

# Analysis of Cellular Automata Diffusion Models in Marketing

Gadi Fibich, Ro'i Gibori and Eitan Muller

February 23, 2009

## Abstract

Diffusion of new products is an important problem in marketing research. One of the most prominent models in diffusion theory is the Bass Diffusion model that describes the number of adopters of new products as a differential equation. More recently, diffusion of products has been studied using agent-based modeling and in particular, stochastic cellular automata models. In this study we explore the relation between the Bass model and the cellular automata models. In particular, we explore the differences between the two models that is due to the fact that time is continuous in the Bass model but discrete in cellular automata models, and describe the conditions under which the cellular automata models converge to the Bass model. Empirical verifications of the main results are also discussed.

## 1 Introduction

### 1.1 Background

An important problem in marketing research is the diffusion of new products, or of products in new markets. The diffusion process begins when the product is introduced into the market and progresses through a series of adoption events. There are various adoption models, each attempting to explain the empirical data gathered on diffusion rates of real-life products, in areas such as retail service, industrial technology, agriculture, and educational, pharmaceutical and consumer-durables markets [12]. In this study we model an innovation diffusion process, in which all the adopters keep the new product. This model is suitable, for example, for consumer-durable products with network externalities, such as CB radios, CD players, DVD players and fax machines [9].

The first and most prominent diffusion model in the marketing literature is the Bass Diffusion Model from 1969 [4]. The Bass model describes the diffusion rate of new products or technologies as a differential equation

$$\frac{dN(t)}{dt} = [M - N(t)][p + \frac{q}{M}N(t)], \quad N(0) = 0, \quad (1.1)$$

where  $N(t)$  is the number of people (or organizations) that adopted the product at time  $t$ ,  $M$  is the Market Potential, or population size,  $p$  is the *coefficient of innovation*, a number describing the likelihood of an individual that has not adopted yet, to adopt the product due to influence by the mass-media, public commercials, etc. (externals sources), and  $q$  is the *coefficient of imitation*, a number describing the likelihood of an individual that

has not adopted yet, to adopt the product due to influence by other people who already adopted the product (internal sources).

The Bass model assumes two means of influence over potential adopters: external sources (e.g. mass media) and internal sources (i.e., other adopters)<sup>1</sup>. Therefore, the probability of a non-adopter to adopt at time  $t$  depends on external sources and on the number of adopters at time  $t$  and is the same for each of the  $M - N(t)$  non-adopters at time  $t$ . The rate of new innovators at time  $t$  is  $p[M - N(t)]$ . The rate of new imitators is  $\frac{q}{M}N(t)[M - N(t)]$ , which is the result of all possible internal communications between  $N(t)$  adopters and  $M - N(t)$  non-adopters at a constant rate of  $\frac{q}{M}$ .

The Bass model was found to describe rather accurately the diffusion rate of many products. Typical values for the parameters were found to be  $p = 0.03/\text{year}$  and  $q = 0.38/\text{year}$  with  $p$  often less than  $0.01/\text{year}$  and  $q$  typically in the range  $0.3$  to  $0.5/\text{year}$  [13].

The Bass model is an aggregate model – it describes the diffusion in terms of the behavior of the entire market, and is generally concerned with total number of adopters at a given time  $t$ . In subsequent studies, marketers modeled the diffusion of new products as based on individual adoption decisions [12, pp. 356]. These models typically assume that each individual in the population adopts at a certain time based on both external sources (e.g., mass media) and internal sources (i.e., influence by individuals that already adopted the product). An important question arising from these models is the aggregate behavior of the population given the individual-based behaviors.

In a series of articles ([6, 7, 8, 10]), Goldenberg, Libai and Muller analyzed individual-level diffusion models by simulating the adoption process using *cellular automata*. In this approach, the diffusion process is simulated by computer simulations, so that the adoption decision of each individual in the simulated population is based on a specific adoption probability that is affected by the adoption state of other individuals in its “neighborhood”.

The cellular automata model can be used to study the assumptions of the Bass model. For example, in the Bass model the coefficients of innovation ( $p$ ) and imitation ( $q$ ) are the same for all members of the population. This assumption can be avoided in cellular automata simulations by using different values of  $p$  and  $q$  for each member of the population [6]. Another assumption of the Bass model is that all members of the population can influence each other. This assumption has been studied with cellular automata simulations with a spatial structure that defines the possible flow of communication between members of the population, see e.g. [1] or [5], or analyzed using a percolation theory approach [11].

One should note that we are addressing the comparison between the classical diffusion paradigm and agent-based modeling but leave for future research the complex interrelationship between the former and some other leading-edge tools such as social network analysis or percolation theory. One of the differences between our approach and social network analysis is the simplifying assumption that we make about the social structure of the ties among the participating individuals, an assumption that is necessary in order to compare cellular automata to the Bass process.

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<sup>1</sup>In the marketing literature, people who adopted because of external sources are called ‘*innovators*’, while people who adopted because of internal sources are called ‘*imitators*’.

Let us consider a cellular automata model in which the values of  $p$  and  $q$  are the same for all members, and all members of the population can influence each other. In this case, there is still a key difference between the Bass model and the cellular automata model: Time is continuous in the Bass model, and discrete in the cellular automata model. In this study, we analyze the effect of this difference, which, to the best of our knowledge, has not been done before.

## 1.2 Cellular Automata and the GLM Model

The adoption probability suggested by Goldenberg, Libai and Muller (which we will refer to as the **GLM model** from now on), is calculated as follows:

Consider an individual  $j$  who has not yet adopted. Let  $A_j$  be the number of adopters amongst the neighbors of  $j$ . Then, the probability that individual  $j$  will adopt during the next step of the simulation is

$$\text{Prob}^{\text{GLM}}(j \text{ adopts}) = 1 - [1 - p_{\text{glm}}(j)][1 - q_{\text{glm}}(j)]^{A_j}, \quad (1.2)$$

i.e., the probability of adoption is the complement of the probability of not adopting during this step; and the probability of not adopting is the product of the probabilities of not adopting due to external influences (the term  $[1 - p_{\text{glm}}(j)]$ ), and of not adopting due to internal influence from each of the  $A_j$  neighboring adopters (the term  $[1 - q_{\text{glm}}(j)]^{A_j}$ ). The probability in (1.2) is different from a linear probability model that resembles the Bass model,

$$\text{Prob}(j \text{ adopts}) = p(j) + q(j)A_j.$$

The terms  $p_{\text{glm}}(j)$  and  $q_{\text{glm}}(j)$  may vary with  $j$ . However, under the homogeneity assumption,

$$p_{\text{glm}}(j) \equiv p_{\text{glm}}, \quad q_{\text{glm}}(j) \equiv q_{\text{glm}}.$$

Using the probability (1.2), the algorithm for a cellular automata simulation of the GLM model is as follows:

- Initialize a population of size  $M$  at the state of “Potential Adopters”. The population is positioned on a graph, each member is a node, and “neighbors” are defined by edges connecting the nodes.
- Start a time step loop.
  - At each time step, the adoption probability is calculated for all potential adopters. For each potential adopter  $j$ , a random number  $U_j$  is drawn from a uniform distribution in the range  $[0, 1]$ . If  $U_j < \text{Prob}^{\text{GLM}}(j \text{ adopts})$ , the state of individual  $j$  becomes “Adopted”.
  - Any individual that became “Adopted”, remains so for the rest of the simulation.
- The time step loop ends when a certain fraction of the population has adopted (e.g., 95% of the population).

### 1.3 Structure of Work

The paper is organized as follows.

