LETTER TO THE EDITOR

A cellular-automata model of flow in ant-trails: non-monotonic variation of speed with density

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Abstract. Generically, in models of driven interacting particles the average speed of the particles decreases monotonically with increasing density. We propose a counter-example, motivated by the motion of ants in a trail, where the average speed of the particles varies *non-monotonically* with their density because of the coupling of their dynamics with another dynamical variable. These results, in principle, can be tested experimentally.

Particle-hopping models, formulated usually in terms of cellular automata (CA) [1], have been used to study the spatio-temporal organization in systems of interacting particles driven far from equilibrium [2, 3, 4, 5] which include, for example, vehicular traffic [6, 7]. In general, the inter-particle interactions tend to hinder their motions so that the average speed decreases *monotonically* with the increasing density of the particles. In this letter we report a counter-example, motivated by the motion of ants in a trail [8], where the average speed of the particles varies *non-monotonically* with their density because of the coupling of their dynamics with another dynamical variable.

The ants communicate with each other through a process called chemotaxis by dropping a chemical (generically called *pheromone*) on the substrate as they crawl forward [9, 10]. Although we cannot smell it, the trail pheromone sticks to the substrate long enough for the other following sniffing ants to pick up its smell and follow the trail. In this letter we develope a CA model which may be interpreted as a model of unidirectional flow in an ant-trail. Rather than addressing the question of the emergence of the ant-trail, we focus attention here on the traffic of ants on a trail which has already been formed.

Each site of our one-dimensional ant-trail model represents a cell that can accomodate at most one ant at a time (see fig.1). The lattice sites are labelled

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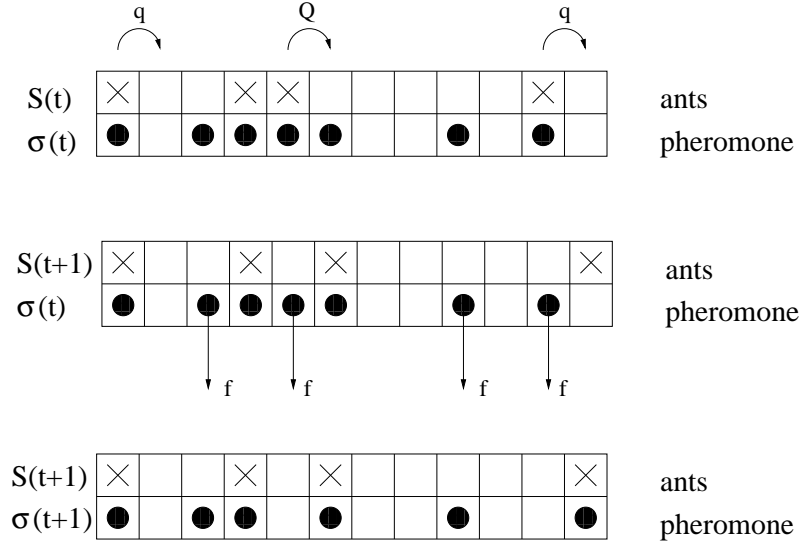
Figure 1. Schematic representation of typical configurations; it also illustrates the update procedure. Top: Configuration at time t, i.e. *before* stage I of the update. The non-vanishing hopping probabilities of the ants are also shown explicitly. Middle: Configuration *after* one possible realisation of *stage I*. Two ants have moved compared to the top part of the figure. Also indicated are the pheromones that may evaporate in stage II of the update scheme. Bottom: Configuration *after* one possible realization of *stage II*. Two pheromones have evaporated and one pheromone has been created due to the motion of an ant.

by the index i ($i = 1, 2, ..., L$); L being the length of the lattice. We associate two binary variables S_i and σ_i with each site i where S_i takes the value 0 or 1 depending on whether the cell is empty or occupied by an ant. Similarly, $\sigma_i = 1$ if the cell i contains pheromone; otherwise, $\sigma_i = 0$. Thus, we have two subsets of dynamical variables in this model, namely, $\{S(t)\} \equiv (S_1(t), S_2(t), ..., S_i(t), ..., S_L(t))$ and $\{\sigma(t)\} \equiv (\sigma_1(t), \sigma_2(t), ..., \sigma_i(t), ..., \sigma_L(t))$. The instantaneous state (i.e., the configuration) of the system at any time is specified completely by the set $(\{S\}, \{\sigma\})$.

