Memory and self-induced shocks in an evolutionary population competing for limited resources

Roland Kay and Neil F. Johnson

Physics Department, Oxford University, Parks Road, Oxford, OX1 3PU, U.K.
(Dated: February 2, 2008)

We present a detailed discussion of the role played by memory, and the nature of self-induced shocks, in an evolutionary population competing for limited resources. Our study builds on a previously introduced multi-agent system [Phys. Rev. Lett 82, 3360 (1999)] which has attracted significant attention in the literature. This system exhibits self-segregation of the population based on the ‘gene’ value $p$ (where $0 \leq p \leq 1$), transitions to ‘frozen’ populations as a function of the global resource level, and self-induced large changes which spontaneously arise as the dynamical system evolves. We find that the large, macroscopic self-induced shocks which arise, are controlled by microscopic changes within extreme subgroups of the population (i.e. subgroups with ‘gene’ values $p \sim 0$ and $p \sim 1$).

I. INTRODUCTION

The dynamical behavior of a population of objects or ‘agents’ (e.g. software or hardware modules, cellular organisms such as bacteria or viruses, human beings, animals) is of interest across a range of disciplines. Physics is arguably luckier than most disciplines in that the ‘agents’ of interest (i.e. particles) do not adapt their behavior according to past failure, hence evolving new sets of rules as time progresses. Nor do the agents in question have any individual memory. Biological and social disciplines are not so lucky. Through a desire to develop a minimal model which could incorporate such features into a manageable yet non-trivial system, Arthur introduced the so-called ‘El Farol’ Bar Problem, which concerns the repeated competition between bar-goers to attend a popular bar with limited seating. Challet and Zhang subsequently introduced a binary version of this bar problem for the case where the amount of resource (e.g. number of seats) is just less than half the number of agents (e.g. possible attendees). This system is referred to as the Minority Game.

The Minority Game does not allow an agent to continuously evolve new strategies and hence explore the entire strategy space. The Minority Game is also essentially deterministic, apart from occasional coin-tosses which are used to break ties in strategy scores. Furthermore the resource level is set at just less than half the number of agents, so that there are always more losers than winners. To help overcome these limitations, Johnson et al. introduced a stochastic version of the Minority Game which is subsequently referred to as the Genetic Model, in which an agent’s strategy (characterized by a ‘gene’ value $p$) can evolve indefinitely in time, and is in principle allowed to access the entire space of strategies (i.e. all $p$ values). The resulting Genetic Model has provoked much interest in the literature (for example see Refs. 3 4 5 6 7 8).

II. EFFECTS OF MEMORY IN THE GENETIC MODEL

Various papers have made claims with regard to the role of memory in the Genetic Model. To date though, no one has performed a detailed analysis of this problem. In this section we present such an analysis which involves comparing the behavior of the original model with that of a memoryless variant. The results presented here for the Genetic Model are reminiscent of earlier results for the Minority Game. In particular, Hart et al. showed that a crowd-anticrowd theory which assumes random history, provides a quantitative description of the time-averaged fluctuations in the Minority Game. Subsequently Cavagna demonstrated numerically that the time-averaged fluctuations were indeed largely unaffected if the global history was replaced with randomly generated data.

As commented in the original paper of Johnson et al. and confirmed by Burgos et al., the self-segregation observed in the Genetic Model is insensitive to changes in an agent’s memory length $m$.

In this paper we present a detailed discussion of the role of memory in the Genetic Model. We also explain the origin of the remarkable step-like structure in the global output time series as a function of the resource level, which was first observed in by Johnson et al. in Ref. 3. We then introduce (Sec. III) a new variant of the Genetic Model in which the number of agents competing at a given time step, is allowed to fluctuate. Because of the analogy with the Grand Canonical Ensemble in physics, we shall refer to this model as the ‘Grand Canonical Genetic Model’ (GCGM) By considering versions of the GCGM both with and without memory, we shall investigate the endogenous (i.e. self-induced) large changes which arise in the system. These large changes represent abrupt macroscopic ‘shocks’, and occur with a greater probability than would be expected based on random walk statistics. We provide a detailed analysis of the mechanism that generates these large changes.

*Electronic address: roland.kay@physics.ox.ac.uk
Ceva and Burgos investigated explicitly the role of memory in the Genetic Model, however the results are restricted to a comparison of the gene value distributions in the minority case, in which the amount of resource is just less than half the number of agents. In contrast, in this section we shall treat the general case, in which the amount of resource is unrestricted, and provide some theoretical analysis to explain the differences that we shall observe between the two models. We shall show in Secs. III C and III H that the observation that the gene value distributions are identical only holds in the special case considered in Ref. [5]. Furthermore, we shall show that the feedback introduced by the existence of memory does influence the behavior of the model in that it controls the time-average of the prediction (Sec. II G) and introduces autocorrelations into the mean attendance time series (Sec. II H). By comparing and contrasting the memoryless Genetic Model with the original model we shall be able to make some important observations about the memory’s true significance. We shall also answer some important questions as to the extent to which memory is of benefit to the agents and the system as a whole.

Before going on to describe the Genetic Model, we note that all of the numerical results presented in this paper were obtained using the model parameters listed in Table I unless otherwise stated. Similarly all time averages are taken over the period 10000 < t < 60000. The first 10 000 time steps being neglected to allow any transients due to the initial conditions to die away.

### A. Original Genetic Model

In this section we present expressions for some of the most basic quantities in the original Genetic Model, which includes the memory. In Sec. III B we shall consider the equivalent expressions in the memoryless variant. We start with a brief summary of the Genetic Model. Fuller details are given in Ref. [2].

The Genetic Model consists of a population of agents who must decide at every time step between two possible choices. We shall refer to the decision of an agent i as its action, a_{i;t}. Each agent is defined by a gene value, p_{i;t}, which can take any value 0 \leq p_{i;t} \leq 1. At each time step the model makes a prediction, h_t, of the outcome of the time step available to all of the agents. Each agent chooses its action to be equal or opposite to this prediction with probabilities p_{i;t} and 1 − p_{i;t} respectively. h_t is calculated based on a global memory that the model maintains of the outcome of the previous m time steps and the assumption that patterns that have occurred in the time series of these outcomes in the past will recur in the future. The parameter m is known as the memory length. The outcome of each time step is determined based on the actions of all of the agents. From now on we shall refer to the outcome as the global action at time t, A_t.

Agent gene values are not constant with time. Each agent maintains a record of its score, s_{i;t}, which determines when it changes its gene value. At every time step, s_{i;t} increases by one unit if a_{i;t} = +A_t and decreases otherwise. If s_{i;t} = −D then the agent mutates. The parameter D is known as the death score. When an agent mutates it chooses a new gene value at random from a range of values of width 2r centered on the old gene value. The parameter r is known as the mutation range.

Let the possible values taken by h_t be −1 and +1. Agent i makes a choice to follow the prediction (a_{i;t} = +h_t) with probability p_{i;t} or to refuse it (a_{i;t} = −h_t) with probability 1 − p_{i;t}. There are two opposite definitions of the global action A_t used in the literature. For example, Ref. [4] defines A_t by analogy with Zhang and Arthur’s Bar model, to be the state of the bar at time t. Thus, A_t = +1 would denote an overcrowded bar and the optimal action of each agent would be to stay at home (i.e. a_{i;t} = −1). However, in this paper we shall adopt the convention of Ref. [2] whereby A_t represents the optimal decision of each agent at time t. The global action A_t is given, in terms of a model parameter l, which can take values 0 \leq l \leq 1, by:

\[
A_t = \begin{cases} 
+1 & n_t^{l+1} \leq Nl \\
-1 & n_t^{l+1} > Nl
\end{cases}
\]  

where:

\[
n_t^{l+1} = \frac{1}{2} \left( \sum_i a_{i;t} + N \right).
\]

In other words, n_t^{l+1} is the number of agents for which a_{i;t} = +1. We shall refer to l as the resource level.

Let \{p_{i;t}\}_i denote the set of values of p_{i;t} for all agents at time t. It is easy to show that the ensemble average number of agents following the prediction (n_t^{l+h_t}) is given by:

\[
\langle n_t^{l+h_t} \rangle = N\overline{p}_t \quad \text{where:} \quad \overline{p}_t = \frac{1}{N} \sum_{i=1}^{N} p_{i;t}.
\]

In equilibrium, where the population evolves such that \overline{p}_t is approximately constant, the ensemble average \langle n_t^{l+h_t} \rangle and the time average \langle n_t^{l+h_t} \rangle_t will coincide. Thus:

\[
\langle n_t^{l+h_t} \rangle_t \approx N\langle \overline{p}_t \rangle_t.
\]

### B. Memoryless Genetic Model

In this section we introduce a memoryless variant of the original Genetic Model. In contrast to the original

| Table I: Parameters used to generate numerical data. |
|-----------------------------------------------------|
| Number of agents: N = 501 | Memory length: m = 4 |
| Death score: D = 4 | Mutation range: r = 0.2 |
model described above, where the gene value of the \( i \)th agent \( p_i \) gives the probability of it choosing to follow the prediction \( a_{i,t} = +h_t \), in the memoryless model \( p_i \) gives the probability that \( a_{i,t} = +1 \) directly. With this modification the prediction \( h_t \) and hence the global memory that produce it become redundant and can be removed from consideration. The agents in this variant are memoryless, by which we mean that their actions \( a_{i,t} \) at time \( t \) are independent of the state of the model at earlier times. \( a_{i,t} \) is dependent only on \( p_{i,t} \). An equivalent way of considering this is to take \( h_t = +1 \) \( \forall t \). The global action \( A_t \) and the number of agents attending the bar \( n^{+1}_t \) are unchanged and so are given by Eqs. 1 and 2 as before. However, Eq. 3 becomes:

\[
\langle n_t^{+1} \rangle_t = N \langle \mathcal{P}_t \rangle_t .
\]

C. Comparison of the performance of the original and memoryless models

We shall now compare the performance of the two models. In order to quantify performance we define \( U_t \) to be the total number of points scored by all of the agents at time \( t \). Therefore we are considering the performance of the system as a whole, rather than that of individual agents. If we consider the models to be analogous to an economic system then the question that we are investigating becomes, to what extent can the agents in this system exploit the potential wealth available to them as a population. Note that in Ref. [4] Burgos et al. treat the memoryless Genetic Model in terms of a cost function given by the second moment of \( n_t^{+1} \) with respect to \( NL \). However this cost function is symmetric in that it assigns an equal cost to deviations of \( n_t^{+1} \) from \( NL \) of opposite signs. As we shall see, \( U_t \) is not symmetric about \( NL \) and hence can distinguish between positive and negative deviations.

1. Original Genetic Model

First we shall derive expressions for \( U_t \) in the model with memory. Later we will see how these expressions are modified in the absence of the memory. From Eq. 6 the condition that \( A_t = +1 \) is:

\[
\begin{align*}
    n_t^{+h_t} &\leq NL & \text{if } h_t = +1 \\
    n_t^{+h_t} &\geq N(1 - l) & \text{if } h_t = -1 .
\end{align*}
\]

Now consider the total number of points scored by the agents, \( U_t \). Agents for which \( a_{i,t} = +A_t \) will gain one point whereas agents for which \( a_{i,t} = -A_t \) will lose. If \( h_t = +1 \) and \( A_t = +1 \) it will be the \( n_t^{+h_t} \) agents who choose to follow \( h_t \) who will gain. If \( A_t = -1 \), then the \( N - n_t^{+h_t} \) agents who choose to refute \( h_t \) will gain. Thus, using Eq. 6, we have:

For \( h_t = +1 \):

\[
U_t(n_t^{+h_t}) = \begin{cases} 
    2n_t^{+h_t} - N & \text{if } n_t^{+h_t} \leq NL \\
    -2n_t^{+h_t} + N & \text{if } n_t^{+h_t} > NL .
\end{cases}
\]  

(7)

When \( h_t = -1 \) and \( A_t = +1 \) it will be the \( N - n_t^{+h_t} \) agents who choose to refute the prediction who will gain and vice-versa for \( A_t = -1 \). Thus, for \( h_t = -1 \) the above expression becomes:

For \( h_t = -1 \):

\[
U_t(n_t^{+h_t}) = \begin{cases} 
    -2n_t^{+h_t} + N & \text{if } n_t^{+h_t} \geq N(1 - l) \\
    2n_t^{+h_t} - N & \text{if } n_t^{+h_t} < N(1 - l) .
\end{cases}
\]

(8)

The expressions in Eqs. 7 and 8 are plotted in Fig. 1. The black and white circles represent the value of \( n_t^{+h_t} \) at which \( U_t \) is a maximum for \( h_t = +1 \) and \( h_t = -1 \) respectively. We shall call the value of \( n_t^{+h_t} \) at which \( U_t \) is a maximum the optimal value and denote it by \( \text{opt}[n_t^{+h_t}] \). From Fig. 1 we can see that \( \text{opt}[n_t^{+h_t}] \) is given by:

For \( l < 0.5 \):

\[
\text{opt}[n_t^{+h_t}] = \begin{cases} 
    NL + 1 & \text{if } h_t = +1 \\
    N(1 - l) - 1 & \text{if } h_t = -1 .
\end{cases}
\]

(9)

For \( l > 0.5 \):

\[
\text{opt}[n_t^{+h_t}] = \begin{cases} 
    NL & \text{if } h_t = +1 \\
    N(1 - l) & \text{if } h_t = -1 .
\end{cases}
\]

(10)

The most important feature of this equation to recognize is that, in general, there is no unique value of \( \text{opt}[n_t^{+h_t}] \) independent of \( t \). Only if \( h_t = +1 \) or \( -1 \) \( \forall t \) would such a unique solution exist.

