend it inductively to any truncated process of order n . Finally we let $n \rightarrow \infty$.

2 Two-Cluster Analysis For $n = 1$

This method is described fully in [8]. We suppose that the occupancy of neighbouring cell pairs is independent and we seek to compute the so-called *two-cluster* probabilities P_2 for all possible combinations of occupancy of two adjacent cells, i.e., the probabilities of two adjacent cells having states $(1, 0)$, $(0, 1)$, $(1, 1)$ and $(0, 0)$, where 0 and 1 denote empty and occupied respectively. It can be shown that all such two-cluster probabilities can be calculated from $y := P_2(1, 0)$ and hence the goal is to seek this quantity.

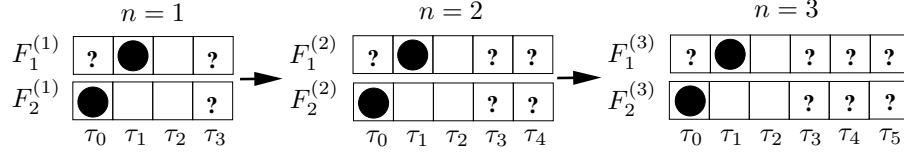


Fig. 2. The propagation of $F_i^{(n)}$ states as n increases. These states correspond to the left-hand column in Fig. 1 for $n = 1$. The added right hand cell in each window takes the value ? meaning that it can be either occupied or empty but we need not consider which, since it has no effect on the ability or probability to produce $(\sigma_1, \sigma_2) = (1, 0)$

The strategy is to list all possible configurations S at time $t^* - 1$ which can give rise to $(1, 0)$ in a monitored two-cluster at time t^* . If we can calculate the transition probability $W(S)$ for each configuration, in addition to the probability $P(S)$ of the configuration itself (which is usually expressed in terms of y), and if we assume the process has reached statistical stationarity, then we may employ conditional probability to write $y = \sum_S P(S)W(S)$, which for the truncation of order n we re-write and express in the form $f_n(y; c, p) = 0$ where c is the mean density and p is the parameter of rule (R2).

The truncated model with $n = 1$ is identical to the parallel update rule of Nagel and Schreckenberg [1], and for this standard case the two-cluster calculations are derived in detail in [8]. Note further that the two-cluster method has been shown to be exact in this case, in the sense that the spatial independence assumption for neighbouring two-clusters is exact.

For the case $n = 1$, Fig. 1 gives a listing of the relevant configurations and their probabilities P and transition probabilities W . Rather than construct $f_1(y; c, p)$ and analyse its zeroes, we instead show now how inductive arguments may be used to extend Fig. 1 to truncated processes of arbitrarily large order n .

3 Inductive Construction for Truncated Processes

We now generalise to look at the truncated process for arbitrary order n . As n is increased, we need to consider bigger families of states, because there are more ways of obtaining $(\sigma_1, \sigma_2) = (1, 0)$. The states also have wider windows, because as n increases, (σ_1, σ_2) can be affected by more sites further downstream. The key is to build the families of cell windows inductively from those with lower n . Our choice of labels for the states was chosen with this process in mind, and we treat the $F_i^{(n)}$ and $G_i^{(n),m}$ states separately as they extend in quite different ways, summarised in Figs. 2–4.

By considering Fig. 2, we observe that the $F_i^{(n)}$ states and their probabilities do not change in any substantive way, so that $P(F_i^{(n)}) = P(F_i^{(1)})$, $W(F_i^{(n)}) = W(F_i^{(1)})$, for all n .

Now we look at Fig. 3 and consider the $G_i^{(n),m}$ states. Let us look at the $n = 2$ case and see how the P and W values relate to those for $n = 1$. Note $P(G_i^{(2),1}) =$