We assume that the ant does not move backward; its forward-hopping probability, however, is higher if it smells pheromone ahead of it. The state of the system is updated at each time step in *two stages*. At the end of stage I we obtain the subset $\{S(t+1)\}$ at the time step $t+1$ using the full information $(\{S(t)\}, \{\sigma(t)\})$ at time t. At the end of the stage II we obtain the subset $\{\sigma(t+1)\}$ at the time step $t+1$ using the subsets $\{S(t+1)\}$ and $\{\sigma(t)\}$.

Stage I: The subset $\{S\}$ (i.e., the *positions* of the ants) is updated *in parallel* according to the following rules:

If $S_i(t) = 1$, i.e., the cell i is occupied by an ant at the time step t, then the ant hops forward to the next cell $i+1$ with

$$\text{probability} = \begin{cases} Q & \text{if } S_{i+1}(t) = 0 \text{ but } \sigma_{i+1}(t) = 1, \\ q & \text{if } S_{i+1}(t) = 0 \text{ and } \sigma_{i+1}(t) = 0, \\ 0 & \text{if } S_{i+1}(t) = 1. \end{cases} \tag{1}$$

where, to be consistent with real ant-trails, we assume $q < Q$.

Stage II: The subset $\{\sigma\}$ (i.e., the presence or absence of pheromones) is updated *in parallel* according to the following rules:

If $\sigma_i(t) = 1$, i.e., the cell i contains pheromone at the time step t, then it contains pheromone also in the next time step, i.e., $\sigma_i(t+1) = 1$, with

$$\text{probability} = \begin{cases} 1 & \text{if } S_i(t+1) = 1 \text{ at the end of stage I,} \\ 1 - f & \text{if } S_i(t+1) = 0 \text{ at the end of stage I.} \end{cases} \tag{2}$$

where f is the pheromone evaporation probability per unit time.
On the other hand, if $\sigma_i(t) = 0$, i.e., the cell i does not contain pheromone at the time step t, then

$$\sigma_i(t+1) = 1 \quad \text{iff } S_i(t+1) = 1 \text{ at the end of stage I.} \tag{3}$$

In certain limits our model reduces to the Nagel-Schreckenberg (NS) model ¶ [11] which is the minimal particle-hopping model for vehicular traffic on freeways. The most important quantity of interest in the context of flow properties of the traffic models is the *fundamental diagram*, i.e., the flux-versus-density relation, where flux is the product of the density and the average speed. For a hopping probability q_{NS} at a given density c the exact flux $F(c)$ in the NS model is given by [6, 12]

$$F_{NS}(c) = \frac{1}{2}\left[1 - \sqrt{1 \; - \; 4\, q_{NS}\, c(1-c)}\right]. \tag{4}$$

which reduces to $F_{NS}(c) = \min(c, 1 - c)$ in the deterministic limit $q_{NS} = 1$.

Note that in the two special cases $f = 0$ and $f = 1$ the ant-trail model becomes identical to the NS model with $q_{NS} = Q$ and $q_{NS} = q$, respectively. Extensions of the NS model have been used not only to capture different aspects of vehicular traffic [6] but also to simulate pedestrian dynamics [7, 13, 14]. In a closely related CA model for pedestrian dynamics [14] the floor fields, albeit *virtual*, are analogs of the pheromone fields $\{\sigma\}$ in the ant-trail model. However, in the pedestrian model there is no exclusion principle for the floor field.

The ant-trail model we propose here is also closely related to the bus route model (BRM) [15, 16]. The variables S and σ in the ant-trail model are the analogs of the variables representing the presence (or absence) of bus and passengers, respectively, in the BRM. Because of the periodic boundary conditions, the number of ants and buses are conserved while the pheromone and passengers are not conserved. However, unlike the BRM, the pheromones are not dropped independently from outside, but by the ants themselves. Another crucial difference between these two models is that in the bus-route model $Q < q$ (as the buses must *slow down* to pick up the waiting passengers) whereas in our ant-trail model $Q > q$ (because an ant is more likely to move forward if it smells pheromone ahead of it).