We note in passing that since \( N = n_t^{+1} + n_t^{-1} \) the optimal value of \( n_t^{+1} \) in the original model is:

\[
\text{opt}[n_t^{+1}] = NL .
\]

(11)

In contrast to \( \text{opt}[n_t^{+h_t}] \), the optimal value of \( n_t^{+1} \) is independent of \( t \). Nevertheless the most important quantity for the analysis that we present here is \( \text{opt}[n_t^{+h_t}] \) in the case of the original model since, as we shall see later, it is the value of \( n_t^{+h_t} \) that the agents can directly control and not that of \( n_t^{+1} \).

Ref. [7] demonstrated the existence of so-called frozen regimes which exist when \( l \) lies outside of the region bounded by two critical values, which we shall label here \( l_{c1} \) and \( l_{c2} \). These regimes were described as quenched by Burgos et al. in Ref. [7]. The frozen regime obtains when \( l < l_{c1} \) or \( l > l_{c2} \). The behavior of the Genetic Model in these regimes is well understood [4, 7], therefore we shall restrict ourselves to a consideration of the dynamic regime. In what follows, unless otherwise stated, \( l \) takes values on the interval \( l_{c1} < l < l_{c2} \). Therefore, inequalities such as \( l < 0.5 \) should be taken as shorthand for \( l_{c1} < l < 0.5 \).
Compared with the variation of $h_t$, agent mutation is a slow process. The value of $h_t$ changes on a timescale of $\Delta t \sim 1$ while agents mutate on a time scale $\Delta t \gg D$. The result of this is that we should not expect the agents to be sensitive to the instantaneous value of $U_t$ given in Eqs. (7) and (8). They will only be sensitive to the time average $\langle U_t \rangle$. Translated to the conventions used here, Ref. [4] found that:

$$\langle h_t \rangle = \begin{cases} +0.5 & l > 0.5 \\ -0.5 & l < 0.5 \end{cases} . \quad (12)$$

Therefore, for $l < 0.5$, $h_t = +1$ for a fraction 0.25 of the time steps whereas the fraction is 0.75 for $l > 0.5$. Thus we can calculate the following expression for $\langle U_t(n_{t,hi}) \rangle$:

For $l < 0.5$:

$$\langle U_t \rangle = \begin{cases} 2n_{t,hi} - N & n_{t,hi} \leq Nl \\ n_{t,hi} - N/2 & Nl < n_{t,hi} < N \langle 1 - l \rangle \\ -2n_{t,hi} + N & n_{t,hi} \geq N \langle 1 - l \rangle \end{cases} . \quad (13)$$

For $l > 0.5$:

$$\langle U_t \rangle = \begin{cases} 2n_{t,hi} - N & n_{t,hi} < N \langle 1 - l \rangle \\ n_{t,hi} - N/2 & N \langle 1 - l \rangle \leq n_{t,hi} < Nl \\ -2n_{t,hi} + N & n_{t,hi} \geq Nl \end{cases} . \quad (14)$$

This expression is plotted in Fig. 2a. From the figure we can see that the optimal value of $n_{t,hi}$ that maximizes $\langle U_t(n_{t,hi}) \rangle$ is given by:

$$\text{opt}[n_{t,hi}] = \begin{cases} N \langle 1 - l \rangle - 1 & l < 0.5 \\ Nl & l > 0.5 \end{cases} . \quad (15)$$

Note that although we have assumed the values given in Eq. (12) for $\langle h_t \rangle$, the values of opt$[n_{t,hi}]$ given in the above equation in fact only depend upon the signs of the values of $\langle h_t \rangle$. The significance of this will become apparent in Sec. 11C.

Let $P_{i,t}$ be the probability that $n_{t,hi} = i$. Lo et al. demonstrated that $P_{i,t}$ will be approximately Gaussian with mean $\mu = \langle n_{t,hi} \rangle = N\overline{p}_t$ and standard deviation $\sigma = \sqrt{\sum_i p_{i,t}(1 - p_{i,t})}$. From Eq. (16) it follows that the optimal form of $P_{i,t}$ will obtain if $\overline{p}_t$ is as given by the following equation and $\sigma = 0$:

$$\text{opt}[\overline{p}_t] = \begin{cases} 1 - l - \frac{1}{N} & l < 0.5 \\ l & l > 0.5 \end{cases} . \quad (16)$$

The term $\frac{1}{N}$ results from the asymmetry of the condition in Eq. (15) which determines $A_t$ in terms of $n_{t,hi}$. For $l < l_c$ in the case of $N \gg 1$ considered here $\frac{1}{N} \ll 1 - l$ and so we can neglect this term. $\sigma = 0$ if $\{p_{i,t}\}_i$ contains only the values 0 and 1. Let $P(x)$ be the distribution of $\{p_{i,t}\}_i$ such that $NP(x)dx$ is the probability that if an agent $i$ is chosen at random from the set $\{p_{i,t}\}_i$ then $x \leq p_{i,t} \leq x + dx$. The optimal form for $P(x)$ is then:

$$P(x) = (1 - \text{opt}[\overline{p}_t])\delta(x) + \text{opt}[\overline{p}_t]\delta(1 - x) . \quad (17)$$

This represents a distribution which is zero everywhere except for peaks at $x = 0$ and $x = 1$. The relative heights of the peaks being such that $\mu = \text{opt}[\overline{p}_t]$.

It is well known that in the long time limit where $t \rightarrow \infty$ the population of agents evolves such that $P(x)$ is strongly peaked about $x = 0$ and $x = 1$ and $\overline{p}_t$ takes the value given by Eq. (16). Although the agents never manage to achieve a form such that the standard deviation $\sigma(n_{t,hi},t)$ is exactly zero, they do approach the optimal distribution represented by Eq. (17). Thus, we can see that the population of agents is capable of evolving such that $P_{i,t}$ is close to its optimal form and
the time series of values of \( n_t^{h_t} \) contains values clustered around the optimal value \( \text{opt}[n_t^{h_t}] \) given by Eq. 15.

2. Memoryless Genetic Model

In this section we shall see how the above analysis applies to the memoryless variant of the model. \( U_t \) in the memoryless model is given by Eq. 7 above. Thus:

\[
U_t(n_t^{+1}) = \begin{cases} 
2n_t^{+1} - N & \text{if } n_t^{+1} \leq NL \\
-2n_t^{+1} + N & \text{if } n_t^{+1} > NL
\end{cases} \tag{18}
\]

Equation 18 is plotted in Fig. 2b. Once again the black circle represents the value of \( n_t^{+1} \) at which \( U_t \) is a maximum. From the figure we can see that the optimal value of \( n_t^{+1} \) is now:

\[
\text{opt}[n_t^{+1}] = \begin{cases} 
NL + 1 & \text{if } l < 0.5 \\
NL & \text{if } l > 0.5
\end{cases} \tag{19}
\]

Unlike the original Genetic Model, this optimal value of \( n_t^{+1} \) is independent of \( t \). As before, the optimal form of \( \Pi_{i,t} \) will be that for which \( \sigma = \sigma(n_t^{+1}, t) = 0 \) and \( \mu = \langle n_t^{+1} \rangle t = N \overline{p}_t \) with \( \overline{p}_t \) given by:

\[
\text{opt}[\overline{p}_t] = \begin{cases} 
l + \frac{1}{2} & \text{if } l < 0.5 \\
l & \text{if } l > 0.5
\end{cases} \tag{20}
\]

Note that, from Eqs. 10 and 20, this will mean that the gene value distribution of the agents for \( l < 0.5 \) in the original and memoryless models will not be identical, but will be related by the transformation \( \{p_{i,t}\} \rightarrow \{1-p_{i,t}\} \).

3. Direct comparison of the models

In this section we shall compare the value of \( U_t(\text{opt}[n_t^{h_t}]) \) in the original Genetic Model with that of \( U_t(\text{opt}[n_t^{h_t}]) \) in the memoryless Genetic Model in order to establish what effect the memory has on the performance of the model. In both the original Genetic Model with memory and the memoryless Genetic model, the agents are rewarded based on the value of \( n_t^{+1} \). This is because the value of the global action is determined from the condition on \( n_t^{+1} \) in Eq. 14 and an agent \( i \) gains or loses one point depending on whether \( a_{i,t} = \pm A_i \). There is, however, one difference between the two models that will be extremely important in what follows. The population of agents can control \( \Pi_{i,t} \) through their effect on \( \overline{p}_t \) and \( \sigma = \sqrt{\sum_i p_{i,t}(1-p_{i,t})} \). In the memoryless model \( \Pi_{i,t} \) represents the probability distribution for \( n_t^{+1} \) whereas in the original model \( \Pi_{i,t} \) represents the distribution function for \( n_t^{h_t} \). The result of this is that in the memoryless model the population of agents can directly control the values that occur in the time series of \( n_t^{+1} \) whereas in the original model they can only control the values of \( n_t^{h_t} \).

In the latter case \( n_t^{+1} \) will also depend on the value of \( h_t \) over which the agents have no direct control.

From Eqs. 15, 16 and 15 it follows that the maximum values of \( U_t \) (which obtain at \( \text{opt}[n_t^{h_t}] \) and \( \text{opt}[n_t^{+1}] \) given by Eqs. 10 and 19) are:

\[
U_t(\text{opt}[n_t^{h_t}]) = \begin{cases} 
\frac{N}{2}(1-2l) - 1 & \text{if } l < 0.5 \\
\frac{N}{2}(2l-1) & \text{if } l \geq 0.5
\end{cases} \tag{21}
\]

no memory:

\[
U_t(\text{opt}[n_t^{+1}]) = \begin{cases} 
N(1-2l) - 2 & \text{if } l < 0.5 \\
N(2l-1) & \text{if } l \geq 0.5
\end{cases} \tag{22}
\]

Thus the optimal value of \( U_t \) in the original model is exactly half that achieved by the memoryless model. As we suggested above, the reason for this is because in the original model \( n_t^{h_t} \) is a function of both \( h_t \) and \( \Pi_{i,t} \). The instantaneous optimal value of \( n_t^{h_t} \) will therefore depend on \( h_t \) (see Fig. 1 and Eq. 19). Note that the value of \( n_t^{h_t} \) that maximizes the time average \( \langle U_t(n_t^{h_t}) \rangle_t \), \( \text{opt}[n_t^{h_t}] \) given by Eq. 14 will always be one of the instantaneous optimal values given in Eq. 21. Thus the agents cannot improve the global utility by varying \( \overline{p}_t \).

They adopt the value of \( \overline{p}_t \) that is optimal for the most common value of \( h_t \), but they must pay the penalty when \( h_t \) takes the opposite value. In contrast, in the memoryless model the instantaneous optimal value of \( n_t^{+1} \) in Eq. 22 is independent of \( t \). Thus, by evolving such that \( \overline{p}_t = \text{opt}[\overline{p}_t] \) the agents can insure that \( n_t^{+1} \) is close to the optimal value at each time step.

D. Analytical expressions for \( \langle n_t^{+1} \rangle_t \) and \( \sigma(n_t^{+1}, t) \)

We can use the same method that we used to derive the expression for \( \langle U_t(n_t^{h_t}) \rangle_t \) in Eqs. 13 and 14 to obtain expressions for \( \langle n_t^{+1} \rangle_t \) and the standard deviation \( \sigma(n_t^{+1}, t) \) of the \( n_t^{+1} \) time series. From Eq. 3:

\[
\langle n_t^{+1} \rangle_t = N \overline{p}_t. \tag{23}
\]

This leads to the following expression for \( \langle n_t^{+1} \rangle_t \):

\[
\langle n_t^{+1} \rangle_t = \begin{cases} 
N(1-\overline{p}_t) & \text{if } h_t = -1 \\
N\overline{p}_t & \text{if } h_t = +1
\end{cases} \tag{24}
\]

Taking the time average in exactly the same way as in Sec. C, we obtain in equilibrium where \( \overline{p}_t \) is approximately constant, yields expressions for \( \langle n_t^{+1} \rangle_t \) and \( \langle (n_t^{+1})^2 \rangle_t \):

\[
\langle n_t^{+1} \rangle_t = \begin{cases} 
\frac{N^2}{4}(3-2\overline{p}_t)^2 & \text{if } l < 0.5 \\
\frac{N^2}{4}(1+2\overline{p}_t)^2 & \text{if } l > 0.5
\end{cases} \tag{25}
\]

\[
\langle (n_t^{+1})^2 \rangle_t = \begin{cases} 
\frac{N^2}{4}(4\overline{p}_t^2-6\overline{p}_t+3)+\sigma^2 & \text{if } l < 0.5 \\
\frac{N^2}{4}(4\overline{p}_t^2-2\overline{p}_t+1)+\sigma^2 & \text{if } l > 0.5
\end{cases} \tag{26}
\]
where $\sigma$ is the standard deviation of $\Pi_t$ introduced in Sec. II A which will be of order unity. If we assume that the agents adopt the optimal distribution in Eq. (17) then we can take $\sigma = 0$. We now obtain an expression for $\sigma(n_t^+1, t)$ as follows:

$$
[\sigma(n_t^+1, t)]^2 = \langle [n_t^+1]_t^2 \rangle - \langle [n_t^+1]_t \rangle^2 = \frac{3N^2}{4} \left( \langle \overline{p}_t \rangle - \frac{1}{2} \right)^2 + \sigma^2 
$$

Taking $\sigma = 0$ gives:

$$
\sigma(n_t^+1, t) = \frac{N\sqrt{3}}{2} \left| \langle \overline{p}_t \rangle - \frac{1}{2} \right|. 
$$

Ref. [4] used a mean-field approximation to derive expressions for $n_t^+1$ and $\sigma(n_t^+1, t)$ in terms of $\langle h_t \rangle_t$ and $\langle \overline{p}_t \rangle_t$. In particular:

$$
\langle n_t^+1 \rangle_t = \begin{cases} 
\frac{N}{4} (3 - 2 \langle \overline{p}_t \rangle_t) & \text{if } l < 0.5 \\
\frac{N}{4} (1 + 2 \langle \overline{p}_t \rangle_t) & \text{if } l > 0.5 
\end{cases} 
$$

$$
\sigma(n_t^+1, t) = \frac{N\sqrt{3}}{2} \left| \langle \overline{p}_t \rangle_t - \frac{1}{2} \right|. 
$$

Note that we have substituted for $\langle h_t \rangle_t$ in the expressions of Ref. [4], with the values of $\langle h_t \rangle_t$ that obtain for $l_{c1} < l < l_{c2}$ ($\langle h_t \rangle_t = 0.75$ for $l < 0.5$ and $\langle h_t \rangle_t = 0.25$ for $l > 0.5$) [4]. Thus, we can see that the expressions that we derived in Eqs. (25) and (28) are consistent with those obtained in Ref. [4].