In Section 2 we consider the **Linear model**, which is the cellular automata model with adoption probability

$$\text{Prob}\{j \text{ adopts in } (t, t + \Delta t)\} = \left[p + \frac{q}{M}n(t)\right]\Delta t.$$

We show that as the population size  $M \rightarrow \infty$ , this model approaches the **Time-Discrete Bass model**

$$n(t + \Delta t) - n(t) = [M - n(t)]\left[p + \frac{q}{M}n(t)\right]\Delta t.$$

This model, in turn, approaches the Bass model (1.1) as  $\Delta t \rightarrow 0$ . These relations are shown in Figure 1.



Figure 1: The relations between the Linear model, the Time-Discrete Bass model and the (Time-Continuous) Bass model.

In Section 3 we consider the GLM cellular automata model. We first generalize this model by including the length of the time-step  $\Delta t$  in the **GLM model**, which is the cellular automata model with adoption probability

$$\text{Prob}\{j \text{ adopts in } (t, t + \Delta t)\} = 1 - (1 - p\Delta t)\left(1 - \frac{q}{M}\Delta t\right)^{n(t)}.$$

We show that this model and the Linear model converge to each other as  $\Delta t \rightarrow 0$ . We also show that as  $M \rightarrow \infty$ , the GLM model approaches the **Time-Discrete GLM model**

$$n(t + \Delta t) - n(t) = [M - n(t)]\left[1 - (1 - p\Delta t)\left(1 - \frac{q}{M}\Delta t\right)^{n(t)}\right].$$

If we take  $\Delta t \rightarrow 0$ , then the Time-Discrete GLM model converges to the Bass model. Hence, as  $M \rightarrow \infty$  and  $\Delta t \rightarrow 0$ , the GLM model converges to the Bass model. These relations are shown in Figure 2.

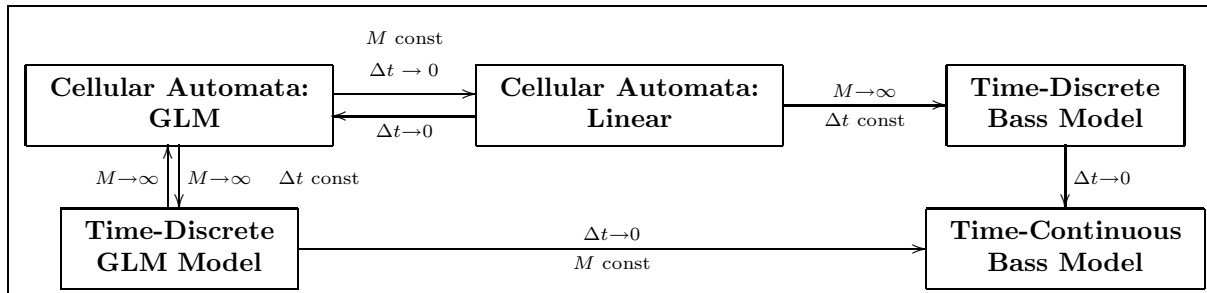


Figure 2: The relations between the GLM model, the Time-Discrete GLM model, the Linear model, the Time-Discrete Bass model, and the (Time-Continuous) Bass model.

In Section 4 we use our results to explain why previous research [6] did not find a good fit between the GLM model parameters and the Bass model parameters.

Finally, in Section 5 we discuss some empirical implications.

## 2 The Linear model

We begin with a description of the basic simple epidemic model with no spatial structure. In this model, we have a population (“market potential”) of size  $M$ . At time  $t = 0$ , none of the members of the population have adopted the new product. A member of the population may choose to adopt the new product due to *external factors* (such as mass media) or due to *internal factors* (influence from other members of the population who already adopted the product). Once a member has adopted the product, he remains an adopter at all later times. The adoption decisions occur at discrete times,  $t_j = j \cdot \Delta t, j = 1, 2, \dots$ . The adoption decision of each non-adopter at  $t_j$  is independent of the decisions of all other non-adopters. For convenience, we denote the time steps  $(t_j, t_{j+1})$  by  $(t, t + \Delta t)$  where  $t = t_j$ .

Let us consider a single member of the population, denoted as Member A, that did not adopt the new product by time  $t = t_j$ .

**Definition 2.1.** Let  $A_{ext.}$  denote the event that Member A adopts due to external influence (mass media, etc.). The event  $A_{ext.}$  is assumed to be random with probability

$$\text{Prob}\{A_{ext.} \text{ in } (t, t + \Delta t)\} = p\Delta t. \quad (2.1)$$

**Definition 2.2.** Suppose member B has already adopted the product. Let  $A_B$  denote the event that member A adopts due to influence from member B. The event  $A_B$  is assumed to be random with probability

$$\text{Prob}\{A_B \text{ in } (t, t + \Delta t)\} = \frac{q}{M}\Delta t. \quad (2.2)$$

We assume that these probabilities are the same for any two members of the population, i.e., that  $p$  and  $q$  are the same for all the members and are independent of  $t$  (the homogeneity assumption).

We further assume the additivity of these probabilities,

$$\begin{aligned} \text{Prob}(\text{A adopts in } (t, t + \Delta t) | \text{State of adopters}) &= \text{Prob}\{A_{ext.} \text{ in } (t, t + \Delta t)\} + \\ &\sum_{\substack{\text{B adopted} \\ \text{by time } t}} \text{Prob}\{A_B \text{ in } (t, t + \Delta t)\}. \end{aligned} \quad (2.3)$$

We now define the *Linear adoption model*:

**Definition 2.3.** The **Linear adoption model** is the following random process. At time  $t = 0$ , no member has adopted. Members can adopt due to external and internal influences, according to relations (2.1), (2.2) and (2.3).

Let us denote by  $n(t)$  the number of members who have adopted by time  $t$ . According to relations (2.1),

(2.2) and (2.3), the conditional probability for a non-adopter  $A$  to adopt in  $(t, t + \Delta t)$  is

$$P_A = \text{Prob}(A \text{ adopts in } (t, t + \Delta t) | n(t) = N) = (p + \frac{q}{M}N)\Delta t.$$

Under the assumptions of our model, adoption decisions are made by every non-adopter at a discrete time  $t_j$ , independently of other non-adopters. Therefore, the number of new adopters at  $(t, t + \Delta t)$  follows the binomial distribution. From the theory of the binomial distribution, we have that the conditional probability for exactly  $k$  new adopters after the adoption decisions at time  $t = t_j$  is given by

$$\text{Prob}(\text{Exactly } k \text{ new adopters in } (t, t + \Delta t) | n(t) = N) = \binom{M - N}{k} P_A^k (1 - P_A)^{M - N - k},$$

and the conditional expected number of new adopters in  $(t, t + \Delta t)$  is given by

$$E\{n(t + \Delta t) - n(t) | n(t) = N\} = (M - N)P_A = (M - N)(p + \frac{q}{M}N)\Delta t. \quad (2.4)$$

One key interest is in the expected value of the number of adopters at time  $t$ , i.e.  $E\{n(t)\}$ , where the expectation is taken over all possible realizations. In what follows, we approximate  $E\{n(t)\}$  using the *deterministic approximation*.

## 2.1 Deterministic approximation

In the deterministic approximation we assume that in each small increment of time, the change in  $n(t)$  is *equal* to the expected change  $E\{n(t + \Delta t) - n(t) | n(t)\}$ . We denote the value of  $n(t)$  under this approximation by  $\bar{n}(t)$ . Notice that while  $n(t)$  is a jump process and assumes only integer values,  $\bar{n}(t)$  may assume any value from 0 to  $M$ . From (2.4), we have the approximation

$$\bar{n}(t + \Delta t) - \bar{n}(t) = [M - \bar{n}(t)][p + \frac{q}{M}\bar{n}(t)]\Delta t. \quad (2.5)$$

If we also let  $\Delta t \rightarrow 0$ , we get that  $\bar{n}(t)$  satisfies the ordinary differential equation:

$$\frac{d\bar{n}(t)}{dt} = [M - \bar{n}(t)][p + \frac{q}{M}\bar{n}(t)], \quad \bar{n}(0) = 0. \quad (2.6)$$

Note that this is exactly the Bass model, equation (1.1). This means that the Bass Diffusion Model can be viewed as a simple epidemic stochastic model, under

1. The deterministic approximation.
2. The limit as  $\Delta t$  goes to zero.

**Definition 2.4.** Because (2.5) is the time-discrete counterpart of the time-continuous Bass model, we will refer to (2.5) as the *Time-Discrete Bass model*.