In fig.2 we show the fundamental diagrams obtained by extensive computer simulations of the ant-trail model for several values of f. The most unusual features of the fundamental diagrams shown in fig.2 are that, over an intermediate range of

¶ By the term 'NS model' in this letter we shall always mean the NS model with maximum allowed speed *unity*, so that each particle can move forward, by one lattice spacing, with probability q_{NS} if the lattice site immediately in front is empty.

(a)

(b)
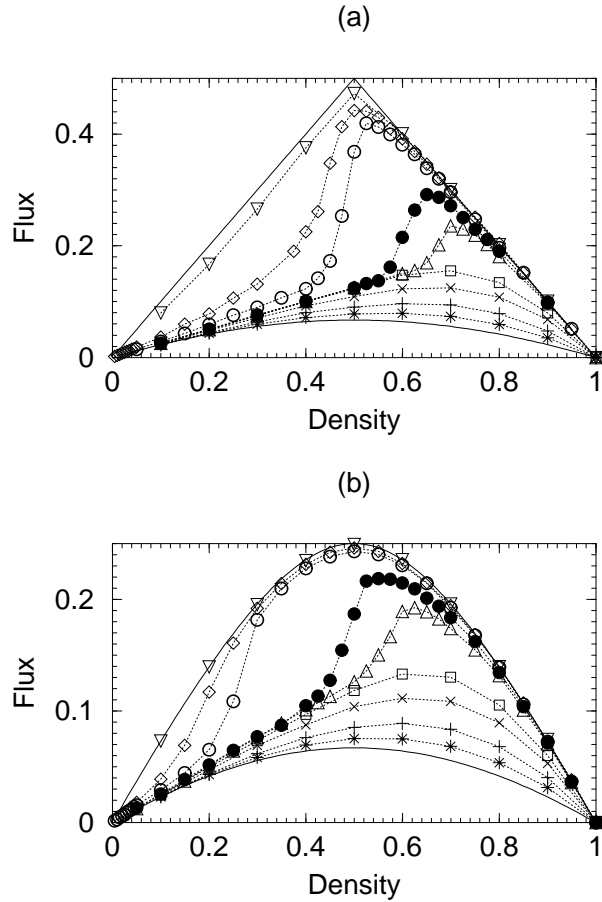
Figure 2. The flux of ants plotted against their densities for the parameters (a) $Q = 1, q = 0.25$ and (b) $Q = 0.75, q = 0.25$. The discrete data points corresponding to $f = 0.0001(\triangledown)$, $0.0005(\diamond)$, $0.001(\circ)$, $0.005(\bullet)$, $0.01(\triangle)$, $0.05(\square)$, $0.10(\times)$, $0.25(+)$, $0.50(*)$ have been obtained from computer simulations; the dotted lines connecting these data points merely serve as the guide to the eye. The two continuous solid curves at the top and bottom correspond to the flux in the NS model for $q_{NS} = 1.0$ and $q_{NS} = 0.25$, respectively, in (a) and for $q_{NS} = 0.75$ and $q_{NS} = 0.25$, respectively, in (b).

values of f (for example, $f = 0.0005, 0.001, 0.005, 0.01$ in fig.2) the flux in the low-density limit $c \to 0$ is very close to that for the NS model with $q_{NS} = q$ whereas in the high-density limit $c \to 1$ the flux for the same f is almost identical to that for the NS model with $q_{NS} = Q$. These unusual features of the fundamental diagrams arise from the *non-monotonic* variation of the average velocity with the density of the ants (see fig.3).

The presence of the pheromone essentially introduces an *effective hopping probability* $q_{\text{eff}}(c)$, which depends on the ant density c. The particle-hole symmetry (and hence the symmetry of the fundamental diagram about $c = 1/2$) observed in the special limits $f = 0$ and $f = 1$, are broken by the c-dependent effective hopping

(a)