\section*{E. Numerical Results}

In this section we present numerical data which supports the analytical results that we presented in the previous sections. Ref. [4] investigated the behavior of $\langle n_t^+1 \rangle_t$ and $\sigma(n_t^+1, t)$ as a function of the resource level $l$. Further work was done with regard to the memoryless Genetic Model with general $l$ by Burgos et al. in Refs. [6, 7]. Figure 3a recalls the results of Ref. [4].

We can clearly see the dynamic and frozen regimes for $l_{c1} < l < l_{c2}$ and $l < l_{c1}$, $l > l_{c2}$ respectively. Figure 3b shows $\langle n_t^+1 \rangle_t$ and $\sigma(n_t^+1, t)$ in the memoryless variant. Figure 4a shows $\langle \overline{p}_t \rangle_t$ as a function of $l$ in the original and memoryless models while Fig. 4b shows $\langle h_t \rangle_t$ in the original model.

First of all note that in Fig. 4b, $\langle \overline{p}_t \rangle_t$ lies to a very good approximation on the following lines:

$$
\langle \overline{p}_t \rangle_t = \begin{cases} 
1 - l & l < 0.5 \\
1 & l > 0.5 
\end{cases} 
$$

This confirms that the population of agents is capable of evolving to achieve the optimal values of $\overline{p}_t$ given in Eqs. (26) and (29).

In Sec. II D we presented expressions in Eqs. (25), (28), (29) and (30) for $\langle n_t^+1 \rangle_t$ and $\sigma(n_t^+1, t)$ If we substitute for $\langle \overline{p}_t \rangle_t$ in these equations with the optimal values from Eq. (16), neglecting the term $\frac{1}{N}$, we obtain the following analytical equations for $\langle n_t^+1 \rangle_t$ and $\sigma(n_t^+1, t)$ for $l_{c1} < l < l_{c2}$:

$$
\langle n_t^+1 \rangle_t = \frac{N}{4} (1 + 2l) \sigma(n_t^+1, t) = \frac{N\sqrt{3}}{2} \left| l - \frac{1}{2} \right|. 
$$

In Fig. 8 we show these analytic expressions together with the numerical data and opt[$n_t^+1$] = $NI$ from Eq. (14). We can see that $\langle n_t^+1 \rangle_t$ deviates from the optimal value of $NI$ for $l_{c1} < l < 0.5$ and $0.5 < l < l_{c2}$ as pointed out in Ref. [4]. We now know, from Sec. II C that the reason for this is that the population of agents can only control $n_t^{+h_1}$ directly and not $n_t^{+1}$. Thus their performance is reduced by the action of $h_t$. We can see that...
\[ \langle n^{t+1} \rangle_t = N_4 (1 + 2l) \]
\[ \sigma(n^{t+1}, t) = N \sqrt{\frac{3}{2} |l - \frac{1}{2}|} \]

**Numerical:**
\[ \sigma(n^{t+1}, t) \]
\[ \langle n^{t+1} \rangle_t \]

**FIG. 3:**
a. Numerical results for \( \langle n^{t+1} \rangle_t \) and \( \sigma(n^{t+1}, t) \) as a function of the resource level \( l \) in the original Genetic Model. We also include lines which represent: \( \text{opt}[n^{t+1}] = Nl \) from Eq. (11) and the analytical expressions for \( \langle n^{t+1} \rangle_t \) and \( \sigma(n^{t+1}, t) \) presented in Eq. (32). 
b. \( \langle n^{t+1} \rangle_t \) and \( \sigma(n^{t+1}, t) \) as a function of the resource level \( l \) in the memoryless Genetic Model.

for \( l_{c1} < l < l_{c2} \), \( \langle n^{t+1} \rangle_t \) instead lies on the line defined by Eq. (32). In Fig. 3, we also see that the numerical data for \( \sigma(n^{t+1}, t) \) agrees to a good approximation with the expressions in Eq. (32). The analytic expression deviates from the numerical data in the vicinity of \( l = 0.5 \). The reason for this is that when we derived the expression for \( \sigma(n^{t+1}, t) \) in Eq. (32), we assumed that the agent gene value distribution is as given by Eq. (17) and so \( \sigma = 0 \). In fact \( \sigma \neq 0 \) and near \( l = 0.5 \) the \( \sigma^2 \) term in Eq. (32) dominates. Therefore \( \sigma(n^{t+1}, t) \) does not go to zero as predicted.

In Fig. 3b we see that, as predicted by Sec. II C 3, \( \langle n^{t+1} \rangle_t \) in the memoryless model does lie on the optimal line defined by \( \text{opt}[n^{t+1}] = Nl \) for \( l_{c1} < l < l_{c2} \). We can also see that \( \sigma(n^{t+1}, t) \) in the memoryless model is much lower than in the original model. The large value of \( \sigma(n^{t+1}, t) \) in the original model results from the fact
that $n_{t}^{+1}$ is a function of both $n_{t}^{h_{t}}$, determined via $\Pi_{c_{t}}$ by the distribution of agent gene values $P(x)$, and $h_{t}$. In the memoryless model $n_{t}^{+1}$ is a function of $P(x)$ only which in equilibrium will be approximately constant in form. The small remaining fluctuations are due to the fact that the agent population does not achieve the ideal distribution of Eq. (17). We can therefore say that the memoryless model is efficient in accessing the available resources.

F. Generation of the prediction from an exogenous source

In Sec. [11] we showed that the effect of the prediction $h_{t}$ is to reduce the agents’ performance via its effect on $n_{t}^{+1}$. This being the case we should expect that the effect of the prediction on the model would be no different to that of an exogenous source provided that the value of $\langle h_{t}\rangle_{t}$ is preserved. In this section we shall check this by comparing the behavior of the original model with a different memoryless variant. In this variant the prediction $h_{t}$ will be generated by a random source, external to the model, rather than taking the value $+1 \forall t$. We shall let $R_{\alpha}$ represent the output of such a random exogenous source which contains only the two values $-1$ and $+1$ and for which $\alpha$ is the time average, $\langle R_{\alpha}\rangle_{t} = \alpha$. We represent the binary sequence generated by the memory for $h_{t}$ in the original Genetic Model by $S$.

Figure 5 shows numerical results for $\langle n_{t}^{+1}\rangle_{t}$ in the memoryless model with $h_{t}$ given by the exogenous sources $R_{0.5}$ and $R_{1.0}$. The results for the original model, $\{h_{t}\}_{t} = S$, are included for comparison. The results for $\{h_{t}\}_{t} = R_{1.0}$ duplicate those presented in Fig. 5 since $\{h_{t}\}_{t} = R_{1.0}$ is equivalent to $h_{t} = +1 \forall t$. In other words taking $\{h_{t}\}_{t} = R_{1.0}$ is exactly equivalent to the memoryless model that we considered in previous sections. In Fig. 6 the data produced using $\{h_{t}\}_{t} = R_{0.5}$ for $\langle n_{t}^{+1}\rangle_{t}$ and $\sigma(n_{t}^{+1}, t)$ agrees with that from the original model for $l_{c1} < l < l_{c2}$. For $l < l_{c1}$ and $l > l_{c2}$ the data from the original model switches to agree with that from the memoryless model with $\{h_{t}\}_{t} = R_{1.0}$ corresponding to the value of $\langle h_{t}\rangle_{t}$ from the original model in these regions. Note there is no need to consider $R_{-0.5}$ and $R_{-1.0}$. The lack of physical significance attached to the labeling of the states of $h_{t}$ means that the model behaves equivalently for $\{h_{t}\}_{t} = R_{\pm \alpha}$.

These results confirm that the original Genetic Model and the memoryless Genetic Model with $h_{t}$ taken from an exogenous source can be regarded as equivalent when considering $\langle n_{t}^{+1}\rangle_{t}$. In contrast we shall see in Sec. [11] that this does not apply when considering higher moments.

G. The values of $\langle h_{t}\rangle_{t}$

So far we have treated the values of $\langle h_{t}\rangle_{t}$ that obtain for $l_{c1} < l < 0.5$ and $0.5 < l < l_{c2}$ as values to be derived empirically by numerical simulation. Now we shall discuss the theoretical reasons for their observed values.

Lo has presented a theory [14] that predicts, using our conventions, the following values for $\langle h_{t}\rangle_{t}$:

$$\langle h_{t}\rangle_{t} = \begin{cases} -1 & \text{For } l < l_{c1} \\ \frac{1}{2} & \text{For } l_{c1} < l < 0.5 \\ +\frac{1}{3} & \text{For } 0.5 < l < l_{c2} \\ +1 & \text{For } l_{c2} < l \end{cases}$$  \hspace{1cm} (33)

However numerical simulation robustly yields values of $\langle h_{t}\rangle_{t} \approx \pm \frac{1}{3}$ in the dynamic regime. In what follows we summarize Lo’s analysis with the addition of some observations which explain why the numerical and analytical results differ. Note that as we pointed out in Sec. [11] the absolute values that obtain for $\langle h_{t}\rangle_{t}$ in the dynamic regime are not important for the theory that we present here. As long as $\langle h_{t}\rangle_{t} < 0$ for $l_{c1} < l < 0.5$ and $\langle h_{t}\rangle_{t} > 0$ for $0.5 < l < l_{c2}$ everything that we have said about $\text{opt}[n_{t}]$ will remain unchanged. Only the magnitude of the relative performance of the original and memoryless Genetic Models depends upon the values taken by $\langle h_{t}\rangle_{t}$.

The analysis hinges on the observation that:

$$\langle A_{t}\rangle_{t} = \langle h_{t}\rangle_{t} .$$  \hspace{1cm} (34)

From Eq. (5) and the definition of $\Pi_{c_{t}}$ the probability that $A_{t} = +1$ is given by:

$$P[A_{t} = +1] = \begin{cases} I_{2} & \text{if } h_{t} = -1 \\ I_{1} & \text{if } h_{t} = +1 \end{cases}$$  \hspace{1cm} (35)
Therefore, the ensemble average values of the global action $A_t$ when $h_t = +1$ and $-1$ are given by:

$$
\langle A_t \rangle = \begin{cases} 
2I_2 - 1 & \text{if } h_t = -1 \\
2I_1 - 1 & \text{if } h_t = +1 
\end{cases}
$$

The time average of the global action is given by the sum of the values of $\langle A_t \rangle$ for $h_t = \pm 1$ weighted by the probabilities that $h_t = \pm 1$. Thus:

$$
\langle A_t \rangle_t = \left( \frac{\langle h_t \rangle_t + 1}{2} \right) (2I_1 - 1) + \left( \frac{1 - \langle h_t \rangle_t}{2} \right) (2I_2 - 1)
$$

Finally, using Eq. \ref{eq:opt} gives:

$$
\langle h_t \rangle_t = \frac{I_1 + I_2 - 1}{I_2 - I_1 + 1}.
$$

In Fig. 6 we illustrate the summations over $\Pi_{i,t}$ in Eq. \ref{eq:sums} that define the values of $I_1$ and $I_2$. For the purposes of calculating these values, we have taken the mean of the distribution to be given by $\mu = \text{opt}[n_t^{+h_t}]$ from Eq. \ref{eq:opt} and the standard deviation to be $\sigma = 8$. We can see from Fig. 6 that the values for $I_1$ and $I_2$ will be given by:

$$
I_1 = \begin{cases} 
0 & \text{if } l < 0.5 \\
\frac{1}{2} & \text{if } l > 0.5 
\end{cases}
$$

$$
I_2 = \begin{cases} 
\frac{1}{2} & \text{if } l < 0.5 \\
1 & \text{if } l > 0.5 
\end{cases}
$$

since the summations either cover the entire peak of the Gaussian, exactly half of it or none at all. From Eqs. \ref{eq:opt} and \ref{eq:sums} we obtain values for $\langle h_t \rangle_t$ in the dynamic regime of:

$$
\langle h_t \rangle_t = \begin{cases} 
-\frac{1}{2} & \text{if } l < 0.5 \\
\frac{3}{2} & \text{if } l > 0.5 
\end{cases}
$$

which agree exactly with the values found by Lo in Ref. \ref{lo}.