Equations (2.5) and (2.6) are only approximations for the expected value of  $n(t)$ . In order to get a deeper insight into the nature of these approximations, we prove the following result:

**Lemma 2.5.** *The deterministic approximation (2.5) is equivalent to neglecting the variance of the adoption process.*

*Proof.* From the definition of expectation, we have:

$$E\{n(t)\} = \sum_{N=0}^M N \cdot \text{Prob}\{n(t) = N\}.$$

If we multiply equation (2.4) by  $\text{Prob}\{n(t) = N\}$  and sum over all possible values of  $N$  we get from the law of total expectation:

$$\begin{aligned} E\{n(t + \Delta t) - n(t)\} &= \sum_{N=0}^M \{E\{n(t + \Delta t) - n(t) | n(t) = N\} \text{Prob}\{n(t) = N\}\} \\ &= \sum_{N=0}^M \{[M - N][p + \frac{q}{M}N]\Delta t \cdot \text{Prob}\{n(t) = N\}\} \\ &= E\{[M - n(t)][p + \frac{q}{M}n(t)]\Delta t\}. \end{aligned}$$

From the linearity of the expectation and using the relation

$$\text{Var}\{n(t)\} = E\{[n(t)]^2\} - [E\{n(t)\}]^2,$$

we get

$$E\{n(t + \Delta t) - n(t)\} = [M - E\{n(t)\}] \left[ p + \frac{q}{M}E\{n(t)\} \right] \Delta t - \frac{q}{M} \Delta t \text{Var}\{n(t)\}. \quad (2.7)$$

Comparing equations (2.7) and (2.5) shows that the deterministic approximation is equivalent to neglecting the variance of the adoption process.  $\square$

Since the deterministic approximation is equivalent to neglecting the variance of the adoption process, it is clear that the expected number of adopters under the deterministic approximation, i.e. the solution of equation (2.5) or (2.6), is different from the average of the actual expected number of adopters given by a stochastic solution of the same process. However, for our adoption process, as well as for other classes of stochastic processes, the stochastic solutions tend to the deterministic solution as the size of the population,  $M$ , goes to infinity (see [3, p. 307], [16], [2, Chapter 5]; see [14] for an analysis in a marketing context).

More specifically, Niu ([14]) showed the following: Let

$$f(t) = \frac{n(t)}{M},$$

be the fraction of individuals that adopted by time  $t$ . Let us denote by  $\bar{f}(t)$  its deterministic approximation,

i.e. the solution of the deterministic equation:

$$\frac{d\bar{f}(t)}{dt} = [1 - \bar{f}(t)][p + q\bar{f}(t)], \quad \bar{f}(0) = 0.$$

Note that this equation identifies with (2.6) if we set  $\bar{f}(t) = \frac{\bar{n}(t)}{M}$ . Then,

$$\lim_{M \rightarrow \infty} \text{Var}\{f(t)\} = 0, \quad \lim_{M \rightarrow \infty} E\{f(t)\} = \bar{f}(t). \quad (2.8)$$

This means that as the size of the population increases to infinity, the variance of the normalized number of adopters at time  $t$  diminishes to zero, or equivalently that the mean of the fractional number of adopters at time  $t$  approaches its deterministic approximation, see (2.7).

The relations (2.8) show that the Linear model converges to the Bass model as  $M \rightarrow \infty$  and  $\Delta t \rightarrow 0$ . We make a stronger conjecture, that the variance of the fraction of adopters in the Linear model goes to zero for all  $\Delta t$ , not just when  $\Delta t \rightarrow 0$ .

**Conjecture 2.6.** *For all  $\Delta t$ , the variance of the fraction of adopters in the Linear model, Definition (2.3), tends to zero for all times  $t$  as  $M \rightarrow \infty$ , i.e.*

$$\lim_{M \rightarrow \infty} \text{Var}\{f(t)\} = 0.$$

We then have the following lemma:

**Lemma 2.7.** *Assume that Conjecture (2.6) holds. Then, the number of adopters in the Linear model, Definition (2.3), converges to the Time-Discrete Bass model, Definition (2.4), as the size of the population  $M$  goes to infinity.*

*Proof.* From (2.7) we have

$$E\{f(t + \Delta t) - f(t)\} = [1 - E\{f(t)\}] [p + qE\{f(t)\}] \Delta t - q\Delta t \text{Var}\{f(t)\}.$$

By applying Conjecture (2.6) and changing back from  $f(t)$  to  $n(t)$  we get the Time-Discrete Bass model.  $\square$

Figure 3 summarizes the results of this section:

1. *The number of adopters in the Linear model, Definition (2.3), converges to the Time-Discrete Bass model, Definition (2.4), as the size of the population  $M$  goes to infinity (by Conjecture (2.6)).*
2. *The Time-Discrete Bass model converges to the (Time-Continuous) Bass model (1.1) as the time-step  $\Delta t$  goes to zero.*

In Figure 4 we compare the average fraction of adopters in simulations of the Linear model, Definition (2.3), with the fraction of adopters according to the Time-Discrete Bass model, Definition (2.4). When the size of the





Figure 3: The relations between the Linear model, Definition (2.3), the Time-Discrete Bass model, Definition (2.4) and the (Time-Continuous) Bass model (1.1).

population is small ( $M = 30$ ), the average fraction of adopters in the Linear model grows significantly slower than the Time-Discrete Bass model. However, when the size of the population is large ( $M = 1000$ ), the average fraction of adopters nearly identifies with the Time-Discrete Bass model. Therefore, these results demonstrate the first phase ( $M \rightarrow \infty$ ) of the diagram in Figure 3, and support Conjecture (2.6).

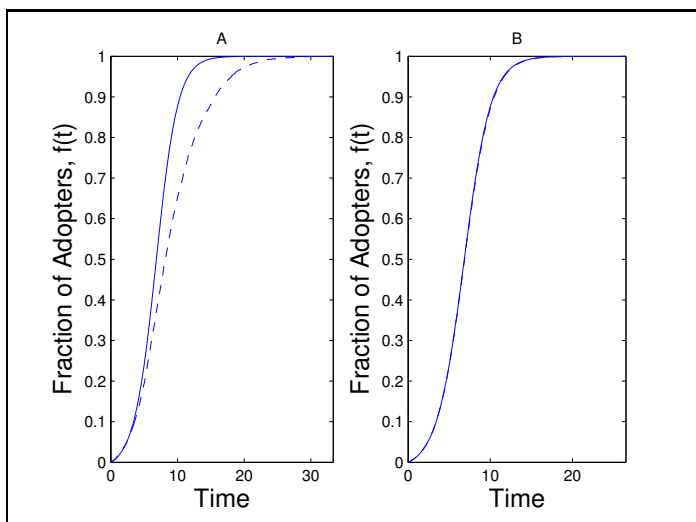


Figure 4: Comparison of the Time-Discrete Bass model, Definition (2.4) (solid) and cellular automata simulations of the Linear model, Definition (2.3) (dashes).  $p = 0.01$ ,  $q = 0.6$ ,  $\Delta t = 1$ , average of 200 simulations. (A)  $M = 30$ , (B)  $M = 1000$ .

