

Diffusion Processes and Event History Analysis*

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Abstract

Several authors (e. g., Brüderl, Diekmann, Yamaguchi) derive hazard rate models of event history analysis from social diffusion processes. This paper also focuses on the integration of diffusion research and survival analysis. After a discussion of Diekmann's flexible diffusion model, we present an alternative approach which clarifies theoretical differences between popular rate models (e. g., the exponential model, log-logistic model, sickle model). Specifically, this approach provides a new rationale for the generalised log-logistic model in the sense of a flexible infection process. In cases with bell-shaped duration dependence, it thus allows a test for social contagion as a result of random contacts between actual and potential adopters. An application to divorce data serves as an illustration.

1 Introduction

Techniques of event history modeling are increasingly used in the social sciences. The range of applications includes labour market studies, demographic analyses, mobility studies, studies in organisational ecology, political science, etc. Undoubtedly, the availability of panel and retrospective data sets (e. g., the German Socioeconomic Panel, Family and Fertility Surveys), different introductory textbooks (e. g., Blossfeld and Rohwer 1995; Courgeau and Lelièvre 1992; Diekmann and Mitter 1984; Lancaster 1990), as well as suitable software (e. g., Rohwer's TDA), have promoted the spreading of these methods.

Parametric approaches to survival analysis have, however, at least one deficiency: a theoretical explanation for the estimated statistical model is usually lacking. Generally, for any given event data, the shape of the empirical transition rate is determined first by using non-parametric procedures (e. g., the Kaplan Meier estimator). This empirical evidence about the course of the so-called hazard rate or risk function is then used for the selection of a suitable parametric model which is subsequently estimated above all by the maximum likelihood method, taking into account covariates. Theoretical considerations rarely refer to the selected hazard rate model, but rather to the selection and interpretation of covariates for the explanation of the risk

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process by endogenisation of at least one process parameter. This is mostly unproblematic if the shape of the empirical risk function suggests a unique parametric model for statistical estimation.¹

However, many social processes are characterised by similarly shaped rates which can be described, from a theoretical point of view, by different models. Such a situation results, for instance, in the case of an approximately bell-shaped hazard rate. This form is found more or less regularly in the investigation of marriage behaviour, divorce risk, or mobility in firms. Different non-monotonous hazard rate models can be used for its representation. In addition to the gamma model, the log-normal model, or the log-logistic standard model, Diekmann and Mitter's (1983, 1984a) sickle model and Brüderl and Diekmann's (1995) generalised log-logistic model, can be applied to the data. A theoretically justified selection between such alternative models would be desirable.

In order to obtain this theoretical foundation, some authors (e. g., Brüderl and Diekmann 1995; Diekmann 1990, 1992; Yamaguchi 1994) link event history models with models from diffusion research (e. g., Hamblin, Jacobsen and Miller 1973; Mahajan and Peterson 1985; Rogers 1983). Here, the idea that the respective event history model can be interpreted in terms of a social diffusion process is fundamental. The common starting point of these works is in each case a general differential equation which covers a multiplicity of diffusion hypotheses as special cases and thus supplies a process-theoretical rationale for different hazard rate models. Similarly shaped rates may also correspond to quite different diffusion processes so that the knowledge of the underlying process hypotheses can in principle be helpful in the selection of a suitable rate model. Under similar conditions (e. g., goodness of fit), preference should be given to that event history model which is accompanied by a theoretically more plausible diffusion hypothesis for the application under consideration. If, on the other hand, there exists a unique hazard rate model that is clearly preferable from a statistical point of view, then the knowledge of the compatible diffusion process at least promotes an understanding of the process under consideration.