The values given in Eq. \ref{eq:opt} depend on the assumption that $\langle n_t^{+h_t} \rangle_t$ is given by the optimal value of Eq. \ref{eq:opt}. In fact, as we see in Fig. 7, numerical simulation using a large number of agents reveals that this is not the case. In the figure $\text{opt}[n_t^{+h_t}] - \langle n_t^{+h_t} \rangle_t \approx 0.002N$ corresponding to $\mu - \langle h_t \rangle_t \approx 0.002$. Careful observation of Fig. 4 reveals that $\langle h_t \rangle_t$ always lies slightly closer to 0.5 than the value predicted by Eq. \ref{eq:sums} in the original model. As we can see from Fig. 7 this changes the values of the summations in Eq. \ref{eq:sums} as follows:

$$
I_1 = \begin{cases} 
0 & \text{if } l < 0.5 \\
0.677 & \text{if } l > 0.5 
\end{cases}
$$

$$
I_2 = \begin{cases} 
0.323 & \text{if } l < 0.5 \\
1 & \text{if } l > 0.5 
\end{cases}
$$

which by Eq. \ref{eq:sums} yields the following values for $\langle h_t \rangle_t$:

$$
\langle h_t \rangle_t = \begin{cases} 
-0.511 & \text{if } l < 0.5 \\
+0.511 & \text{if } l > 0.5 
\end{cases}
$$

These figures agree much more closely with the numerically observed values of $\langle h_t \rangle_t = \pm 0.5$ than the values obtained in Eq. \ref{eq:opt}.

We can therefore see that the values of $\langle h_t \rangle_t = \pm 0.5$ that obtain in the dynamic regime result from the fact that $\langle h_t \rangle_t$ deviates slightly from the optimal value of Eq. \ref{eq:opt}. In the absence of this deviation we would indeed
obtain the values given in Eq. 16 for $\langle h_i \rangle_t$. We can see that the memory does indeed have a non-trivial role to play in the Genetic Model. The feedback between the prediction $h_t$ and the global action $A_t$ represented by Eq. 16 controls the values of $\langle h_i \rangle_t$ that obtain in the dynamic regime $l_{c1} < l < l_{c2}$.

H. Deviation of $\pi_t$ from its optimal value

In Sec. II C when we calculated the optimal values of $\pi_t$ in Eq. 16 we implicitly assumed that the gene value distribution is given by 17 and that therefore $\sigma = 0$. If $\sigma$ is non-zero then the values of $n_t^{l+1}$ will be spread about $\langle n_t^{l+1} \rangle_t$. An examination of Fig. 2 reveals that the reduction in $\Delta t$ resulting from a deviation of $n_t^{l+1}$ towards 0 is less than that of a deviation towards $N$. Therefore we might expect that the agents would evolve such that $\pi_t$ was less than $\text{opt}[\pi_t]$ when $\sigma > 0$ in order to compensate for this. This argument also applies to the memoryless model. We know from Eqs. 15, 14, 15 and Fig. 2 that the change that occurs in $U_t$ at $n_t^{l+1} = Nl$ in the memoryless model is greater than that which occurs in the original model. Therefore, if the argument presented above were correct, we would expect a larger deviation in the memoryless case. However, we can see in Fig. 3 that the deviation of $\pi_t$ from $\text{opt}[\pi_t]$ in the memoryless model is less than that in the original model since $\langle \pi_t \rangle_t$ lies closer to the line described by $\pi_t = l$ in the figure. Figure 5 shows numerical data for $\Pi_{i,t}$ in the memoryless model. It is the equivalent of Fig. 4 Any deviation of the peak of $\Pi_{i,t}$ in Fig. 3 from the optimal value given in Eq. 16 is too small to be observable. Thus we can see that the observed deviation $\text{opt}[\pi_t] - \pi_t$ in the memoryless model is much smaller than that in the original model. Therefore we conclude that a different effect, one most probably related to the variation of the prediction $h_t$, must be responsible for the deviation observed in the original model.

We note in passing that since $\langle \pi_t \rangle_t$ deviates from $\text{opt}[\pi_t]$ given by Eq. 16 in the original model while no such deviation is observed in the memoryless model, the gene value distribution of the agents in the two models differs for general $l$. We would expect this difference to vanish in the case of $l = 0.5$, as found by Burgos and Ceva 2, and for the frozen regimes of $l < l_{c1}$ and $l > l_{c2}$ in which the original and memoryless models are equivalent.

I. Autocorrelation of $n_t^{l+1}$

In this section we consider another property of the Genetic Model: the autocorrelation of the time series $n_t^{l+1}$. First of all we shall present numerical data contrasting the behavior of the autocorrelation in the original and memoryless models. We shall then consider a Markovian analysis of the original Genetic Model which explains the behavior of the autocorrelation of $n_t^{l+1}$ observed therein in the simplest case of $m = 1$.

I. Numerical Results

We define the autocorrelation $C_{\tau}(x_t)$ of a time series $x_t$ as follows:

$$C_{\tau}(x_t) = \frac{\langle x_t x_{t+\tau} \rangle - \langle x_t \rangle^2}{\langle x_t^2 \rangle - \langle x_t \rangle^2},$$

where $\tau$ gives the lag time.

Figure 8 shows the autocorrelation of the attendance time series $C_{\tau}(n_t^{l+1})$ for $0 \leq \tau \leq 10$ and $1 \leq m \leq 5$. We can see from the figure that for $l = 0.5$ there is no significant correlation for $\tau > 0$. For $l \neq 0.5$, in contrast, $C_{\tau}(n_t^{l+1})$ as a function of $\tau$ has a clear structure. The magnitude of $C_{\tau}(n_t^{l+1})$ is non-zero for $\tau = (m + 1)/i$, where $i = 1, 2, 3 \ldots n_{t+1}^{l+1}$ and $n_{t+1}^{l+1}$ are anticorrelated for odd values of $i$ and correlated for even values. Figure 11 shows $C_{\tau}(n_t^{l+1})$ for the same values of $\tau$ and $l$ depicted in Fig. 8. However, this time $h_t$ was derived from a random exogenous source rather than the memory. It is clear from a comparison of Figs. 8 and 11 that the structure observed in $C_{\tau}(n_t^{l+1})$ in Fig. 8 is only present in the original model with memory. Figure 11 shows the autocorrelation of the prediction time series $h_t$. From this we can see that the structure present in Fig. 8 derives from structure present in the prediction time series.

From Figs. 8 and 11 we can see that one of the functions of the memory is to introduce non-zero autocorrelations into the prediction time series $h_t$. These will clearly not be present in either of the memoryless models in which either $h_t \equiv +1 \forall t$ or $h_t \equiv R_o$. In Ref. 2 Burgos et al.
found that for $l = 0.5$ the gene value distribution functions in the Genetic Model and the memoryless Genetic Model are equivalent. Further in Ref. [7] Burgos et al. stated that “a simplified version of the model, that makes no use of memory is indistinguishable from the original formulation”. In contrast however, the numerical data presented in Figs. [8] and [11] demonstrates that the two formulations are distinguishable. While the memoryless model yields equivalent results for $(n_t^{+1})_t$, it does not do so for higher moments. Any analysis in which possible autocorrelations in the $n_t^{+1}$ time series could be a factor could not be conducted using the memoryless model. However, this effect would not be noticeable in an investigation restricted to the minority case of $l = 0.5$.

2. Markovian analysis

In this section we will present a Markovian analysis of the action of the memory in the Genetic Model. This analysis must be performed separately for each value of $m$ of interest since each leads to a distinct state space. Here we shall present the analysis for $m = 1$ only. Treatment of higher values of $m$ is possible, although cumbersome since they lead to state spaces which are too large to be treated conveniently by hand.

The first stage of our analysis is to define a convention for labeling the states of the memory. Each state label must define the values of $h_t$, $A_t$ and the state of the memory. This is the minimum set of information needed to calculate the state transition probabilities. For $m = 1$ the memory will contain $2^{m-1} = 2$ entries corresponding to the two possible histories $A_{t-1} = -1$ and $A_{t-1} = +1$. We shall label these entries $m_t^{-1}$ and $m_t^{+1}$ respectively. Each state therefore comprises four attributes each of which can take values $±1$. There are therefore sixteen possible states which we denote using the shorthand notation described in Fig. [12]. We label these states by analogy with the binary number system as shown in Fig. [12].

For the sake of clarity we shall consider the case of $l < 0.5$. By symmetry the results that we derive will also apply to $l > 0.5$. From Eqs. [35] and [12], we have the following expression for the probability that $A_t = +1$:

$$P[A_t = +1] = \begin{cases} I_2 = \alpha & \text{if } h_t = -1 \\ I_1 = 0 & \text{if } h_t = +1 \end{cases}, \quad (45)$$

where $\alpha$ represents the numerical value of $I_2$ in Eq. [12]. The result of this is that if the prediction $h_t = +1$ then the global action $A_t = -1$ with probability $P = 1$. We can therefore discard states 3, 7, 11 and 15 from consideration. In each of these states $h_t = +1$ and $A_t = +1$ and thus they will never be visited by the model.

Using Eq. [45] we derive the state transitions shown in Fig. [13]. We can see that each state either makes a transition to one other state with probability $P = 1$ or to one of two possible states with probability $P = \alpha$ respectively. This information can be used to further simplify the state space. We need not consider states which have no inward transitions or states which only have inwards transitions from states that we have removed. This allows us to remove states 2, 8, 9, 10, 12 or 13 from consideration. The model will not visit these states once initial transients have died away. This reduces our state space from sixteen states to only six: 0, 1, 4, 5, 6 and 14.

Figure [14] shows the state transition diagram corresponding to Fig. [13] in the simplified state space described above. From this we can form the following Markov transition matrix, in which the remaining states are arranged in numerical order:

$$
T = \begin{pmatrix}
1 - \alpha & 1 - \alpha & 0 & 0 & 0 & 0 \\
0 & 0 & 1 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 1 \\
\alpha & \alpha & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \alpha & 0
\end{pmatrix}, \quad (46)
$$

which defines the stationary Markov chain.

From Eq. [46] we can derive the $n$-step autocorrelation functions $C_n(h_t)$. Recall the oscillatory dependence of $C_n(h_t)$ on $\tau$ in Fig. [11]. If $C_1(h_t) = 0$ and $C_2(h_t) = -\epsilon$ (where $\epsilon$ is of order 0.1) then we would expect to observe the dependence depicted in the figure. If $h_t$ and $h_{t+2}$ are anticorrelated and $|C_2(h_t)| < 1$ then we should expect $h_t$ and $h_{t+4}$ to be correlated and $|C_4(h_t)| < |C_2(h_t)|$ and so on. Thus the form of $C_2(h_t)$ depicted in Fig. [11] for $m = 1$ depends only on the values of $C_1(h_t)$ and $C_2(h_t)$.

First we calculate the stationary state $s$ of the Markov chain defined by Eq. [46]. This gives:

$$s = \frac{1}{(1 + \alpha)^2} \begin{pmatrix}
1 - \alpha \\
\alpha \\
\alpha(1 - \alpha) \\
\alpha^2 \\
\alpha \\
\alpha^2
\end{pmatrix}, \quad (47)$$

From Eq. [47], the one-step autocorrelation $C_1(h_t)$ is given by:

$$C_1(h_t) = \frac{\langle h_t h_{t+1} \rangle_t - \langle h_t \rangle_t^2}{\langle h_t^2 \rangle_t - \langle h_t \rangle_t^2}. \quad (48)$$

Therefore we need to calculate values for $\langle h_t^2 \rangle_t$, $\langle h_t \rangle_t$ and $\langle h_t h_{t+1} \rangle_t$. Since $h_t = \pm 1$, $\langle h_t^2 \rangle_t = 1$. In order to calculate values for the other two averages it is necessary to form the vectors $h_0$ and $h_1$ which respectively give the values of $h_t$ and $h_{t+1}$ for each of the states in the simplified state space. The elements of $h_0$ can be read directly from Fig. [12]. This gives:

$$h_0 = \begin{pmatrix}
-1 & +1 & -1 & +1 & -1
\end{pmatrix}. \quad (49)$$
Taking the scalar product of $h_0$ with $s$ gives:
\[
\langle h_t \rangle_t = h_0 \cdot s = \frac{\alpha - 1}{\alpha + 1}.
\] (50)

In Sec. II G we used an alternative method, not restricted to $m = 1$, to derive the expression for $\langle h_t \rangle_t$ in Eq. (39). Substituting $I_1 = 0$ and $I_2 = \alpha$ in Eq. (49) yields Eq. (50) above. Thus, the analysis presented here and in Sec. II G are consistent.

We can derive $h_1$ by multiplying the values of $h_t$ and $h_{t+1}$ in Fig. 13. This gives:
\[
h_1 = \left( +1 \ -1 \ -1 \ +1 \ +1 \ -1 \right).
\] (51)

Once again taking the scalar product with $s$ gives:
\[
\langle h_t h_{t+1} \rangle_t = h_1 \cdot s = \left( \frac{\alpha - 1}{\alpha + 1} \right)^2.
\] (52)
Lag: $\tau$

$$C_1(h_t) = 0.$$  \hspace{1cm} (53)

Thus, we expect $h_t$ and $h_{t+1}$ to be uncorrelated which is in agreement with Fig. 11.

The two-step autocorrelation $C_2(h_t)$ is given by:

$$C_2(h_t) = \frac{\langle h_t h_{t+2} \rangle_t - \langle h_t \rangle_t^2}{\langle h_t^2 \rangle_t - \langle h_t \rangle_t^2}. \hspace{1cm} (54)$$

Therefore in order to calculate the two-step autocorrelation function $C_2(h_t)$ we must calculate $\langle h_t h_{t+2} \rangle_t$. As 

FIG. 11: Autocorrelation of the $h_t$ time series for the range of values of $m$ shown. Model parameters: $n = 1000$, a) $l = 0.4$, b) $l = 0.5$.

Therefore, from Eqs. 48, 50 and 52 we have:

$$C_1(h_t) = 0.$$

Thus, we expect $h_t$ and $h_{t+1}$ to be uncorrelated which is in agreement with Fig. 11.