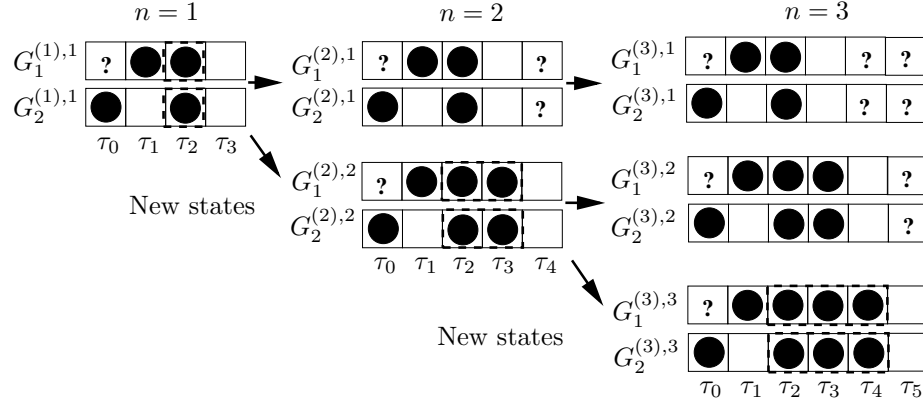


Fig. 3. Propagation of the $G_i^{(n),m}$ states as n increases. Existing states breed new ones as well as propagating in the same manner as the $F_i^{(n)}$ states (shown in Fig. 2). The characteristic feature of states which breed is that all cells with the dashed outline should be filled. For any given n , $F_i^{(n)}$ and $G_i^{(n),m}$ encompass all states capable of producing $(\sigma_1, \sigma_2) = (1, 0)$ at the next time step. The breeding of $G_i^{(n),m}$ means that the number of states increases by two each time n is increased by one

$n = 2$			$n = 3$			
	P	W		P	W	
$G_1^{(2),1}$	$y(1 - \frac{y}{c})$	$p - \frac{p^2}{2}$	→	$G_1^{(3),1}$	$y(1 - \frac{y}{c})$	$p - \frac{p^2}{2}$
$G_2^{(2),1}$	$\frac{y^3}{c(1-c)}$	p^2	→	$G_2^{(3),1}$	$\frac{y^3}{c(1-c)}$	p^2
$G_1^{(2),2}$	$y(1 - \frac{y}{c})^2$	$\frac{p^2}{2}$	↘	$G_1^{(3),2}$	$y(1 - \frac{y}{c})^2$	$\frac{p^2}{2} - \frac{p^3}{6}$
$G_2^{(2),2}$	$\frac{y^3}{c(1-c)}(1 - \frac{y}{c})$	$\frac{p^3}{2}$	↘	$G_2^{(3),2}$	$\frac{y^3}{c(1-c)}(1 - \frac{y}{c})$	$\frac{p^3}{2}$
				$G_1^{(3),3}$	$y(1 - \frac{y}{c})^3$	$\frac{p^3}{6}$
				$G_2^{(3),3}$	$\frac{y^3}{c(1-c)}(1 - \frac{y}{c})^2$	$\frac{p^4}{6}$

Fig. 4. The state and transition probabilities for the $G_i^{(n),m}$ for increasing n . We see the state probabilities unaltered along the propagating (horizontal) arrows, and gaining a factor of the conditional probability $1 - y/c$ on the breeding (diagonal) arrow. Transition probabilities gain a factor of p/n on a diagonal arrow, while $W(G_1^{(n),n-1}) = W(G_1^{(n-1),n-1})(1 - p/n)$. All others remain unchanged on the horizontal arrows

$P(G_i^{(1),1})$, since a ? contributes a factor of one to the probability, and $P(G_i^{(2),2}) = (1 - y/c)P(G_i^{(1),1})$, gaining a factor of the conditional probability $1 - y/c$ from the extra agent appearing in the blocks at τ_3 . For the transition probabilities we find $W(G_2^{(2),1}) = W(G_2^{(1),1})$. Moreover $W(G_i^{(2),2}) = (p/2)W(G_i^{(1),1})$, because

one more agent is required to move, gaining a factor of p , whilst the $1/2$ comes from the probability that the agents will update in an order which will allow the second agent to move. Finally $W(G_1^{(2),1}) = (1 - p/2)W(G_1^{(1),1})$ because it has become necessary to specify that the second agent in the block does not move, although it now can. These $n = 2$ probabilities are shown in Fig. 4. By looking at both Figs. 3 and 4, we see that the $(n = 1) \mapsto (n = 2)$ transition involved the *breeding* of states. This process generalises inductively to give the breeding behaviour at higher n values. Non-breeding $G_i^{(n),m}$ states propagate unaltered in the manner of the $F_i^{(n)}$ states.