The connection between diffusion research and event history analysis is the focus of the present paper. After an introduction of central concepts, we discuss Diekmann's (1990, 1992) flexible diffusion model (Section 2). Subsequently, we present a more restrictive model (Section 3). This approach illustrates differences in the underlying theoretical processes between established event history models (e. g., the exponential model, log-logistic model, sickle model). Specifically, this approach provides a new rationale for Brüderl and Diekmann's (1995) generalised log-logistic model in the sense of a flexible infection process. In cases with bell-shaped duration dependence it thus allows a test for social contagion due to random contacts between

¹ Some economic models of unemployment durations and job durations have been successful in predicting the shape of the duration dependence. However, they do not rely on diffusion processes but model the job search behaviour with stochastically arriving job offers (see for example the survey in Van den Berg 2001).

actual and potential adopters. An application to divorce data serves as an illustration (Section 4). Because it is especially unlikely that divorce has much to do with social contagion, the suggested approach of connecting diffusion research and event history analysis can be tested to see if it leads to plausible results.

2 Foundations

2.1 Concepts

Let us consider a social system with a large number of individuals who, in a given period of time, are confronted with a binary and absorbing event the occurrence of which can be interpreted as a result of a decision (e. g., marriage, divorce, adopting new technologies).² Let T be a non-negative continuous random variable, representing the duration until the occurrence of an event (arrival time or waiting time, depending upon the viewpoint) with distribution function $F(t)$ and density function $f(t)=dF(t)/dt$. Because $F(t)$ defines the proportion of the population which has already experienced the event up to time t , $1 - F(t)$ represents the complementary proportion without the event up to this point in time. The hazard rate $h(t) = f(t)/(1 - F(t))$ then gives (approximately) the conditional probability of a change in status in the (very small) time interval $[t, t + \Delta t]$ if the event has still not occurred before t .

These concepts were originally introduced and interpreted in the sense of event history analysis. From the perspective of diffusion research, other terms can be used which are at least partly borrowed from epidemiology (cf., e. g., Kramer 1988). Since $F(t)$ defines the proportion of prior adopters or those “infected” at time t , this quantity indicates the period-specific prevalence rate. The derivative or density $dF(t)/dt = f(t)$ can thus be interpreted as the increase in prevalence during a (short) additional time interval.³ Because $1 - F(t)$ defines the respective proportion of potential adopters (population at risk) and $h(t) = f(t)/(1 - F(t))$ applies this by definition, the hazard rate $h(t)$ can be interpreted as the “incidence rate”.⁴ It captures the (relative) influx to the group of adopters during the brief time interval $[t, t + \Delta t]$.

² Biologically or technically caused events, such as deaths or damage to a machine, do not fall into this category.

³ Because $dF(t)/dt = f(t)$ expresses the increase in the proportion of adopters per time unit, $f(t)/F(t)$ indicates the respective growth rate of the prevalence.

⁴ According to Kramer (1988: 27–32) the prevalence rate defines the proportion of adopters in a certain population at a fixed point in time. In contrast, the incidence rate always refers to a time interval. It defines the proportion of non-adopters from this population who become adopters during a certain period. In our context (ignoring absolute sizes) the incidence rate corresponds therefore to the hazard rate $h(t)$, while the respective prevalence rate is given by the distribution function $F(t)$. For a very small prevalence rate of a feature (e.g., the proportion of regular consumers of hard drugs in the total population) one can capture the incidence rate by the density function $f(t)$, because in this case $f(t)$ and $h(t) = f(t)/1 - F(t)$ are approximately equal.

Thus, a process such as spreading of behaviours (or the occurrence of events) takes account of a connection between incidence and prevalence. In other words, a diffusion process reflects a functional relationship between $h(t)$ and $F(t)$. Due to the large number of possible relations and the definition of the hazard rate, the density $f(t)$ should be expressed as a sufficiently general function of the prevalence $F(t)$. We now turn to such an integration of diffusion research and event history analysis.