The two-step autocorrelation $C_2(h_t)$ is given by:

$$C_2(h_t) = \frac{\langle h_t h_{t+2} \rangle_t - \langle h_t \rangle_t^2}{\langle h_t^2 \rangle_t - \langle h_t \rangle_t^2}. \hspace{1cm} (54)$$

Therefore in order to calculate the two-step autocorrelation function $C_2(h_t)$ we must calculate $\langle h_t h_{t+2} \rangle_t$. As 

FIG. 12: a) The labels used to index the sixteen possible states. The states that are crossed out are those in which $h_t = +1$ and $A_t = +1$. These can be omitted due to Eq. 45. b) A key for the graphical representation of each state.

FIG. 13: List of the one-step transitions that the model can make from each of the states listed in Fig. 12.

FIG. 14: State transition diagram corresponding to the transitions depicted in Fig. 12 in the simplified state space. The arrow labels give the transition probabilities.
before we must form the vector $h_2$ corresponding to the values of $h_t h_{t+2}$ for each of the states in the simplified space. This can be done following the method described in Fig. 15 which gives:

$$h_2 = \left( +1 \quad -1 \quad +1 \quad -1 \quad -1 \quad -1 \right). \tag{55}$$

Taking the scalar product with $s$ gives:

$$\langle h_t h_{t+2} \rangle_t = h_2 \cdot s = \frac{(1 - 3\alpha)(1 + \alpha)}{(1 + \alpha)^2}. \tag{56}$$

From Eqs. 55 and 54 and 56 we have:

$$C_2(h_t) = -\alpha. \tag{57}$$

Therefore, from Eqs. 53 and 57 we have that:

$$C_2(h_t) = 1, 0, -\alpha, 0, \alpha^2, 0, -\alpha^3, \ldots \tag{58}$$

for:

$$\tau = 0, 1, 2, 3, 4, 5, 6, \ldots$$

Note that as a result of this the autocorrelation of $h_t$ at $m = 1$ gives a direct measurement of the value of $\alpha$. This provides a much more convenient measure of $\alpha$ than computing the summation for $I_2$ in Eq. 39, as was done in Sec. II E.

Figure 16 shows a comparison of the theoretical values of $C(h_t)$, obtained with the numerical value of $\alpha = 0.323$ from Sec. II E, with the numerical values given in Fig. 15. We can see from Fig. 16 that Eq. 58 correctly predicts the form of $C_2(h_t)$ although it does underestimate the correlation for $\tau = 4$. One possible explanation of this slight deviation is that in the analysis above we have assumed that $\alpha$ is a constant. However, the value of $\alpha$ depends very sensitively on the form of $\Pi_{i,t}$. Therefore fluctuations in the gene value distribution of the agents could cause significant fluctuations in $\alpha$. Markovian analysis of the $l = 0.5$ case confirms that $C(h_t) = 0$ for $\tau > 1$, in agreement with the numerical results of Fig. 16.

J. Summary of Memory Characteristics

We conclude from the results presented in this section that the Genetic Model performs better in the absence of memory. By this we mean that the average total number of points scored per time step when $h_t = +1 \forall t$ is twice that when $h_t$ is determined by the global memory. This was established semi-analytically in Sec. II F and supporting numerical data was presented in Sec. II E. We showed in Sec. II C that the reason for this reduction in the performance in the presence of memory is that the agents cannot directly control the distribution of values for $n_t$ as they can in the memoryless model, because $n_t$ is now also a function of $h_t$. In Sec. II D we presented numerical data to show that the values of $\langle h_t \rangle_t$ and $\sigma(n_t^+)$ can be reproduced if the prediction $h_t$ is taken from an exogenous source providing that the value of $\langle h_t \rangle_t$ is preserved. Thus, the feedback between the global action of the agents and $h_t$ is of no benefit to the population of agents. The only function of this feedback is to regulate the value of $\langle h_t \rangle_t$.

We also investigated the values observed for the time average of the prediction $\langle h_t \rangle_t$ as a function of the resource level $l$. We showed that the values of $\langle h_t \rangle_t$ of $\pm 0.5$ that obtain in the dynamic regime of $l_{c1} < l < l_{c2}$ are due to the deviation observed between the mean of the agent gene value distribution $P(x)$ and the optimal value predicted by Eq. 29.

In Sec. III we showed that the form of the autocorrelation function of the $n_t^+$ time series at $l \neq 0.5$ occurs as a result of the cycles in state space performed by the memory. Finally we demonstrated that the two-step autocorrelation of the prediction $C_2(h_t)$ can be used to provide a direct measurement of the deviation described above.

III. SELF-INDUCED SHOCKS IN THE GRAND CANONICAL GENETIC MODEL

In this section we move on to consider the important practical property of self-induce shocks, otherwise known
as endogenous large changes (ELC). Such large changes are arguably a defining characteristic of complex systems, yet there is no rigorous quantitative description of such events in real-world realizations of complex systems (for examples see Refs. [15, 16, 17, 18, 19, 20, 21, 22]).

A. Introduction

As we show here, the Genetic Model can be generalized in a straightforward way to produce a model system which demonstrates such large changes. The extent to which these large changes are insensitive to the memory, then provides a useful tool for analyzing the microscopic causes underlying these large changes. In particular, we introduce an extension of the Genetic Model in Sec. II in which the number (or ‘volume’) of active agents is a time dependent quantity. We shall refer to this variant of the Genetic Model as the Grand Canonical Genetic Model (GCGM).

One particular application might be to financial markets, where large changes are called crashes or drawdowns. However the Genetic Model does not directly yield a price time series. Therefore, if we want to consider the effect of endogenous large changes on price, we must derive one from fundamental observables such as $\pi_t$. By definition the threshold value of $\eta^{-1} = Nl$ corresponds to the state in which the volume of the item that is being traded which is available for sale is equal to the demand. Therefore, the more general case of $l \neq 0.5$ represents a system in which the volumes in which an item are bought and sold are not equal. The excess demand is then given by:

$$\Delta = \left( \frac{l}{1-l} \right) N_{\text{buy}} - N_{\text{sell}}$$  \hspace{1cm} (59)

If we let the action of an agent $a_{it} = -1, +1$ represent choosing to buy or sell respectively then we obtain the following expression for the price $\pi_{t+1}$ at time $t + 1$ in terms of the price at $t$:

$$\pi_{t+1} = \pi_t + \frac{\lambda}{(1-l)} \left[ \frac{l}{1-l} \right] n_{t-1} - n_{t+1}$$  \hspace{1cm} (60)

where $\lambda$ is known as the market depth and determines the magnitude of the change in price caused by a unit change in $\Delta$. Different expressions for the price $\pi_t$ in terms of the excess demand $\Delta$ have been discussed in the literature (see, for example, Refs. [23 and 24]). The linear expression in Eq. (60) represents the simplest of these and is not as realistic as expressions in higher powers of $\Delta$. Nevertheless it is more than adequate for the illustrative purposes for which we shall need it. Since in all that follows the units of the price $\pi_t$ are arbitrary we will take $\lambda = 1$.

An example of a large volume change observed in the GCGM is given in Fig. 17. We can see that large changes occur in the volume accompanied by large price movements. However, the behavior of the volume in the figure is qualitatively different to that observed in the GCMG: Ref. [21] reported two distinct types of behavior. For traders with a long memory the volume was observed to be continuously fluctuating with occasional particularly large fluctuations which were not instantaneous; much like the ‘drawdowns’ and ‘drawups’ discussed by Sornette in Ref. [25]. For traders with short memories the volume was frequently zero with occasional large instantaneous spikes and corresponding instantaneous price movements. In contrast, in Fig. 17 the volume exhibits small fluctuations and occasional instantaneous changes which are accompanied by periods of large fluctuations in the price. We shall see that the behavior that we observe in these figures is typical of the behavior of the volume in the GCMG.

B. The Grand Canonical Genetic Model

The Genetic Model represents an abstract model of a population competing for a limited resource and as such it often discussed in the context of financial markets [2, 3, 4, 5, 6, 12, 13, 26]. In such a context, however, it does not seem realistic that the agents trade at every time step. A real market trader would also have the option of withdrawing from the market and returning when s/he felt confident of a successful outcome. In order to model this extra degree of freedom, and in keeping with the work of Johnson et al. in Ref. [21], we shall introduce an extension of the Genetic Model in which the agents are free to opt in and out of the game.

As in the original Genetic Model described in Sec. III and Ref. [8] there are $N$ agents participating in the model. However, unlike the original model they do not all play at each time step. At any time $t$ there will be two populations of agents, an active population and an inactive one. Active agents participate in exactly the same way as they do in the original model. In contrast an inactive agent $i$ will continue to make its choice as if it were participating, however it will not be considered when calculating the global action and its score will not be updated. We can imagine that inactive agents represent traders who do not make a trade at time $t$. In-
stead they make a prediction of whether their best choice would have been to follow the prediction $a_{i,t} = +h_t$ or to refute it $a_{i,t} = -h_t$. Since such a trade is *virtual* in that the trader does not act on it, it has no effect on the market and the trader is protected from losing, or even making, money. The only effect of such a virtual trade is that the agent reevaluates its confidence level depending on whether the trade would have been successful or not. These *virtual trades* are analogous to the *virtual points* earned by strategies in the Minority Game [2]. They allow the agents to keep track of their potential performance without in any way representing an agent’s wealth.

These modifications necessitate some minor changes to the basic equations of the Genetic Model that we introduced in Sec. III. Let the activity of an agent $i$ be given by $z_{i,t}$. If $z_{i,t} = 0$ then agent $i$ belongs to the population of inactive agents and vice-versa for $z_{i,t} = 1$. Equation 3 for the global action $A_t$ now becomes:

$$A_t = \begin{cases} +1 & n_{t+1}^z \leq n_t \\ -1 & n_{t+1}^z > n_t \end{cases} \text{ where: } n_t = \sum_i z_{i,t}. \quad (61)$$

Inactive agents become active and active agents become inactive according to their performance in the recent past. We defined a new model parameter known as the *confidence interval*, $T$. An inactive agent will become active if it would have won for $T$ consecutive time steps. In other words, an agent $i$ for which $z_{i,t} = 0$ will activate, $z_{i,t+1} = 1$, if $a_{i,t} = +A_t$ for $t - T < \tau \leq t$. In the same way, an active agent will become inactive if it loses for $T$ consecutive time steps. In order to control the activation and deactivation of agents we assign each agent a new quantity with we shall call its *virtual points* $v_{i,t}$, in keeping with the virtual points allocated to strategies in the Minority Game. For an active agent $v_{i,t}$ is increased each time the agent loses and is reset to zero if it wins. Thus, for active agents $v_{i,t}$ is the number of consecutive time steps for which the agent has lost. For an inactive agent $v_{i,t}$ is increased each time that the agent would have won and is reset to zero each time it would have lost. The updating rules for $v_{i,t}$ can be summarized as follows. If $z_{i,t} = 0$:

$$v_{i,t+1} = \begin{cases} 0 & \text{if } a_{i,t} = -A_t \\ v_{i,t} + 1 & \text{if } a_{i,t} = +A_t \end{cases} \quad (62)$$

If $z_{i,t} = 1$:

$$v_{i,t+1} = \begin{cases} v_{i,t} + 1 & \text{if } a_{i,t} = -A_t \\ 0 & \text{if } a_{i,t} = +A_t \end{cases}. \quad (63)$$

The rules for agent activation and deactivation are then, If $z_{i,t} = 0$:

$$z_{i,t+1} = \begin{cases} 0 & \text{if } v_{i,t} < T \\ 1 & \text{if } v_{i,t} = T \end{cases} \quad (64)$$

If $z_{i,t} = 1$:

$$z_{i,t+1} = \begin{cases} 1 & \text{if } v_{i,t} < T \\ 0 & \text{if } v_{i,t} = T \end{cases}. \quad (65)$$

The expression in Eq. (2) for the number of agents for which $a_{i,t} = +1$ becomes:

$$n_{t+1}^+ = \frac{1}{2} \sum_i z_{i,t} (a_{i,t} + 1). \quad (66)$$

In this section we shall define $\overline{p}_t$ to be the mean gene value of the active agent population. Thus, $\overline{p}_t$ is given by:

$$\overline{p}_t = \frac{1}{n_t} \sum_i z_{i,t} p_{i,t} \quad (67)$$

Therefore, the expression in Eq. (3) for the mean number of agents following the prediction $h_t$ becomes:

$$\langle n_{t+h_t} \rangle = \sum_i z_{i,t} p_{i,t} = n_t \overline{p}_t \quad (68)$$

C. Price Time-Series

As we stated in Sec. III A the cutoff, now given by $n_{t+1}^z = n_l$, in the Genetic Model, defined by Eq. (51), is by definition the state in which the excess demand $\Delta = 0$. From Eq. (60) we can see that the price change $\Delta \pi = \pi_t - \pi_{t-1}$ is positive and negative for $n_{t+1}^z < n_l$ and $n_{t+1}^z > n_l$ respectively. By comparison with Eq. (61) we can see that the condition that determines the sign of the price change at time $t$ is the same as that which determines the global action $A_t$; with the exception that the equality in Eq. (61) gives a price change of zero. With reference to Eq. (6) we have the condition that $\Delta \pi \geq 0$ in terms of $n_{t+1}^z$:

$$n_{t+1}^z \geq n_l (1 - l) \quad \text{if } h_t = -1$$

$$n_{t+1}^z \leq n_l \quad \text{if } h_t = +1. \quad (69)$$

From this it follows that the probability $P[\Delta \pi \geq 0]$ that the price rises or remains the same at time $t$ is given by:

$$P[\Delta \pi \geq 0] = \begin{cases} I_2 & \text{if } h_t = -1 \\ I_1 & \text{if } h_t = +1 \end{cases}, \quad (70)$$

where $I_1$ and $I_2$ represent the summations defined by Eq. (60) and illustrated by Fig. 5 with the substitution $N \rightarrow n_t$. We can see from Eq. (61) and Fig. 5 that for $l < 0.5 \ P[\Delta \pi \geq 0] = 0$ for $h_t = +1$ and for $l > 0.5 \ P[\Delta \pi \geq 0] = 1$ for $h_t = -1$. The result of this is that, in the dynamic regime of the original GCGM with memory,
one of the values that \( h_t \) can take will cause the price to rise or fall with probability \( P = 1 \). Note that in the cases of \( l < 0.5, h_t = -1 \) and \( l > 0.5, h_t = +1 \) we do not expect that \( P[\Delta p \geq 0] = 0.5 \) as might be expected from Fig. 6. Recall that, as we discussed in Sec. II. C, \( p_t \) deviates from the optimum values given in Eq. (19) in the Genetic Model. Furthermore, because the GCGM is frequently perturbed by ELC it does not settle into equilibrium in the same way as the Genetic Model and so \( p_t \) is more variable although, as we shall see, it does remain close to the values given by Eq. (19) in the periods between ELC.