In Figure 5 we compare the fraction of adopters according to the Time-Discrete Bass model, Definition (2.4), with the fraction of adopters according to the (Time-Continuous) Bass model (1.1). When  $\Delta t = 1$ , the fraction of adopters according to the Time-Discrete Bass model grows considerably slower than the Bass model. However, when  $\Delta t$  is small (Figure 5B) the fraction of adopters according to the Time-Discrete Bass model nearly identifies with the Bass model. Therefore, these results demonstrate the second phase ( $\Delta t \rightarrow 0$ ) of the diagram in Figure 3.

We now explore the differences between the Time-Discrete and Time-Continuous Bass models. Since for most products the influence of internal sources was found to be much stronger than external sources [13], we first focus on the case  $p \ll q$ .

**Lemma 2.8.** *If  $p \ll q$ , then for  $0 \leq n \leq \left(\frac{q-p}{2q}\right)M \approx \frac{M}{2}$ , the Time-Discrete Bass model grows slower than the Time-Continuous Bass model.*

*Proof.* The Time-Discrete Bass model can be viewed as the Euler approximation to the Time-Continuous Bass model, i.e.

$$n(t + \Delta t) - n(t) \approx \dot{n}(t)\Delta t. \tag{2.9}$$

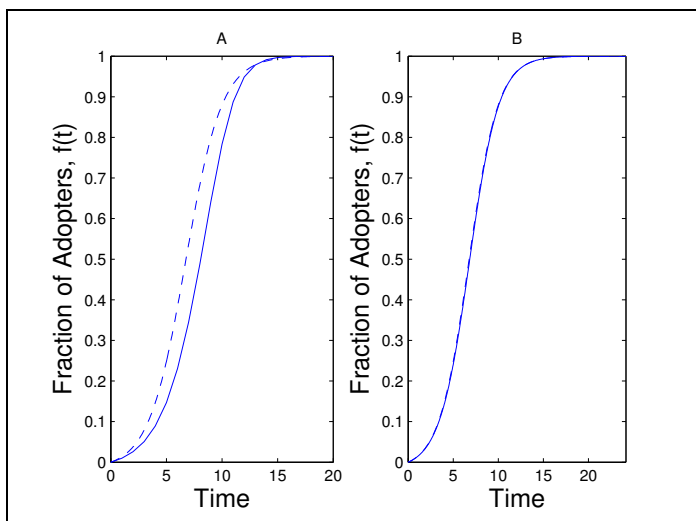


Figure 5: Comparison of the Time-Discrete Bass model, Definition (2.4) (solid) and the Bass model (1.1) (dashes).  $p = 0.01$ ,  $q = 0.6$ ,  $M = 1000$ . (A)  $\Delta t = 1$ , (B)  $\Delta t = 0.05$ .

Let us compare this with the exact expression

$$n(t + \Delta t) - n(t) = \dot{n}(t)\Delta t + \ddot{n}(\Theta)\frac{\Delta t^2}{2}, \quad t < \Theta < t + \Delta t. \quad (2.10)$$

From the Bass model (1.1), we have

$$\dot{n} = Mp + (q - p)n - \frac{q}{M}n^2.$$

Therefore

$$\ddot{n} = \dot{n}(q - p - 2\frac{q}{M}n). \quad (2.11)$$

Since  $\dot{n} > 0$ ,

$$\ddot{n} > 0, \quad \text{for } 0 \leq n < \left(\frac{q-p}{2q}\right)M.$$

Therefore, for  $n < \left(\frac{q-p}{2q}\right)M$ , (2.10) grows faster than (2.9).  $\square$

In the case  $q \ll p$  we find a different behavior:

**Lemma 2.9.** *If  $q \ll p$ , then the Time-Discrete Bass model grows faster than the Time-Continuous Bass model for all  $n$ .*

*Proof.* From (2.11), we find that  $\ddot{n} < 0$  for all  $t$ . Therefore, (2.10) grows slower than (2.9).  $\square$

### 3 Deterministic Approximation of the GLM Model

Let us now derive the time evolution of the deterministic approximation for the GLM model (see section 1.2), using the same approach. We assume again homogeneity of the parameters  $p$  and  $q$ . We also assume that all

the nodes in the population graph are connected to each other (full-connectivity), so this eliminates the spatial dependency of the model.

We begin by generalizing the GLM model as follows. In the original model, the probability of any non-adopter to adopt during the next time step, under the assumptions of homogeneity and full-connectivity, conditioned on the number of adopters at time  $t$ , is given by:

$$\text{Prob}^{\text{GLM}} = 1 - [1 - p_{\text{glm}}][1 - q_{\text{glm}}]^{n(t)}$$

The length of the time step is not explicitly included in this model, or, equivalently, is given by  $\Delta t = 1$ . In order to be able to relate the GLM model to the Linear model, Definition (2.3), we allow the GLM model to include the time step  $\Delta t$ . To do that, we define  $p_{\text{glm}} = p_{\text{glm}}(\Delta t)$  as the probability of a non-adopter to adopt from time  $t$  to time  $t + \Delta t$  due only to external influences, and  $q_{\text{glm}} = q_{\text{glm}}(\Delta t)$  as the probability of a non-adopter to adopt from time  $t$  to time  $t + \Delta t$  due only to internal influence from another adopter. The total adoption probability for a non-adopter  $A$  to adopt from time  $t$  to time  $t + \Delta t$  is then given by:

$$P_A^{\text{GLM}} = \text{Prob}^{\text{GLM}}(A \text{ adopts in } (t, t + \Delta t) | n(t) = N) = 1 - [1 - p_{\text{glm}}(\Delta t)][1 - q_{\text{glm}}(\Delta t)]^N. \quad (3.1)$$

**Definition 3.1.** The *GLM model* is the adoption process with the adoption probability (3.1).

In order to relate the GLM model, Definition (3.1), to the Linear model, Definition (2.3), we prove the following lemma:

**Lemma 3.2.** *Let*

$$p_{\text{glm}} = p\Delta t, \quad q_{\text{glm}} = \frac{q}{M}\Delta t. \quad (3.2)$$

*Then, as  $\Delta t \rightarrow 0$ , the conditional adoption probability for a single non-adopter  $A$  is*

$$\text{Prob}^{\text{GLM}}(A \text{ adopts in } (t, t + \Delta t) | n(t) = N) = \left[p + \frac{q}{M}N\right]\Delta t + O(\Delta t^2).$$

*Proof.* Using equation (3.1) we get that the conditional probability for a non-adopter to adopt during  $(t, t + \Delta t)$  is

$$\begin{aligned} \text{Prob}^{\text{GLM}}(A \text{ adopts in } (t, t + \Delta t) | n(t) = N) &= 1 - (1 - p_{\text{glm}})(1 - q_{\text{glm}})^N \\ &= 1 - (1 - p\Delta t) \left[1 - \left(\frac{q}{M}\Delta t\right)\right]^N \\ &= 1 - (1 - p\Delta t) \left[1 - \frac{q}{M}\Delta t \cdot N + O(\Delta t^2)\right] \\ &= \left[p + \frac{q}{M}N\right]\Delta t + O(\Delta t^2). \end{aligned} \quad (3.3)$$

□

**Corollary 3.3.** *Let  $p_{glm}$  and  $q_{glm}$  be defined as in (3.2). As  $\Delta t \rightarrow 0$ , the expected number of adopters in the GLM model, Definition (3.1), and in the Linear model, Definition (2.3), converge to each other.*

*Proof.* As we have seen in (2.4), since the adoption decision of every non-adopter at each discrete time step  $t = t_j$  is independent from the adoption decisions of other non-adopters, the number of new adopters in  $(t, t + \Delta t)$  is a binomial random variable, and the conditional expected number of new adopters is given by

$$E\{n(t + \Delta t) - n(t) | n(t) = N\} = (M - N)P_A^{\text{GLM}} = (M - N)[1 - (1 - p_{glm})(1 - q_{glm})^N]. \quad (3.4)$$

Using (3.3) we have

$$E\{n(t + \Delta t) - n(t) | n(t) = N\} = (M - N)\left\{ \left[ p + \frac{q}{M}N \right] \Delta t + O(\Delta t^2) \right\} = (M - N)\left[ p + \frac{q}{M}N \right] \Delta t + O(\Delta t^2). \quad (3.5)$$

By comparing (3.5) with (2.4) we conclude that the GLM model, Definition (3.1), and the Linear model, Definition (2.3), converge to each other as  $\Delta t \rightarrow 0$ .  $\square$

The relation between the GLM model and the Linear model is depicted in Figure 6.