2.2 Flexible diffusion model

A general model for connecting the logic of diffusion and event history analysis is suggested by Diekmann (1990, 1992). His model is based on a differential equation. Accordingly, the spread of the feature under consideration, or the occurrence of the relevant event, can be thought of as a consequence of the information flow within the system. The adoption of a behaviour or the occurrence of an event is a result of information that is passed on either through interaction with adopters or by sources of influence (e. g., the mass media) that are present throughout the system. To capture different diffusion processes, Diekmann makes the assumption that the information transfer takes place by contacts between a subset of the already infected and not infected portions of the population.⁵ The mixing assumption is $p(t) = F(t)^m(1 - F(t))^n$, where m and n are arbitrarily selectable parameters not interpreted as to content. Because this product indicates the proportion of interactions between sections of the population at t , one can view $p = p(t)$ as the probability of an informative and thus potentially infectious contact for members of the risk population at time t .⁶ Its weighting with an arbitrarily selectable adoption rate $s(t) > 0$ then determines the increase on the proportion of adopters per unit of time:

$$\frac{dF(t)}{dt} = s(t)F(t)^m(1 - F(t))^n. \quad (1)$$

Therefore, the corresponding hazard rate is:

$$h(t) = s(t)F(t)^m(1 - F(t))^{n-1}, \quad (2)$$

⁵ The related assumption of a “homogeneous mixing” of the population, concerning infection status, characterises standard models in epidemiology as well (e.g., Anderson and May 1991; Bailey 1975). The actors do not differ with regard to age, education, sex etc. Research on socially structured diffusion expanded enormously as a result of the AIDS epidemic. Morris (1994) presents an overview and a modeling suggestion for dealing with non-homogeneous mixing in epidemiological models which is based on log-linear methods. Strang (1991) discusses the role of event history analysis when introducing social-structural features into models of social diffusion.

⁶ The function $p(t)$ can also be related to the popular economic concept of the matching function or meeting function in economics, specifying the flow of filled jobs as a function of the stock of unemployed and the stock of vacancies (see e.g. the survey by Petrongolo and Pissarides 2001).

so that very different connections between incidence and prevalence are possible.⁷ The type of diffusion process as well as the interpretation of the adoption rate $s(t)$ is determined to a large degree by the selection of the parameters m and n . In particular, we can differentiate three processes:

- The parameter combination $m = 1$ and $n = 1$ defines the probability of a potential infection of possible adopters per unit of time through $p(t) = F(t)(1 - F(t))$. Individual instances of adopting behaviour or of events can thus be interpreted as resulting from coincidental interactions between prior and potential adopters. This scenario is based on the assumption of homogeneous mixing after contagion. It thus illustrates pure infection processes. According to Diekmann, $s(t)$ represents the contagion rate for interactions between actors with and without a given feature (event).⁸
- As a result of the parameter constellation $m = 0$ and $n = 1$, the probability of a potentially influential contact for potential adopters per unit of time arises through $p(t) = 1 - F(t)$, the proportion of the population at risk. Adopting a behaviour can be understood here as a result of contacts of this part of the population with the total system. One can thus regard this as consequences of the influence of system-wide sources (e. g., mass media), so that $s(t)$ is interpretable in Diekmann's sense as a time-dependent influence rate.⁹
- The parameter combination $m = 0$ and $n = 2$ determines the probability of a potentially influential contact for members of the risk population per unit of time through $p(t) = (1 - F(t))^2$. In this scenario the crucial role is played by interactions between potential adopters. Diekmann (1990) speaks of matching processes (e. g., a sales contract, marriage) in this case, in which $s(t)$ is to be understood as the time-dependent matching rate.

Diekmann's approach certainly offers an elegant connection between diffusion-theoretical logic and event-analytic methodology. However, there are also arguments that justify the formulation of an alternative approach for the integration of diffusion research and event history analysis:

⁷ Diekmann (1990, 1992), Yamaguchi (1994), and Brüderl and Diekmann (1995) present detailed discussions of special cases of this approach for integrating diffusion research and event history analysis.

⁸ The example of such an infection process that is probably the most well-known is the logistic model applied by Coleman, Katz and Menzel (1957) which results from (1) for $m = n = 1$ and $s(t) = \alpha$.