### D. Endogenous Large Changes (ELC) in the GCGM

As we shall see the behavior of the model in this regime is rich and complex. For this reason we shall initially consider a simplified memoryless variant of the GCGM which is analogous to the memoryless Genetic Model considered in Sec. II. C. Subsequently we shall consider how the inclusion of memory affects the behavior of the full GCGM.

ELC in the GCGM result from a combination of two factors, both of which must be present if a large change is to occur. We shall later see that the capacity of the model to undergo an ELC depends sensitively on the distribution of gene values \( P(p) \). However, a suitable \( P(p) \) is not a sufficient condition for an ELC to occur. It is also necessary for a particular pattern to occur in the global action time series. We can think of this pattern as a trigger that initiates the ELC, but only if \( P(p) \) is in a susceptible state. Furthermore we shall see that the natural evolution of the model causes \( P(p) \) to evolve towards the most susceptible state while ELCs move \( P(p) \) towards the state in which it is least susceptible. Thus, rather than settling into equilibrium like the original Genetic Model, the evolution of the GCGM is characterized by a cyclic behavior: \( P(p) \) periodically evolving towards a more susceptible state until its progress is reversed by an ELC.

#### 1. Susceptibility of \( P(p) \)

ELC like the one illustrated in Fig. 17 are the result of highly correlated behavior of the agents. By this we mean that a significant number of agents activate or deactivate at the same time step. This implies highly correlated behavior since in order to do so the actions of all of the agents involved must be identical for the \( T \) preceding time steps. It is initially surprising that such a high degree of correlation could arise in the GCGM because, unlike Minority Game agents, GCGM agents make their decisions stochastically. The probability of coincidence between the actions of a large group of agents will usually be very small. However, there are two groups of agents in the model whose behavior is well correlated. These two groups are those agents whose gene values lie within a certain small range \( \delta \) of 0 and 1. We shall call agents belonging to these groups zero agents and one agents respectively. The degree of correlation of these agents is a decreasing function of \( \delta \), being a maximum for \( \delta = 0 \). It is easy to show that if we set an upper limit on the fraction \( f_d \) of zero and one agents whose actions are not perfectly correlated over a period of \( T \) time steps, \( \delta \) is given by:

\[
\delta = 1 - (1 - f_d)^{\frac{1}{T}} \tag{71}
\]

The precise value chosen for \( \delta \) is not important since it only serves to give a measure of the population of zero and one agents. Therefore it is more convenient to choose a fixed value for \( \delta \) which gives rise to values of \( f_d \) which lie within an acceptable range, rather than choosing a different \( \delta \) for each value of \( T \). In all that follows we shall take \( \delta = 0.02 \) which gives \( f_d < 0.33 \) for \( T \leq 20 \).

In short, we see that the probability of highly correlated agent behavior increases rapidly as the number of zero and one agents increases. Thus, gene values distribution functions \( P(p) \) which are biased to favor agents with gene values near to \( p = 0 \) and \( p = 1 \) will be the most susceptible to ELC.

Now that we’ve considered what forms of \( P(p) \) are most susceptible we will discuss how \( P(p) \) evolves in the GCGM. In the periods between the ELC the number of active agents \( n_t \) given by Eq. (61) is a slowly varying function of time. As we remarked above, correlations between the behavior of large numbers agents are expected to be rare and so \( n_t \) will fluctuate slowly with time as individual agents activate and deactivate. Hence the results of Refs. 4, 13 can be applied to the GCGM in these periods. Refs. 4, 13 describe how in the Genetic Model the agents self-segregate into two populations having low and high gene values – these two populations can be thought of as a ‘Crowd‘ and ‘Anticrowd‘. Thus, although we have yet to consider what the effect of an ELC will be on \( P(p) \) we can see that after such an event \( P(p) \) will evolve continuously towards the extremised distribution described by Ref. 13. From our discussion above we know that it is this type of extremised gene value distribution which is most susceptible to ELC.

#### 2. Triggers in the global action time series

We saw above that it is only the zero and one agents which can participate in the highly correlated behavior necessary for an ELC. Therefore, in order to think about what patterns in the global action time series might induce an ELC it is necessary to consider these agents. If at time step \( t \), \( A_t = +h_t \) then each zero agent will lose while each one agent will win. If \( A_t = +h_t \) for \( T \) consecutive time steps then immediately following the \( T \)th time step a fraction \( 1 - f_d \) of the active zero agents will deactivate while the same fraction of the inactive one
agents will activate. Similarly if \( A_t = -h_t \) for \( T \) time steps then a fraction \( 1 - f_A \) of the inactive zero agents will activate and a fraction \( 1 - f_A \) of the active one agents will deactivate. Thus we can see that sequences of time steps in which \( A_t = +h_t \) or \( A_t = -h_t \) for \( T \) time steps will be important for the correlated agent activations and deactivations that make up an ELC.

Since such sequences are important in the occurrence of ELC it would be useful to have an expression for the probability that they will occur. The first step is to derive expressions for the probability that \( A_t = \pm h_t \). We shall see later that these expressions are important in their own right. From Eq. (65), substituting \( n_t \) for \( N \), we have the following expressions for the probability that \( A_t = \pm h_t \):

\[
P[A_t = -h_t] = \begin{cases} \sum_{i = 1}^{n_t} \Pi_{i:t} & \text{if } h_t = -1 \\ \sum_{i = h_t + 1}^{n_t} \Pi_{i:t} & \text{if } h_t = +1 \end{cases} \tag{72}
\]

\[
P[A_t = +h_t] = \begin{cases} \sum_{i = 0}^{(1) n_t - 1} \Pi_{i:t} & \text{if } h_t = -1 \\ \sum_{i = 0}^{n_t} \Pi_{i:t} & \text{if } h_t = +1 \end{cases} \tag{73}
\]

We shall see later that \( n_t \gg 1 \). Therefore we can use the continuous approximation of \( \Pi_t(x) \) for \( \Pi_{i:t} \). As demonstrated in Ref. [12], \( \Pi_{i:t} \) will be a Gaussian. In the GCGM only active agents contribute to the mean \( \mu \) and variance \( \sigma^2 \) of \( \Pi_t(x) \). Therefore:

\[
\Pi(x) = \frac{1}{\sigma \sqrt{2\pi}} e^{-\frac{1}{2}(\frac{x - \mu}{\sigma})^2} , \tag{74}
\]

where:

\[
\mu = n_t \bar{p}_t , \quad \sigma^2 = \sum_{i} \varepsilon_{i:t} p_{i:t}(1 - p_{i:t}) . \tag{75}
\]

In the continuous approximation we have:

\[
P[A_t = -h_t] \approx \int_{(1) n_t}^{+\infty} \Pi_t(x) \, dx \quad \text{if } h_t = -1 \]

\[
P[A_t = +h_t] \approx \begin{cases} \int_{l_t}^{+\infty} \Pi_t(x) \, dx & \text{if } h_t = -1 \\ \int_{l_t}^{+\infty} \Pi_t(x) \, dx & \text{if } h_t = +1 \end{cases} \tag{76}
\]

Finally we can express Eq. (76) in terms of erf functions as, for \( h_t = \pm 1 \):

\[
P[A_t = -h_t] \approx \frac{1}{2} \left[ 1 + \text{erf} \left( \frac{1}{\sigma \sqrt{2}} \frac{x - n_t \lambda_t^+}{\sigma} \right) \right] , \tag{77}
\]

\[
P[A_t = +h_t] \approx \frac{1}{2} \left[ 1 + \text{erf} \left( \frac{1}{\sigma \sqrt{2}} \frac{x + n_t \lambda_t^-}{\sigma} \right) \right] , \tag{78}
\]

where for convenience we have defined \( \lambda_t^\pm \) as follows:

\[
\lambda_t^- = p_t - (1 - l) \quad \lambda_t^+ = p_t + l . \tag{79}
\]

The erf function is defined as:

\[
\text{erf}(x) = \frac{2}{\sqrt{\pi}} \int_{0}^{x} e^{-t^2} \, dt . \tag{80}
\]

We can see from Eq. (70) that the expressions for the probability that \( A_t = \pm h_t \) depend upon the the values taken by \( h_t \). For this reason it will not be possible in general to derive a simple expression for the probability that \( A_t = \pm h_t \) for \( T \) consecutive time steps. Such an expression would depend upon the realization of the prediction time series during the specific \( T \) time steps under consideration. In the next section, however, we shall see that a simple expression can be derived in the case of the memoryless model.

Ref. [27] presented an analysis of crashes in financial markets such as the one that occurred on the NASDAQ in April 2000. The authors propose that such crashes result from speculative bubbles in which large numbers of traders share the same unrealistic expectations of the future performance of the companies in question. These bubbles eventually burst, apparently in response to some event which acts as a trigger. We can draw a broad qualitative analogy between this and the GCGM. The extremised gene value distribution function discussed in Sec. III D 4 corresponds to a state of the model in which large numbers of agents share the same unrealistic expectation that the global action will be equal to or the opposite of the prediction. It is this speculative distribution that is most susceptible to triggers that occur from time to time in the global action time series.

\[\text{E. ELC in the memoryless GCGM}\]

We form the memoryless GCGM from the full model described in Sec. II C by taking \( h_t = +1 \forall t \) in exactly the same way as we did in Sec. II. Our discussion of the susceptibility of the gene value distribution function \( P(p) \) in Sec. II D 1 applies equally to the memoryless and the full GCGM. The equivalent of the patterns of \( T \) time steps in which \( A_t = -h_t \) or \( A_t = +h_t \) are those in which \( A_t = -1 \) or \( A_t = +1 \). In the memoryless case, the expressions in Eq. (70) become:

\[
P[A_t = \pm 1] \approx \frac{1}{2} \left[ 1 \pm \text{erf} \left( \frac{1}{\lambda_t^\beta} \frac{x - n_t \lambda_t^\pm}{\sigma \sqrt{2}} \right) \right] , \tag{81}
\]

where we have used the fact that since \( \sigma \) is of order unity the integrands in Eq. (65) will approximately vanish for \( x < 0 \) and \( x > N \). This has allowed us to replace lower limits of 0 with \( -\infty \) and upper limits of \( N \) with \( +\infty \).
This expression is no longer dependent on \( h_t \), since \( h_t = +1 \) if \( t \). Therefore, in the case of the memoryless GCGM, we can derive the following simple expression for the probability \( \Lambda_t \) that \( A_t = \pm 1 \) for \( T \) consecutive time steps:

\[
\Lambda_t = \frac{1}{2} \left[ 1 - \text{erf} \left( \frac{1 - n_t \lambda^+_t}{\sigma \sqrt{2}} \right) \right]^T + \frac{1}{2^T} \left[ 1 + \text{erf} \left( \frac{1 - n_t \lambda^+_t}{\sigma \sqrt{2}} \right) \right]^T. \tag{80}
\]

Figure 18a shows \( \Lambda_t \) given by Eq. (80) as a function of \( \lambda^+_t \). However, it is easier to interpret a plot of the average waiting time, given by \( \Lambda_t^{-1} \). A plot of this is included in Fig. 18b.

There are a couple of points to notice in Fig. 18. First of all the minimum of \( \Lambda_t \) does not occur at \( \lambda^+_t = 0 \) but at a value of \( \lambda^+_t = \frac{1}{2n_t} \). This results from the fact that in the case of \( n_t + 1 = \text{ln} \) our model tie breaks by declaring the global action \( A_t = +1 \). The most obvious feature of Fig. 18 is that \( \Lambda_t \) increases rapidly with increasing \( \lambda^+_t \). This means that the probability of a trigger sequence occurring in the global action time series \( A_t \) increases with the deviation of \( \bar{p}_t^i \) from \( I \). Therefore we can consider the value of \( \lambda^+_t \) to be controlling the probability that a trigger sequence will occur. Furthermore, note that \( \Lambda_t \) never vanishes and so the average waiting time never goes to infinity. Crucially, this means that regardless of the value of \( \bar{p}_t^i \) there is always a non-zero probability of that a trigger sequence will occur.

1. Price Time-Series in the memoryless GCGM

One of the advantages of the memoryless GCGM is that the dynamics of the price time series are particularly simple. We saw in Sec. 111C that the probability of a price fall at time \( t \) is given by the same condition that the global action \( A_t = -1 \). Therefore, \( P[\Delta \pi < 0] = P[A_t = -1] \) given by Eq. (79). Thus the price will fall with probability \( P < 0.5 \) if \( \lambda^+_t < 0 \) and with probability \( P > 0.5 \) if \( \lambda^+_t > 0 \).