4 General Solution for the Two-Cluster Probability

By employing conditional probability we may write

$$y_n = \sum_i P(F_i^{(1)})W(F_i^{(1)}) + \sum_{i,m} P(G_i^{(n),m})W(G_i^{(n),m}), \quad (1)$$

where y_n denotes $P_2(1, 0)$ for the truncated process of order n and $F_i^{(n)}$, $G_i^{(n),m}$ are the families of states described in the previous section. This formula, on substitution of the relevant quantities, may be rearranged in the form $f_n(y; c, p) = 0$, where

$$f_n(y_n; c, p) = p - \frac{py}{1-c} + \sum_{i=1}^n \left(\frac{-y}{c}\right)^i \sum_{j=i}^n \frac{p^j}{j!} \binom{j-1}{i-1} \left(1 - \frac{py}{1-c}\right). \quad (2)$$

By letting $n \rightarrow \infty$ we solve $f(y; c, p) = 0$ for the two-cluster probability of the full process, where

$$f(y; c, p) = -(1-p) + \frac{1}{c-y} \left(1 - \frac{py}{1-c}\right) \left(c - ye^{p(1-y/c)}\right). \quad (3)$$

In general, this equation appears to have a unique solution for y , but requires numerical solution.

5 Steady State Velocities and Flow Rates

We now find the mean velocity and flow rate in terms of the two-cluster probability y . We proceed by using y to find the probability distribution of the length of the block to which an agent chosen at random belongs. This quantity may be constructed from conditional two-cluster probabilities in the form

$$\mathcal{P}_l = \left(\frac{y}{c}\right)^2 \left(1 - \frac{y}{c}\right)^{l-1}, \quad (4)$$

where l is the length of the block in question. We now use the fact that the agent is equally likely to be in any position within the block, and we sum the

probability that it moves from the k th position over all $k = 1, 2, \dots, l$ positions. By using (4), we thus obtain the mean velocity (equivalent to the probability that an agent chosen at random moves) in the form

$$\begin{aligned} \hat{v} &= \sum_{l=1}^{\infty} l \mathcal{P}_l \frac{1}{l} \sum_{k=i}^l P(\text{block serves at least } k \text{ agents}) \\ &= \left(\frac{y}{c-y} \right) \left(\exp \left(\frac{p}{c} (c-y) \right) - 1 \right). \end{aligned} \quad (5)$$

We can therefore write down flow rate

$$q = \left(\frac{cy}{c-y} \right) \left(\exp \left(\frac{p}{c} (c-y) \right) - 1 \right), \quad (6)$$

as the product of the system density and mean velocity.

6 Conclusion

By extending the two-cluster analysis of the well-known parallel update model [1,8], we have been able to derive expressions for steady state distributions and flow rates of the more complicated shuffle update case. The results found here agree with the recent paper of Wölki *et al* [5] who employed a car-oriented mean field (COMF) method, as opposed to the site-oriented (SOMF) method that we use. However, it remains to be shown whether exactness, i.e. the spatial independence of neighbouring clusters, holds for the full model and the truncated processes of order $n > 1$.

References

1. K. Nagel, M. Schreckenberg: *Journal de Physique I* **2**, 2221 (1992)
2. N. Rajewsky, L. Santen, A. Schadschneider, M. Schreckenberg: *J. Stat. Phys.* **92**, 151 (1998)
3. D. Chowdhury, L. Santen, A. Schadschneider: *Phys. Rep.* **329**, 199 (2000)
4. G. Lunt: *Cellular Automaton Models for Flows Without Momentum*. Masters Thesis, University of Bristol (2001)
5. M. Wölki, A. Schadschneider, M. Schreckenberg: preprint, arXiv:cond-mat/0509546v1 21 Sep 2005
6. D. Smith, R. E. Wilson: preprint
7. B. Derrida, E. Domany, D. Mukamel: *J. Stat. Phys.* **69**, 667 (1992)
8. M. Schreckenberg, A. Schadschneider, K. Nagel, N. Ito: *Phys. Rev. E* **51**, 2939 (1995)