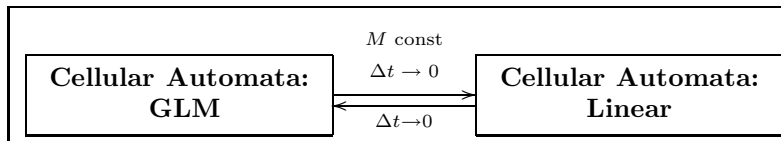


Figure 6: The relation between the Linear model, Definition (2.3) and the GLM model, Definition (3.1).

In Figure 7 we compare the average fraction of adopters in cellular automata simulations of the GLM model and of the Linear model. When  $\Delta t = 1$ , the fraction of adopters according to the GLM model grows slower than the Linear model. However, when  $\Delta t$  is small (Figure 7B) the average fraction of adopters according to the GLM model essentially identifies with the Linear model.

**Corollary 3.4.** *When  $p_{glm}$  and  $q_{glm}$  are defined as in (3.2),  $\Delta t \rightarrow 0$  and  $M \rightarrow \infty$ , the GLM model, Definition (3.1), converges to the (Time-Continuous) Bass model (1.1).*

*Proof.* From Corollary (3.3), we have that as  $\Delta t \rightarrow 0$ , the GLM model identifies with the Linear model. In addition, since  $\Delta t \rightarrow 0$  and  $M \rightarrow \infty$ , we have from the results of Section 2.1 that the Linear model converges to the Bass model. Together, we have that the GLM model converges to the Bass model.  $\square$

Figure 8 depicts the result of Corollary (3.4).

We now show another way to derive Corollary (3.4). Let us consider now the case where  $\Delta t$  does not approach zero. This corresponds, for example, to the original GLM simulations with  $\Delta t = 1$ . The conditional expected number of new adopters in each time increment is still given by (3.4). Let us denote by  $\bar{n}_{glm}(t)$  the deterministic approximation of the number of adopters in time  $t$  according to the GLM model, and define  $p_{glm}$

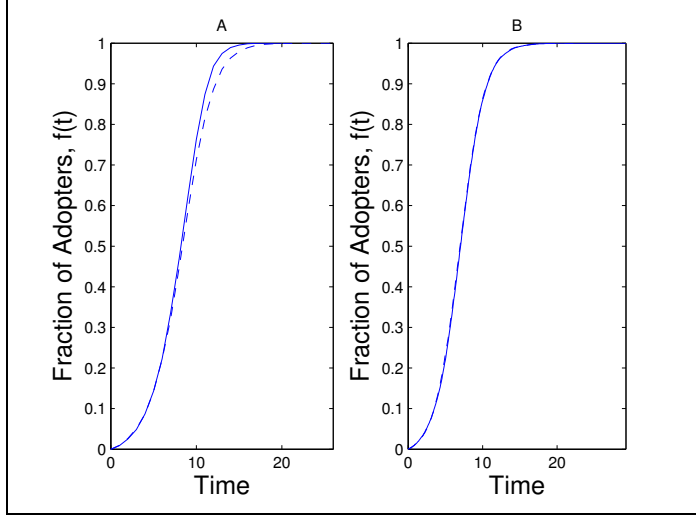


Figure 7: Comparison of the GLM model, Definition (3.1) (dashes) and the Linear model, Definition (2.3) (solid). Here,  $p = 0.01$ ,  $q = 0.6$ ,  $M = 1000$ , average of 20 simulations. (A)  $\Delta t = 1$ , (B)  $\Delta t = 0.05$ .

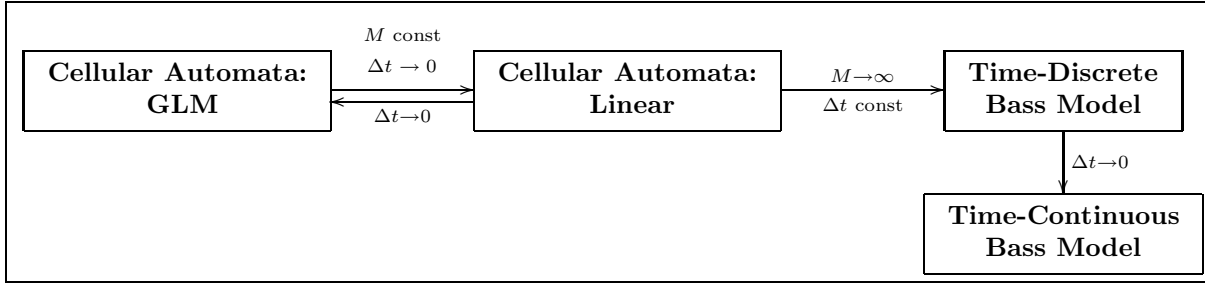


Figure 8: The relations between the GLM model, Definition (3.1), the Linear model, Definition (2.3), the Time-Discrete Bass model, Definition (2.4), and the (Time-Continuous) Bass model (1.1).

and  $q_{\text{glm}}$  as in (3.2). This means that the change in  $\bar{n}_{\text{glm}}(t)$  at each time step is, see (3.4),

$$\begin{aligned}
 \bar{n}_{\text{glm}}(t + \Delta t) - \bar{n}_{\text{glm}}(t) &= E\{n(t + \Delta t) - n(t) | n(t) = \bar{n}_{\text{glm}}(t)\} \\
 &= [M - \bar{n}_{\text{glm}}(t)][1 - (1 - p_{\text{glm}})(1 - q_{\text{glm}})\bar{n}_{\text{glm}}(t)] \\
 &= [M - \bar{n}_{\text{glm}}(t)][1 - (1 - p\Delta t)(1 - \frac{q}{M}\Delta t)\bar{n}_{\text{glm}}(t)].
 \end{aligned} \tag{3.6}$$

**Definition 3.5.** We refer to the deterministic approximation (3.6) as the *Time-Discrete GLM model*.

If we let  $M \rightarrow \infty$ , we conjecture again that the normalized variance of the GLM model approaches zero:

**Conjecture 3.6.** For any  $\Delta t$ , the variance of the fraction of adopters in the GLM model, Definition (3.1), tends to zero for all times  $t$  as  $M \rightarrow \infty$ , i.e.

$$\lim_{M \rightarrow \infty} \text{Var}\{f(t)\} = 0.$$

Using Conjecture (3.6), we get that the expected number of new adopters in each time step converges to the deterministic approximation of the GLM model.

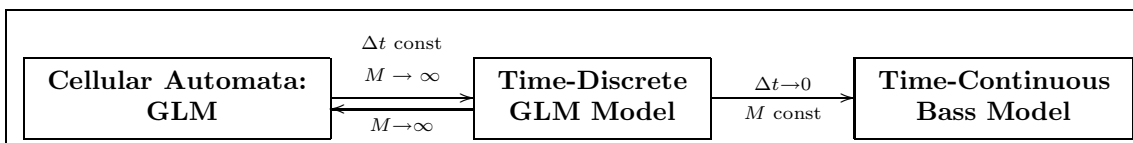


Figure 9: The relations between the GLM model, Definition (3.1), the Time-Discrete GLM model, Definition (3.5), and the (Time-Continuous) Bass model (1.1).