(b)
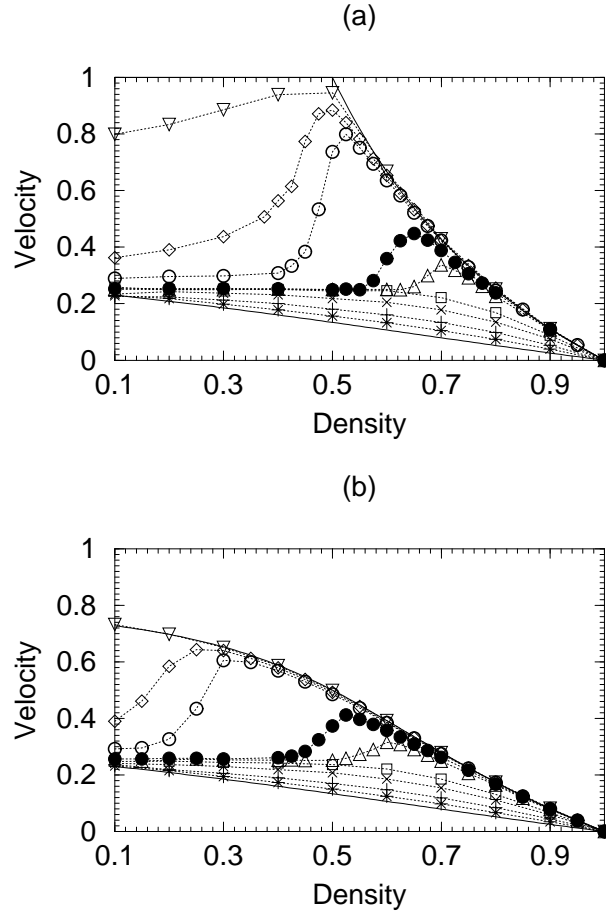
Figure 3. The average velocity of ants plotted against their densities for the parameters (a) $Q = 1, q = 0.25$ and (b) $Q = 0.75, q = 0.25$. Same symbols in the figs.2 and 3 correspond to the same values of the parameter f.

probability for all $0 < f < 1$ leading to a peak at $c > 1/2$. Furthermore, the analysis of correlation functions reveals some interesting clustering properties which will be studied in detail in a future publication [17].

The qualitative features of the c-dependence of q_{eff} can be reproduced by an analytical argument based on a *mean-field approximation* (MFA) [17]. In this MFA, let us assume that all the ants move with the mean velocity $\langle V \rangle$ which depends on the density c of the ants as well as on f; although, to begin with, the nature of these dependences are not known we'll obtain these self-consistently.

Let us consider a pair of ants having a gap of n sites in between. The probability that the site immediately in front of the following ant contains pheromone is $(1 - f)^{n/\langle V \rangle}$ since $\frac{n}{\langle V \rangle}$ is the average time since the pheromone has been dropped. Therefore, in the MFA the effective hopping probability is given by

$$q_{\text{eff}} = Q(1 - f)^{n/\langle V \rangle} + q\{1 - (1 - f)^{n/\langle V \rangle}\}. \tag{5}$$

We replace n by the corresponding exact global mean separation $\langle n \rangle = \frac{1}{c} - 1$ between

successive ants. Moreover, since $\langle V \rangle$ is identical to q_{eff}, we get the equation

$$\left(\frac{q_{\text{eff}} - q}{Q - q} \right)^{q_{\text{eff}}} = (1 - f)^{\frac{1}{c} - 1} \tag{6}$$

which is to be solved self-consistently for q_{eff} as a function of c for a given f. Note that the equation (6) implies that, for *given f*, $\lim_{c \to 0} q_{\text{eff}} = q$; this reflects the fact that, in the low-density regime, the pheromone dropped by an ant gets enough time to completely evaporate before the following ant comes close enough to smell it. Equation (6) also implies $\lim_{c \to 1} q_{\text{eff}} = Q$; this captures the sufficiently high density situations where the ants are too close to miss the smell of the pheromone dropped by the leading ant unless the pheromone evaporation probability f is very high. Similarly, from (6) we get, for *given c*, $\lim_{f \to 1} q_{\text{eff}} = q$ and $\lim_{f \to 0} q_{\text{eff}} = Q$ which are also consistent with intuitive expectations.

In view of the fact [10] that the lifetime of pheromones can be as long as thirty to sixty minutes, the interesting regime of f ($\ll 1$), where the average velocity varies non-monotonically with the ant density, seems to be experimentally accessible. We hope that the non-trivial predictions of this minimal model of ant-trail will stimulate experimental measurement of the ant flux as a function of the ant density for different rates of pheromone evaporation by using different varieties of ants [8].

Acknowledgment

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