⁹ The classical example of such an influence process is the exponential model which has already been applied by Coleman, Katz and Menzel (1957). Instead of "influence by the system", one frequently reads about "external influence" in the diffusion-theoretical literature (e. g., Mahajan and Peterson 1985), whereas infection stemming from contacts between actors with or without the feature is referred to there as "internal influence".

- First, it is striking that the two parameters are unlimited. According to the logic of the diffusion approach, one can interpret $p(t) = F(t)^m(1 - F(t))^n$ as the probability of an informative contact for potential adopters. Because $F(\cdot)$ is a distribution function, however, $p(t) = F(t)^m(1 - F(t))^n \leq 1$ must apply. This condition is possibly violated with unrestricted values of m and n (example: $m = -1$, $n = 1$ and $F = 0,4$). It is fulfilled, for example, by the restrictions $m \geq 0$ and $n \geq 0$.
- If one is limited to the scenario $m \geq 0$ and $n \geq 0$, then m and n determine the interacting parts of the groups of prior and potential adopters. It is unclear whether and how the two parameters m and n can be interpreted according to their content. It is not clear here, for instance, why $m = n = 0$ always means that $p = 1$, but $m \rightarrow \infty$ and/or $n \rightarrow \infty$ always leads to $p = 0$.
- Apart from the selection of the respective interaction pattern by specification of m and n , the approach also permits an arbitrary definition of the adoption function $s(t)$. In principle the number of parameters, and the functional form of $s(t)$, can be freely determined. This flexibility is reflected in the fact that there are different diffusion-theoretical explanations for one and the same hazard rate model. Thus, the log-logistic standard model can be interpreted both as an infection process and a matching process.¹⁰ For other standard models of event history analysis (e. g., exponential distribution, generalised log-logistic model, sickle model), ambiguous diffusion-theoretical interpretations are also possible since one can freely choose m , n , and $s(t)$ (Braun 1998). In order to arrive at a unique derivative of individual event models from (1), one could follow, e. g., Yamaguchi (1994), and concentrate on pure contagion processes ($m = n = 1$) with flexible selection of the adoption rate $s(t)$.

In the following section we will focus on an alternative way to avoid such ambiguities and interpretation problems. This approach deviates substantially from Diekmann's approach in at least two aspects. The arbitrary adoption function $s(t)$ is replaced by a flexible function, and the parameters m and n which are unclear as far as content is concerned, are eliminated in favour of an interpretable quantity. Although fundamental considerations and established concepts are maintained wherever possible, these differences already find expression in the model assumptions we specify below.

¹⁰ According to Diekmann (1992), one gets the infection theory explanation for the log-logistic standard model by the parameter selection $m = n = 1$ and the infection rate $s(t) = \alpha/t$ in (1), whereas the interpretation of the model as a matching process results from the specifications $m = 0$, $n = 2$ and $s(t) = \alpha\gamma(\gamma t)^{\alpha-1}$ with $\alpha, \gamma > 0$ in (1).

3 An alternative model

3.1 Model assumptions

Once again, we assume that spreading processes result from appropriate information about the characteristic or event under consideration and the respective willingness of the actors to adopt them. Sources of information are interactions between actors in the system. However, only a subset of all contacts is informative with regard to the feature, and not every informative contact necessarily leads to the occurrence of an event. It therefore makes sense to first determine the probability of an interaction with an adopter per unit of time and then to specify accordingly the time-dependent adoption function of potential adopters. A simple assumption for linking these quantities results finally in a flexible hazard rate function and thus in a general diffusion model.