Therefore, we have the following lemma (see also Figure 9),

**Lemma 3.7.** *Assume that Conjecture (3.6) holds. Then, As  $M \rightarrow \infty$ , the GLM model, Definition (3.1) converges to the Time-Discrete GLM model, Definition (3.5).*

To see that, in Figure 10 we compare the average fraction of adopters in simulations of the GLM model, Definition (3.1), with the fraction of adopters according to the Time-Discrete GLM model, Definition (3.5). When the size of the population is small ( $M = 30$ ), the average fraction of adopters in the GLM model grows significantly slower than the Time-Discrete GLM model. However, when the size of the population is large ( $M = 1000$ ), the average fraction of adopters nearly identifies with the Time-Discrete GLM model, in support of Conjecture (3.6).

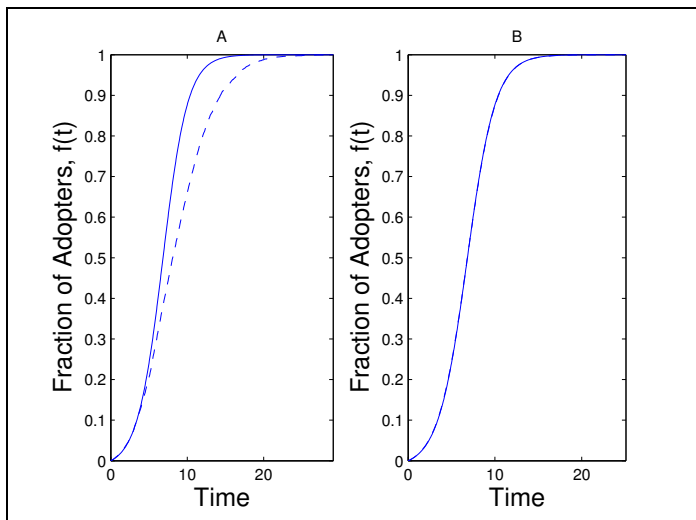


Figure 10: Comparison of the Time-Discrete GLM model, Definition (3.5) (solid) and the GLM model, Definition (3.1) (dashes).  $p = 0.01$ ,  $q = 0.6$ ,  $\Delta t = 1$ , average of 200 simulations. (A)  $M = 30$ , (B)  $M = 1000$ .

We now show that as  $\Delta t \rightarrow 0$ , the Time-Discrete GLM model converges to the Time-Continuous Bass Model (see Figure 9).

**Lemma 3.8.** *Let  $p_{glm}$  and  $q_{glm}$  be defined as in (3.2). Then, as  $\Delta t \rightarrow 0$ ,  $\bar{n}_{glm}(t)$  satisfies*

$$\frac{d\bar{n}_{glm}(t)}{dt} = [M - \bar{n}_{glm}(t)][p + \frac{q}{M}\bar{n}_{glm}(t)], \quad \bar{n}_{glm}(0) = 0.$$

*Proof.* Using (3.3), by the same arguments used in the derivation of equation (2.4), the change in the determin-

istic approximation  $\bar{n}_{\text{glm}}(t)$  in each time increment is then:

$$\begin{aligned}\bar{n}_{\text{glm}}(t + \Delta t) - \bar{n}_{\text{glm}}(t) &= [M - \bar{n}_{\text{glm}}(t)] \left[ 1 - (1 - p\Delta t) \left( 1 - \frac{q}{M} \Delta t \right) \bar{n}_{\text{glm}}(t) \right] \\ &= [M - \bar{n}_{\text{glm}}(t)] \left\{ \left[ p + \frac{q}{M} \bar{n}_{\text{glm}}(t) \right] \Delta t + O(\Delta t^2) \right\}.\end{aligned}$$

If we divide by  $\Delta t$  and take  $\Delta t \rightarrow 0$  we get

$$\frac{d\bar{n}_{\text{glm}}(t)}{dt} = [M - \bar{n}_{\text{glm}}(t)] \left\{ \left[ p + \frac{q}{M} \bar{n}_{\text{glm}}(t) \right] + \lim_{\Delta t \rightarrow 0} \frac{O(\Delta t^2)}{\Delta t} \right\} = [M - \bar{n}_{\text{glm}}(t)] \left[ p + \frac{q}{M} \bar{n}_{\text{glm}}(t) \right],$$

which is the same as the Bass model (1.1).  $\square$

In Figure 11 we compare the fraction of adopters according to the Time-Discrete GLM model, Definition (3.5), with the fraction of adopters according to the Bass model (1.1). When  $\Delta t = 1$ , the fraction of adopters according to the Time-Discrete GLM model grows considerably slower than the Bass model. However, when  $\Delta t$  is small (Figure 11B) the fraction of adopters according to the Time-Discrete GLM model nearly identifies with the Bass model.

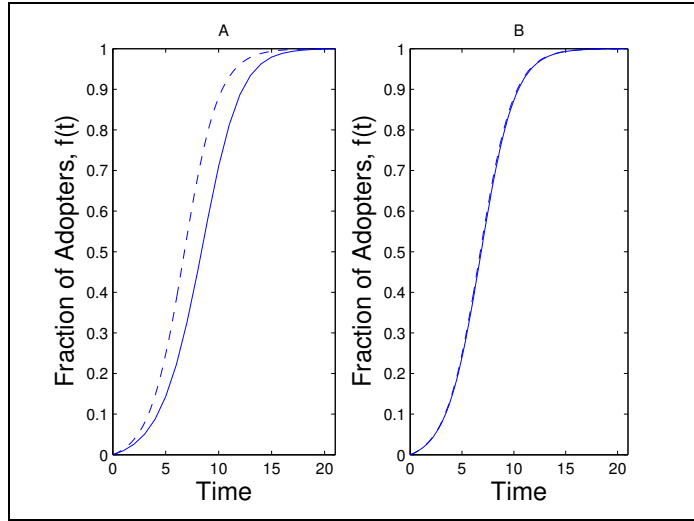


Figure 11: Comparison of the Time-Discrete GLM model, Definition (3.5) (solid) and the Bass model (1.1) (dashes).  $p = 0.01$ ,  $q = 0.6$ ,  $M = 1000$ . (A)  $\Delta t = 1$ , (B)  $\Delta t = 0.05$ .

Previously, we saw that when  $M \rightarrow \infty$  and  $\Delta t \rightarrow 0$ , the GLM model converges to the Bass model, see the diagram in Figure 9. In order to see this numerically, in Figure 12A we compare the averaged fraction of adopters in the GLM model, Definition (3.1), with the fraction of adopters in the Bass model (1.1). The fraction of adopters in the GLM model was averaged over 1000 simulations, and is indeed very close to the fraction of adopters in the Bass model.

In the marketing literature, the predictions of diffusion models are usually tested against the rate of the diffusion, rather than against the fraction of adopters. Therefore, let  $\frac{\Delta n(t)}{M}$  denote the fraction of new (noncu-

mulative) adopters at time  $t = t_j$ ,

$$\frac{\Delta n(t_j)}{M} = \frac{n(t_j) - n(t_{j-1})}{M}. \quad (3.7)$$

In Figure 12B we show the same data as in Figure 12A, in terms of the fraction of new adopters. In agreement with the theoretical prediction, the average fraction of new adopters in the GLM model is in good agreement with the Bass model.