2. Example ELC

Now that we have introduced the memoryless GCGM we shall consider a specific example of an ELC. This will allow us to see how the elements discussed in Sec. 111D are involved in ELC in the GCGM. In order to do this, however, we need to introduce one further quantity which we shall call the prediction performance and denote by \( \eta_t \). At time step \( t \) the value of \( \eta_t \) gives the number of previous consecutive time steps at which the prediction was the same as the global action \( A_t = +h_t \). In the memoryless GCGM the value of \( \eta_t \) gives the number of consecutive time steps preceding \( t \) at which \( A_t = +1 \). The reason that \( \eta_t \) is useful is that during one of the so called trigger sequences that we discussed in Sec. 111D \( \eta_t \) will become large and, thus, it can be used to identify these events.

Figure 19 lists the values of the global action \( A_t \) and the prediction performance \( \eta_t \) for a period of time in which an ELC occurs in the memoryless GCGM with \( l = 0.4 \) and \( T = 12 \). In order to show the behavior of the one and zero agents that we discussed in Sec. 111D we have also included the virtual points \( v_{i,t} \) of an agent \( i \) which is inactive and has \( p_{i,t} = 1.0 \) at the beginning of the time period shown. Since the actions of zero and one agents are anti-correlated (as we saw in Sec. 111D) the virtual points of inactive one agents and active zero agents will always be the same. The same applies to the virtual points of active one and inactive zero agents. For this reason it is only necessary to give \( v_{i,t} \) for one of these four groups in Fig. 111D since from this we can infer the virtual points of the others. Figure 20 shows \( \eta_t \) graphically for the same time period as well as the probability \( P[A_t = -1] \) that the global action \( A_t = -1 \) at each time step, given in terms of \( \lambda^+_t \) by Eq. (29). Figure 21b shows the deviation of \( \bar{p}_t^i \) from \( I, \lambda^+_t \), over the same time period. The quantities depicted in Figs. 19 and 20 are those that play an important role in the mechanism that causes ELC. Later, in Fig. 23 we shall demonstrate what effect the ELC described here has on
external observables such as the price and the volume. In the following paragraphs we describe the significant features in Figs. 19 and 20. The paragraph labels a-e correspond to the identically labeled time intervals in Fig. 19.

a. This sequence of $T$ time steps in which $A_t = +1$ provides the trigger sequence discussed in Sec. 11.1 The model reaches the final time step in this period $v_{kt} = T = 12$ for both inactive one agents and active zero agents. The inactive one agents will then activate while the active zero agents will deactivate. The virtual points of these agents will then be reset to 0. Unless the numbers of one agents activating and zero agents deactivating are approximately equal, this correlated behavior will lead to a step change in the volume like the one depicted in Fig. 17. Only active agents contribute to $P_t$ (see Eq. (74)) and so this instantaneous loss of zero agents and gain of one agents causes $P_t$, and therefore $\lambda^+_t$, to undergo a step increase. We can see this clearly in Fig. 20.

b. Throughout the period of $T$ time steps labeled b in Fig. 18, $\lambda^+_t \approx 0.16$. Equation (73) gives $P[A_t = -1]$ in terms of $\lambda^+_t$ and this is depicted graphically in Fig. 21 where we have taken values for $n_t$ and $\sigma_t$ corresponding to their mean values over the period described by Figs. 19 and 20. We can see from Fig. 21 that for $\lambda^+_t < -0.05$ and $\lambda^+_t > 0.05$, $P[A_t = -1] \approx 0$ and 1 respectively. Therefore, if the magnitude of $\lambda^+_t$ exceeds 0.05 the model becomes quasi-deterministic at time step $t$. Thus, for the period labeled b, $A_t = -1$. The effect of this on the zero and one agents is exactly the opposite of that of period a: the virtual points of the inactive zero agents and the active one agents now increases at each time step. Once again $v_{kt} = T = 12$ for both these populations at the end of period b and so the inactive zero agents activate while the active one agents deactivate. Note that the inactive zero agents activating at the end of period b are not just those that deactivated at the end of period a. Any zero agents that were inactive at the start of period a would have been unaffected by the trigger sequence, however they now activate along with those that previously deactivated. The result of this is that $\lambda^+_t$ does not return to the value of $\lambda^+_t \approx 0.4$ that it had at the end of period a. That would have returned the model to its non-deterministic state. Instead, however, $\lambda^+_t \approx -0.06$ and so at the start of period c $P[A_t = -1] = 0$.

c. This period of $T$ time steps in which $A_t = +1$ is identical to period a in terms of its effect on the one and zero agents. Thus, at the end of period c the inactive one agents reactivate and the active zero deactivate resulting in the same step increase in $\lambda^+_t$ that we observed before. The important difference between periods a and c is that the first occurred stochastically (there was a significant non-zero probability that $A_t = \pm 1$ at each time step) whereas period c occurs quasi-deterministically (the probability that $A_t = +1$ for the $T$ time steps in period c is $P \approx 1$).

d. Similarly period d is identical to period b except that at the end $\lambda^+_t = -0.03$. For Fig. 21 we can see that this gives $P[A_t = -1] > 0$.

e. $P[A_t = -1]$ is no longer $\approx 0$ and so the model returns to its usual stochastic behavior, $A_t$ taking values $-1$ and +1 probabilistically. This represents the end of the ELC since there is now no mechanism for the synchronized activation and deactivation that occurs during periods a-e. The model now returns slowly to the equilibrium state. In other words the state that it is in once transients due to any ELC have died away.

From the analysis that we have presented above we might have expected that the periodic synchronized activations and deactivations that we described above would continue indefinitely and that the model would never return to the stochastic state. One question that we did not address above, however, is that of how the model manages to break out of the deterministic behavior that it exhibits during the ELC. We have considered the effect of a period of $T$ time steps in which $A_t = \pm 1$ on the zero and one agents in terms of agent activation and deactivation. However, we have not considered agent mutation. We shall see in what follows that it is agent mutation that allows the model to return to the stochastic state. During periods b-d the one agents are only active at time steps at which $A_t = -1$ and the zero agents are only active when $A_t = +1$. Because of this the scores of zero and one agents are decreasing functions of time. Their scores are fixed when they are inactive and when they are active their individual actions are the inverse of the global action: $a_{id} = -A_i$. While these agents are inactive the model is favorable to them and so after $T$ time steps they reactive. However, because the behavior of all these agents is so highly correlated, in doing so they change the dynamic of the model so that it is no longer favorable. This has a clear analogy with the phenomenon of market impact in economic systems.

Since the scores of the zero and one agents are decreasing functions of time during the ELC the scores of these agents will rapidly reach the death score $s_{id} = -D$ at which they mutate. If $r \gg \delta = 0.02$ (defined by Eq. 71) then with a very high probability of $\frac{\lambda^+_t}{\lambda^+_t} + \delta$ a mutating zero or one agent will mutate to a gene value of $p_{id} > \delta$ or $p_{id} < 1 - \delta$ respectively. The result of this is that the population of zero and one agents that participate in the synchronized activations and deactivations steadily decreases throughout the ELC. Eventually there are no longer enough of these agents to maintain $\lambda^+_t$ at a magnitude greater than 0.05 and so $P[A_t = -1] \neq 0$ or 1. The model then returns to the stochastic state.

3. Summary of ELC in the memoryless GCGM

In this section we shall bring together the elements that we have introduced so far in order to give a broad
FIG. 19: The prediction performance $\eta_t$, $A_t$ and the virtual points $v_{i,t}$ of an agent $i$ which initially is inactive and has a gene values of $p_{i,t} = 1.0$. The model is the memoryless GCGM with $n = 500$, $l = 0.4$, $T = 12$, $r = 0.2$ and $m = 3$.

FIG. 20: Various important quantities plotted over the time period corresponding to Fig. 19: a) The prediction performance $\eta_t$ (measured against the left hand axis) and the probability $P[A_t = -1]$ that the global action $A_t = -1$ (measured against the right hand axis). b) The deviation of $\lambda_t$ from $l$, $\lambda_t^\tau$. Overview of ELC in the memoryless model. We demonstrated in Sec. [HID 1] that in, what we now call, the stochastic state the agents migrate towards gene values $p = 0.0$ and $p = 1.0$. Therefore, while the model is in the stochastic state the number of zero and one agents increases. This increases the susceptibility of the gene value distribution $P(p)$ to any trigger sequences that might occur and also increases the duration of the next ELC. If a trigger sequence occurs in the evolution of the model then if there are enough zero and one agents an ELC will take place as described in the previous section. One of the effects of the ELC is to reduce the numbers of zero and one agents. This decreases the probability of a subsequent ELC occurring.

In order to make this clear we show in Fig. 22, the numbers of zero and one agents during the time period leading up to and after that depicted in Figs. 19 and 20. Figure 22a shows $\lambda_t^\tau$ over the same time period. As we saw in Sec. [HID 2] ELC can be identified by the spikes that occur in the $\lambda_t^\tau$ time series. We can see in Fig. 22 that, while the ELC that we examined in Sec. [HID 2] causes a large decrease in the numbers of zero and one agents, significant numbers remain and so the initial ELC is followed by several smaller ones. The most important feature of Fig. 22 to notice, however, is that sudden decreases in the numbers of zero and one agents that occur at each ELC and the steady increase that these quantities exhibit in the periods between ELC.

FIG. 21: Probability $P[A_t = -1]$ that the global action $A_t = -1$ in terms of $\lambda_t^\tau$ given by Eq. (79) with $n_t = 205$ and $\sigma = 4.9$. These values correspond to the mean values of these quantities over the time period depicted in Figs. 19 and 20.
Thus we can see that the magnitude of the price changes during the ELC exceeds that of the negative excursions. In the oscillations in $\lambda^+$ such as the remarked in Sec. III A, ELC in the GCGM also affect the price rises and falls as we see in Fig. 23a. In the period described by Figs. 19 and 20. We can see from the plot of $P$ which is in turn given in terms of $\lambda^+$ we can see from the figure that during periods $\text{d}$ and $\text{e}$ $\lambda^+ = 0.552$ and that this is not sufficiently large to yield $P[A_t = -1] = 1.0$. Because of this period $\text{e}$, in which $A_t = -1$, does not occur deterministically. However, since $P[A_t = -1] = 0.967$ it is more probable that $A_t = -1$ for $T$ time steps than when the system is in dynamic equilibrium. From Fig. 24 we see that at the last time step of period $\text{d}$ $A_t = +1$ because $P[A_t = -1] \neq 1.0$ however $T$ time steps then follow (period $\text{e}$) in which $A_t = -1$. Thus the model is fairly robust against stochastic fluctuations. It’s not important if there is a period like $\text{d}$ in which the oscillatory pattern is briefly broken. During this interjected period, however, agent mutation will act to bring $\lambda^+$ closer to 0.0. Therefore the longer the interjected period the lower the probability that the ELC will continue.

4. Another example ELC

In Figs. 24 and 25 we give a second example of an ELC in the memoryless GCGM. We can see that the behavior of the model depicted therein is much the same as that exhibited in Figs. 19 and 20. The period labeled $\text{a}$ provides the trigger sequence of $T$ time steps for which $A_t = +1$. As before $\lambda^+$ exhibits decaying step-like oscillations during periods $b, c$ and $e$ until the model returns to dynamic equilibrium at the end of $e$. Note, however that the periods $c$ and $e$, for which $A_t = -1$ and $A_t = +1$ respectively, are separated by three time steps, $\text{d}$, in which $A_t = -1, -1, +1$. Figure 24 demonstrates why this occurs. We can see from the figure that during periods $\text{d}$ and $\text{e}$ $\lambda^+ = 0.552$ and that this is not sufficiently large to yield $P[A_t = -1] = 1.0$. Because of this period $\text{e}$, in which $A_t = -1$, does not occur deterministically. However, since $P[A_t = -1] = 0.967$ it is more probable that $A_t = -1$ for $T$ time steps than when the system is in dynamic equilibrium. From Fig. 24 we see that at the last time step of period $\text{d}$ $A_t = +1$ because $P[A_t = -1] \neq 1.0$ however $T$ time steps then follow (period $\text{e}$) in which $A_t = -1$. Thus the model is fairly robust against stochastic fluctuations. It’s not important if there is a period like $\text{d}$ in which the oscillatory pattern is briefly broken. During this interjected period, however, agent mutation will act to bring $\lambda^+$ closer to 0.0. Therefore the longer the interjected period the lower the probability that the ELC will continue.

F. ELC in the full GCGM: an idealized case

Before we examine some examples of numerically observed ELC in the full GCGM we shall consider a theoretically idealized case. In this section we will assume that in equilibrium $(\bar{p}_t)_t$ is equal to the optimal value $\text{opt}[\bar{p}_t]$ given by Eq. (10) of $1 - l$ for $l < 0.5$ and $l$ for $l > 0.5$. During the ELC we will assume that $\bar{p}_t$ oscillates between values that are greater and less than the equilibrium value by a magnitude sufficiently large that $P[A_t = -h_t]$, given by Eq. (10), takes only the values 0 and 1. This yields the following values for $P[A_t = -h_t]$,

FIG. 22: a) The evolution of the numbers of agents for which $p_{i,t} < \delta$ (zero agents) and $p_{i,t} > 1 - \delta$ (one agents) over a time period that includes that depicted in Figs. 19 and 20. b) $\lambda^+$ over the same time period. The occurrence of ELC is indicated by spikes in the $\lambda^+$ time series. The first ELC identifiable is that depicted in Figs. 19 and 20.

FIG. 23: Evolution of the number of active agents (also know as the volume) and the price (defined by Eq. (60)) over the same time period described by Figs. 19 and 20.
for $l < 0.5$:

\[
\begin{align*}
\bar{p}_t < \text{opt} [\bar{p}_t] : & \quad P[A_t = -h_t] = \begin{cases} 
0 & \text{if } h_t = -1 \\
1 & \text{if } h_t = +1
\end{cases} \\
\bar{p}_t > \text{opt} [\bar{p}_t] : & \quad P[A_t = -h_t] = \begin{cases} 
1 & \text{if } h_t = -1 \\
1 & \text{if } h_t = +1
\end{cases}
\end{align*}
\]

for $l > 0.5$:

\[
\begin{align*}
\bar{p}_t < \text{opt} [\bar{p}_t] : & \quad P[A_t = -h_t] = \begin{cases} 
1 & \text{if } h_t = -1 \\
0 & \text{if } h_t = +1
\end{cases} \\
\bar{p}_t > \text{opt} [\bar{p}_t] : & \quad P[A_t = -h_t] = \begin{cases} 
1 & \text{if } h_t = -1 \\
1 & \text{if } h_t = +1
\end{cases}
\end{align*}
\]

As we saw in Sec. [III D 2] it is sequences of $T$ time steps in which $A_t = -h_t$ or $A_t = +h_t$ which act as the triggers.
for ELC in the full GCGM. We can see from Eqs. [28] and [30] that \( A_t = -h_t \) with probability \( P = 1\) when \( \overline{p}_t > \text{opt}[\overline{p}_t] \). Thus, \( \overline{p}_t > \text{opt}[\overline{p}_t] \) leads to the sequences of time steps which have the same effect on the zero and one agents as the sequences of time steps in which \( A_t = 1\) that we saw in the memoryless GCGM. The situation when \( \overline{p}_t < \text{opt}[\overline{p}_t] \) is more complicated. We can see from the above expressions that for \( l < 0.5\), \( A_t = +1\) while for \( l > 0.5\), \( A_t = -1\). Thus, for \( \overline{p}_t < \text{opt}[\overline{p}_t] \) we expect sequences of time steps in which \( A_t = -1\) and \( A_t = +1\) respectively. However, it is not immediately apparent that \( A_t = +h_t \) as we might expect.

By application of the same Markovian analysis that we used in Sec. [12] to the \( m = 1\) case, we can derive the state transition diagrams given in Fig. [28]. The state labels are as defined by Fig. [12]. We can see from Fig. [28] that when \( \overline{p}_t < \text{opt}[\overline{p}_t] \) the transition diagrams each contain two attractor states in which \( h_t = -1\) and \(+1\) for \( l < 0.5\) and \( l > 0.5\) respectively. Thus, when the model is in these states \( P[A_t = -h_t] = 0\) and therefore \( A_t = +h_t\).

The reason that they can be divided into two congruent sub-diagrams is that in each case, as we remarked above, \( A_t \) only takes a single value. Therefore, the value of the memory bit that corresponds to the opposite value of \( A_t \) has no significance. This leads to the two-fold state degeneracy that we observe; states which only differ in the value of this attribute are equivalent. Another feature to note in Fig. [28] is that, depending on the state that the model is in when it changes from \( \overline{p}_t > \text{opt}[\overline{p}_t] \) to \( \overline{p}_t < \text{opt}[\overline{p}_t] \), it may take several time steps to reach the attractor. Thus, unlike in the case of the memoryless GCGM, we should not expect oscillations with period \( T \). There will likely be interjected time steps while the model finds the attractor.

We can see that this analysis will apply to the case of general \( m \) by considering Eq. [28]. For \( \overline{p}_t < \text{opt}[\overline{p}_t] \), \( A_t = -1 \) or \(+1\) consistently. At the first time step after the activation and deactivation of one and zero agents the history will contain a mixture of \(-1s\) and \(+1s\). However, it is clear that after \( m+1\) time steps it will contain only \(-1s\) and \(+1s\) for \( l < 0.5\) and \( l > 0.5\) respectively and the memory bit corresponding to this history will also take the same value. These states in which the history is \( \{-1, -1, \ldots, -1\} \) and \( h_t = -1 \) or \( \{+1, +1, \ldots, +1\} \) and \( h_t = +1 \) correspond to the attractor states in Fig. [28].

1. Example ELC

Now we shall look at a numerical example. Figure [29] gives the values of the global action \( A_t \), the prediction \( h_t \) and the prediction performance \( \eta_t \). Once again we have also included the virtual points \( v_{i,t} \) of an agent \( i \) which is inactive and has \( p_{i,t} = 1.0 \) at the beginning of the time period shown. Figure [29] is equivalent to Figs. [13] and [24] except that we have additionally included the value of the prediction \( h_t \). Figure [30] shows \( \lambda_t^+ \), \( \eta_t \) and \( P[A_t = -h_t] \) given by Eq. [28]. The paragraph labels below correspond to the labels in Fig. [29].

a Period a, in which \( A_t = +h_t \), provides the trigger which causes the activation and deactivation of zero and one agents.

b,c The (de)activation that is the result of a causes a step increase in \( \lambda_t^+ \) as we expect. However, the magnitude of \( \lambda_t^+ \) during b and c is not sufficiently large that \( P[A_t = -h_t] = 1 \) when \( h_t = +1 \). In fact, as we see from Fig. [31], \( P[A_t = -h_t] \approx 0.9 \) when \( h_t = +1 \). Thus we can see that in this regard the realization of an ELC described here is not ideal in the sense discussed in the previous section. It is because \( P[A_t = -h_t] \neq 1 \) that for the second time step of b \( A_t = +h_t \) resulting in these two interjected time steps. Throughout period c \( A_t = -h_t \) as expected.

d,e,f The interjected period d corresponds to the model finding one of the attractor states in which \( A_t = +h_t \). During period e, \( A_t = +h_t \) once again. However, after the reactivation and deactivation at the end of e...
Therefore, by chance \( A_t = +h_t \) for the next three time steps as well, resulting in the interjected period \( f \). This extra long period in which \( A_t = +h_t \) allows some zero and one agents who had failed to (de)activate during the \( T \) time steps \( e \) to do so. Thus, \( \lambda^2_i \) increases and so therefore does \( P[A_t = -h_t] \) for \( h = +1 \).

**g,h,i** During \( g \), \( A_t = -h_t \) despite the fact that \( P[A_t = -h_t] \approx 0.7 \) (for \( h = +1 \)). \( h \) once again corresponds the model finding the attractor state. \( i \) represents the final period in which \( A_t = +h_t \) before \( \lambda^2_i \) returns to approximately the equilibrium value and the ELC comes to an end.

Note that the periods like \( c \) and \( g \), in which the magnitude of \( \lambda^2_i \) is not sufficiently large that \( P[A_t = -h_t] = 1 \) when \( h_t = +1 \), occur with a much greater probability that they do in the memoryless model. The reason for this is that \( P[A_t = -h_t] = 1 \) when \( h_t = -1 \), unless the magnitude of the oscillations in \( \pi_t \) is so great that \( \lambda^2_i = 0 \). Therefore, for any time steps during periods like \( c \) and \( g \) for which \( h_t = -1 \), \( A_t = -h_t \) with probability \( P = 1 \). We can see this clearly in the plot of \( P[A_t = -h_t] \) in Fig. 31. In Fig. 31 we show once again the volume \( n_t \) and the price \( \pi_t \) over the same period described by Figs. 29 and 30. In Fig. 31a we can clearly see the effect of the discussion in Sec. III C. Each time that \( h_t = -1 \) the price rises with probability \( P = 1 \). Furthermore the result of the deviation of the equilibrium value of \( \pi_t \) from \( \text{opt}(\pi_t) \) (see Sec. II C) is that it is more probable that the price will rise rather than fall when \( h_t = +1 \). These two effects ensure that in equilibrium (between ELC) the price \( \pi_t \) is an increasing function of time. We can see in Fig. 31b that one of the effects of the ELC described in this section is to halt and even briefly reverse this continuous price rise.

The fundamental reason for this behavior is that, as we remarked in Sec. II the agents in the GCGM are unable to control directly whether they will buy or sell at each time step. They can only control the probability with which they will follow the prediction \( h_t \). As we saw in Sec. II the optimum behavior for the agents is to evolve such that the excess demand will be zero when \( h_t \) takes it’s most common value \( (h_t = +1 \) in the case of \( l > 0.5 \)). Therefore, in the asymmetric case of \( l \neq 0.5 \), the magnitude of the excess demand \( \Delta \) will be large when \( h_t \) takes the opposite value. This represents the agents mistakenly believing the prediction which in turn leads to an excess of buyers or sellers for \( l < 0.5 \) and \( l > 0.5 \) respectively.

Johansen and Sornette have provided evidence\(^{25, 27}\) that large price changes in financial markets are outliers. By this it is meant that the frequency with which large price changes occur cannot be predicted using the distribution of smaller price changes. From the results presented in this section, we can see that the large changes that occur in the volume during ELC are also outliers in this sense. The distribution of volume changes between ELC is such that changes of the magnitude observed during an ELC occur with a very small probability. As we saw in Sec. II D a different mechanism (i.e. that of the susceptibility of \( P(p) \) and the occurrence of triggers in \( A_t \)) is responsible of the occurrence of ELC, which therefore occur with a much greater probability.

### G. Summary of ELC Characteristics

We have seen how ELC can occur in the GCGM as a result of the susceptibility of the gene value distribution \( P(p) \) to triggers in the global action time series \( A_t \). We also saw that between ELC the self-segregation of the agents increases the susceptibility of \( P(p) \) while this process is reversed during an ELC. Furthermore we saw that an ELC in the the memoryless GCGM leads to an approximately periodic oscillation in a derived price time series. In contrast the price time series in the full GCGM is a divergent quantity resulting from the inability of the agents to control \( n_t \) directly. In both models ELC lead to approximately periodic volume \( n_t \) oscillations.

### IV. CONCLUSION AND FUTURE DIRECTIONS

In conclusion, we have presented a detailed discussion of the role played by memory, and the nature of self-induced shocks, in an evolutionary population competing for limited resources. We have left open several interesting questions that we hope will be addressed by future work. First of all in Sec. III we have only considered the case in which the death score \( D \) is less than the confidence interval \( T \). The result of this is that agents mutate over a shorter time scale than the period of oscillation of an ELC. We would expect that values of \( D > T \) would lead to ELC that persisted for many more periods.

We have taken the ratio of the number of points gained by an agent when \( a_{i,t} = +A_t \) to that lost when \( a_{i,t} = -A_t \) to be unity. Hod, Nakar and Burgos et al. Refs. \(^{26, 27}\) demonstrated that for values of this prize-to-fine ratio \( R < 1 \) the self-segregation of the gene value distribution observed by Johnson et al.\(^{17}\) is replaced by clustering behavior. In this case the agents tend to evolve towards \( p_{i,t} = 0.5 \) in equilibrium. This has implications for the occurrence of ELC since, as we saw in Sec. III D this clustered gene value distribution is not susceptible to the trigger sequences that cause ELC. Therefore we expect that reducing the prize-to-fine ratio would suppress the occurrence of ELC in the GCGM.

Perhaps most importantly, we showed in Secs. IV and II that for the original Genetic Model in equilibrium \( \pi_t \) deviates from the optimal value given in Eq. (16). This apparently small deviation has some important consequences as it determines the values taken by \( \langle h_t \rangle \) and the magnitude of the autocorrelations observed in the \( h_t \) time series. We have shown that since this effect is not present in the memoryless Genetic Model it does not result from the finite standard deviation of the gene value
FIG. 29: The prediction performance $\eta_t$, $A_t$ and the virtual points $v_{ij}$ of an agent $i$ which initially is inactive and has a gene values of $p_{i,t} = 1.0$. The model is the full GCGM with $n = 500$, $l = 0.5$, $T = 12$, $r = 0.2$ and $m = 3$. The symbols in the margins denote the positions of the step change of $\lambda^i_t$ in Fig. 29.

distribution as we might expect but must instead result from the action of the global memory. We hope that future work will provide clarification of this point.

Acknowledgments

We are extremely grateful to P.M. Hui and T.S. Lo (Chinese University of Hong Kong) for detailed discussions, and for sharing their results with us. RK is financed by an EPSRC studentship.
FIG. 31: Evolution of the number of active agents (also known as the *volume*) and the price (defined by Eq. (60)) over the same time period described by Figs. 29 and 30.

[14] T. S. Lo, Master’s thesis, Physics Department, Chinese University of Hong Kong (2000).
[15] I. Giardina and J.-P. Bouchaud, arXiv:cond-mat/0206222 (2002).
[16] D. Challet, M. Marsili, and Y.-C. Zhang, Physica A 294, 514 (2001).
[17] V. Eguíluz and M. G. Zimmermann, Phys. Rev. Lett. 85, 5659 (2000).
[18] M. L. Hart, D. Lamper, and N. F. Johnson, Physica A 316, 649 (2002).
[19] P. Jefferies, D. Lamper, and N. F. Johnson, Physica A 318, 592 (2003).
[20] P. Jefferies and N. Johnson, arXiv:cond-mat/0207523 (2002).
[21] N. F. Johnson, M. Hart, P. M. Hui, and D. Zheng, Journal of Theoretical and Applied Finance 3, 443 (2000).
[22] D. Lamper, S. D. Howison, and N. F. Johnson, Phys. Rev. Lett. 88, 017902 (2002).
[23] J.-P. Bouchaud and R. Cont, Euro. Phys. J. B 6, 543 (1998).
[24] Y.-C. Zhang, Physica A 269, 30 (1999).
[25] D. Sornette and A. Johansen, Journal of Risk 4 (2001/02).
[26] T. S. Lo, S. W. Lim, P. M. Hui, and N. F. Johnson, Physica A 287, 313 (2000).
[27] A. Johansen and D. Sornette, Euro. Phys. J. B 17, 319 (2000).
[28] Note that in fact $\langle n_i^{t+1} \rangle_t$ lies slightly closer to $N$ than the expression in Eq. (32). This is due to the deviation depicted in Fig. 6 which we shall discuss in Secs. II G and II H.