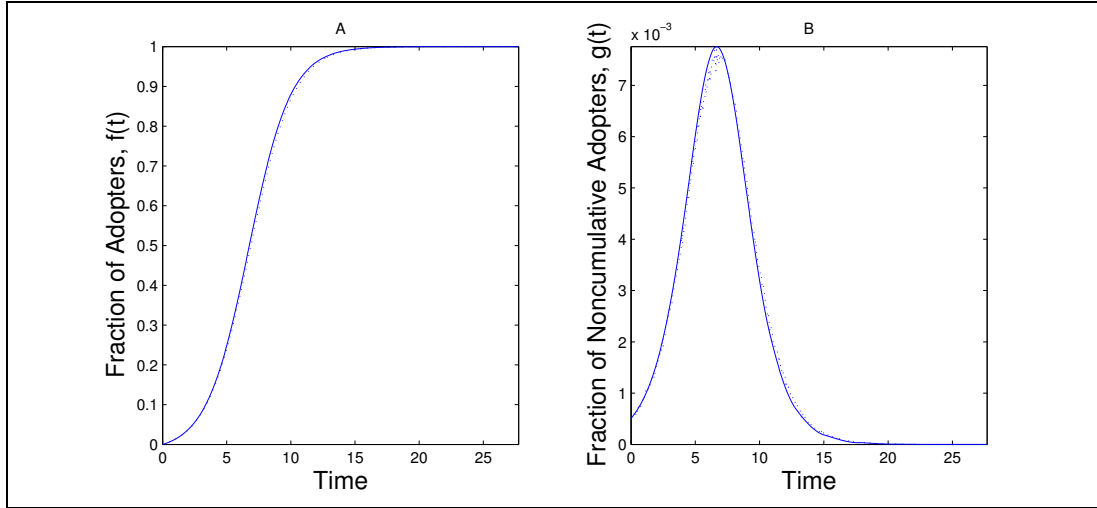


Figure 12: Comparison of the fraction of adopters in the GLM model, Definition (3.1) (dots) and the Bass model (1.1) (solid).  $p = 0.01$ ,  $q = 0.6$ ,  $M = 1000$ ,  $\Delta t = 0.05$ , average of 1000 simulations. (A) Total (cumulative) adopters, (B) New (noncumulative) adopters, see (3.7).

### 3.1 Convergence of the GLM Model to the Bass Model

In summary, we showed that the GLM model converges to the Bass model as  $\Delta t \rightarrow 0$  and  $M \rightarrow \infty$  in two ways (see Figure 13):

1. As  $\Delta t \rightarrow 0$ , the GLM model converges to the Linear model, which, as  $M \rightarrow \infty$  and  $\Delta t \rightarrow 0$ , converges to the Bass model.
2. As  $M \rightarrow \infty$ , the GLM model converges to the Time-Discrete GLM model, which, as  $\Delta t \rightarrow 0$  converges to the Bass model.

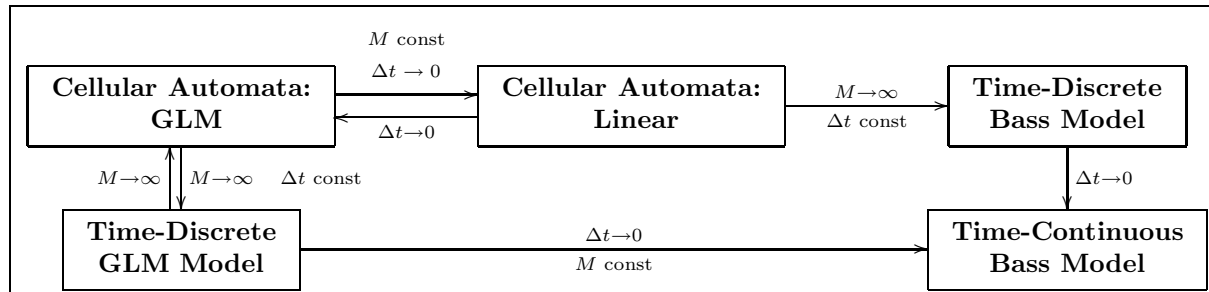


Figure 13: The relations between the GLM model, Definition (3.1), the Time-Discrete GLM model, Definition (3.5), the Linear model, Definition (2.3), the Time-Discrete Bass model, Definition (2.4), and the (Time-Continuous) Bass model (1.1).



## 4 Relationship Between Individual and Market-Averaged Parameters

In [6], Goldenberg, Libai and Muller explored the relation between the parameters in their cellular automata model ( $p_{\text{glm}}$  and  $q_{\text{glm}}$ ), and the parameters in the Bass model ( $p$  and  $q$ ) as follows. They conducted a series of experiments with different values of  $p_{\text{glm}}$  and  $q_{\text{glm}}$ . They expected the relationship to be

$$p_{\text{glm}} \approx p, \tag{4.1}$$

$$q_{\text{glm}} \approx \frac{q}{M}. \tag{4.2}$$

They varied  $p_{\text{glm}}$  in the range 0.004 to 0.04, which is a typical range for  $p$  from previous marketing research. Since 0.001 to 1 is a typical range for  $q$  from previous marketing research, and because they used in their simulations populations of size  $M = 1000$ , they varied  $q_{\text{glm}}$  in the range 0.00001 to 0.001. They used a total of 100 combinations of  $p_{\text{glm}}$  and  $q_{\text{glm}}$ . For each combination, a cellular automata simulation was conducted. Using non-linear least squares fit, the Bass model parameters  $p$  and  $q$  were estimated for the resulting adoption curves. Using ordinary least squares regression, they determined the relationship between the cellular automata parameters and the Bass parameters. As expected, they found that  $q$  was generated almost entirely by  $q_{\text{glm}}$  (the correlation was  $r = 0.99$ ) while  $p_{\text{glm}}$  had almost no effect on  $q$  ( $r = 0.015$ ), in agreement with (4.2). However, they found that both  $p_{\text{glm}}$  and  $q_{\text{glm}}$  had a strong correlation with the parameter  $p$ : although  $p$  was generated mostly by  $p_{\text{glm}}$  ( $r = 0.9$ ), it was also influenced by  $q_{\text{glm}}$  ( $r = -0.29$ ), in disagreement with (4.1).

Let us explain why the results of [6] did not agree with (4.1). We saw that if

$$p_{\text{glm}} = p\Delta t, \quad q_{\text{glm}} = q\Delta t,$$

then as  $M \rightarrow \infty$ , there is an excellent fit between the cellular automata simulations and the Time-Discrete GLM model (see (3.2) and Figure 10). Since  $\Delta t = 1$  in the simulations of [6], their results should agree with the Time-Discrete GLM model with  $\Delta t = 1$  where the relations between  $p_{\text{glm}}$ ,  $q_{\text{glm}}$ ,  $p$  and  $q$  are given by (4.1), (4.2), and not with the Time-Continuous Bass model. Therefore, the disagreement of their results with (4.1) is because they compared their results with the Time-Continuous Bass model instead of the Time-Discrete GLM model. As we saw, when  $\Delta t = 1$ , there are significant differences between these two models (see Figure 11).

## 5 Empirical verification

We now show some empirical verification of our main results. Indeed, while the Bass model is time-continuous, empirical data are always time-discrete. Therefore, when we try to find the values of  $p$  and  $q$  from empirical data, the sampling period  $\Delta t$  may affect the values of  $p$  and  $q$  that we obtain. Indeed, our analysis highlighted the importance of the discrete-time period  $\Delta t$ , and that it should be sufficiently small in order to agree with

the continuous model. We now confirm this consequence using empirical data.

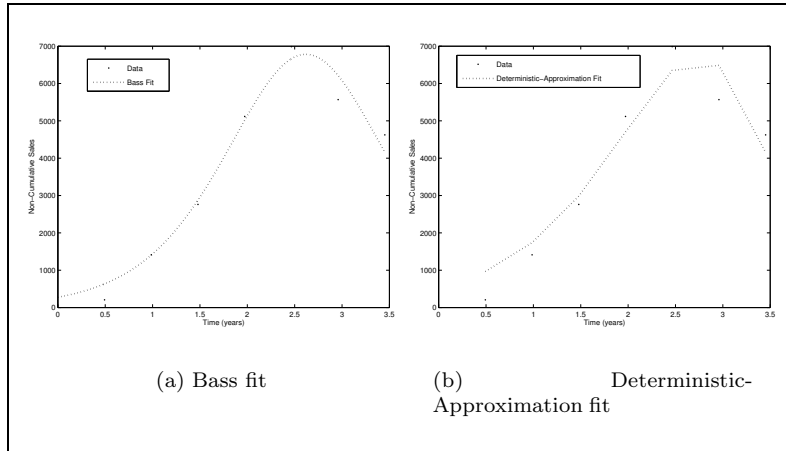


Figure 14: UK non-cumulative sales during periods of  $\Delta t = 6$ -months, fitted with derivatives of the Bass model (left panel) and the Deterministic-Approximation model (right panel).

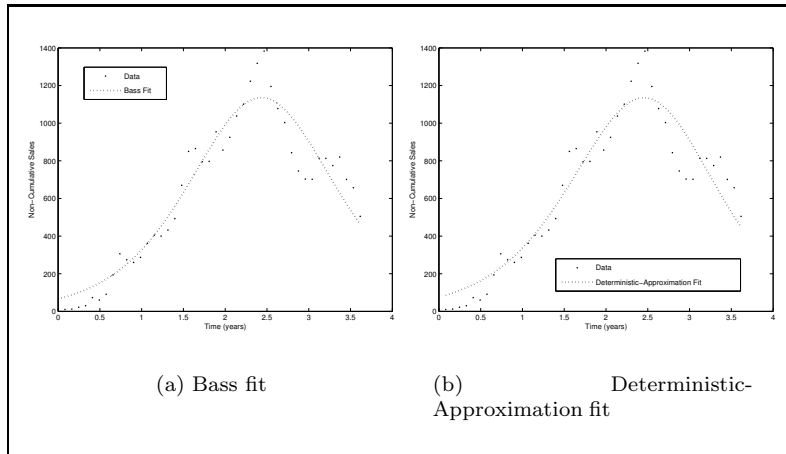


Figure 15: Same as Figure 14 with  $\Delta t = 1$ -month.

We now apply our theoretical analysis to the analysis of data of daily sales of a software tool in the UK, over a period of 3.5 years. We denote by  $N(t)$  the total number of sales by time  $t$ , and by  $\Delta N(t) = N(t) - N(t - \Delta t)$  the number of sales between  $t - \Delta t$  and  $t$ . According to the Bass model,

$$\Delta N(t) \approx N'(t) \cdot \Delta t = M \frac{p(p+q)^2 e^{-(p+q)t}}{[p + qe^{-(p+q)t}]^2} \Delta t. \quad (5.1)$$

According to the deterministic approximation,

$$\Delta N(t) \approx [M - N(t)] \left[ p + \frac{q}{M} N(t) \right] \Delta t. \quad (5.2)$$

In Figure 14 we present the non-cumulative sales over a period of  $\Delta t = 180$  days, and find the values of  $p$  and  $q$  that provide the best fit to the Bass model, see equation (5.1), and to the Discrete approximation model, see equation (5.2). We then repeat the same procedure for  $\Delta t = 30$  days,  $\Delta t = 7$  days and  $\Delta t = 1$  day

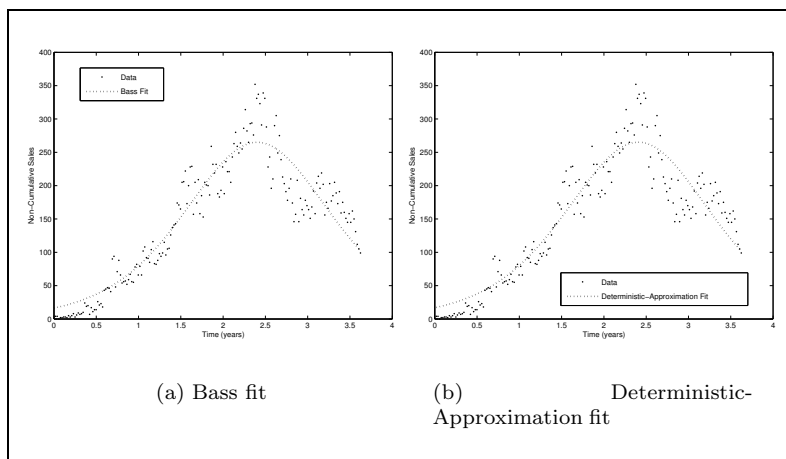


Figure 16: Same as Figure 14 with  $\Delta t = 1$  week.

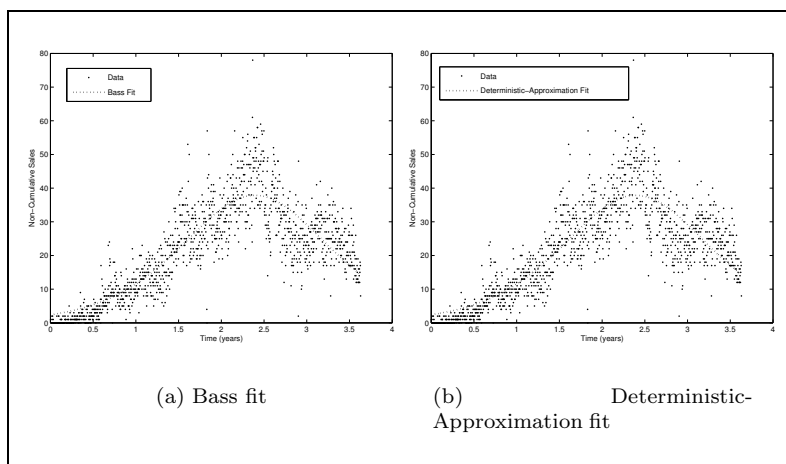


Figure 17: Same as Figure 14 with  $\Delta t = 1$  day.

(Figures 15–17).

In Table 1 we summarize the values  $p$ ,  $q$  and the adjusted  $R^2$  obtained in the fitting process. Obviously, as  $\Delta t$  decreases, the data become more noisy, and therefore the value of the adjusted  $R^2$  decreases. When  $\Delta t = 6$  months, the value of  $p \approx 0.018$  predicted by the Bass model is only 26% of the value of  $p \approx 0.068$  predicted by the DA model. As we reduce the sampling period to  $\Delta t = 1$  months, the values of  $p$  predicted by both models change considerably, and get closer to each other. Further reduction of the sampling period to  $\Delta t = 1$  week and to  $\Delta t = 1$  day has a much smaller effect on the value of  $p$ . In particular, the large difference between the predictions of the two models at large  $\Delta t$ , essentially disappears as  $\Delta t$  “goes to zero”, in agreement with our previous analysis. Unlike  $p$ , the value of  $q$  is nearly independent of  $\Delta t$ , as well as the model being used, but also show a (fast) convergence to the Bass model.

In conclusion, we see that, as predicted by our analysis, the discrete approximation model, as well as the Bass model applied to a time discrete data set, agrees with the continuous Bass model only if  $\Delta t$  is sufficiently small.

Model	$\Delta t$	$p(1/year)$	$q(1/year)$	Adj. $R^2$
Bass	180 days	0.018	1.73	0.96
DA	180 days	0.068	1.74	0.90
Bass	30 days	0.026	1.70	0.91
DA	30 days	0.033	1.70	0.91
Bass	7 days	0.027	1.70	0.88
DA	7 days	0.029	1.70	0.88
Bass	1 day	0.027	1.70	0.76
DA	1 day	0.028	1.70	0.76

Table 1: Empirical values of  $p$  and  $q$  obtained using the Bass model and the Discrete Approximation (DA) model.

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