3.1.1 Probability of informative contacts

The quantities $F(t)$ and $1 - F(t)$ represent the respective proportions of prior and potential adopters in the system. If all actors (independent of their status concerning the event) possess the same chance of beginning an interaction, $F(t)$ determines the probability of an individual coincidentally meeting a prior adopter. On the other hand, $(1 - F(t))$ determines the probability that such a contact is not with an adopter and therefore uninformative with regard to the event. If one now supposes for each actor in the system k statistically independent contacts per unit of time, then $(1 - F(t))^k$ gives the probability that an individual has had no contact with an adopter. Thus,

$$w(t) = 1 - (1 - F(t))^k \quad (3)$$

is the probability that at least one of k 's statistically independent contacts of any given actor with an adopter will occur, and is therefore informative concerning the event.¹¹ The function $w(t)$ increases *ceteris paribus* with k , the statistically independent contacts of each actor in the system per time unit: for $k = 0$, $w(t) = 0$; for $k = 1$, $w(t) = F(t)$; for $k = 2$, $w(t) = F(t)(2 - F(t))$; and $k \rightarrow \infty$ corresponds to $w(t) = 1$. Under otherwise identical conditions, $w(t)$ increases along with the prevalence rate $F(t)$. Because the latter usually increases with time, the probability of a potentially influential contact also tends to increase with time passed (since the beginning of the process). There is also often a positive or negative time dependency that characterises the willingness of potential adopters to adopt the characteristic in question.

¹¹ The quantity $w(t)$ defines the probability of an informative contact for each actor in the system independent of his status concerning the feature. Thus it differs in conception from $p(t)$, the probability of an informative contact for members of the risk population in Diekmann's approach.

3.1.2 The adoption function

In order to achieve a complete parameterisation, a sufficiently general adoption function $r(t) > 0$ is introduced which determines the adoption rate per unit of time.¹² This function possesses the real-number parameters $c > 0$, $\delta > 0$, δ and $\varepsilon \geq 0$:¹³

$$r(t) = ce^{\delta t} t^{\varepsilon-1}, \quad (4)$$

where e defines the base of the natural logarithm, and the scaling parameter c can be re-parameterised if necessary.¹⁴ Thus, the adoption rate for $\delta = 0$ and $\varepsilon = 1$ is a constant. In all other cases it depends on the time t , though the effect is influenced substantially by the combination of the respective parameters δ and ε . The elasticity function of $r(t)$ gives a brief summary of all possibilities. The elasticity of the adoption rate is a linear function of the time passed since the beginning of the process:

$$\frac{dr(t)}{dt} \frac{t}{r(t)} = (\varepsilon - 1) + \delta t. \quad (5)$$

A one per cent increase in the time passed changes the adoption rate by approximately $100(\varepsilon - 1 + \delta t)\%$. The time elasticity of the willingness of adoption is formulated in the definition of diffusion processes and the corresponding hazard models assumptions. Before this can be made clearer, we first need to introduce an assumption about the determinants of the hazard rate.

3.1.3 Hazard rate

The hazard rate, or risk function $h(t)$, indicates the conditional probability of a status change for 'feature-free' actors. If one assumes that a feature spreads as a result of contacts between actors in the system, it is plausible that the risk of the occurrence of the event will depend on the probability of an informative contact $w(t)$ and the adoption rate $r(t)$. A high risk of occurrence might exist in particular when both the probability of an interaction with an adopter and the willingness of adoption are high. Thus, the following assumption for determinants of the hazard seems to make sense:

$$h(t) = r(t)w(t). \quad (6)$$

¹² The flexible function $r(t)$ plays a role similar to that of the arbitrary function $s(t)$ in Diekmann's approach.

¹³ The function $r(t)$ is elementarily integratable only for real numbers of ε . It is a generalisation of the gamma density $g = (b(bt)^{a-1} e^{-bt})/\Gamma(a)$ in which a and b are positive parameters and $\Gamma(\cdot)$ represents the gamma function. Namely, $r(t) = g(t)$ for $\varepsilon = a > 0$, $\delta = -b < 0$ and $c = b^a/\Gamma(a)$. Due to the characteristics of the gamma function, $c = b^a/(\varepsilon - 1)!$ if ε is a positive real number.

¹⁴ Typical re-parameterisations are $c = \alpha\beta/\gamma$ and $c = \alpha\gamma^a$, whereby α , β , γ represent positive parameters.

The hazard rate arises then as a result of the product of the time-dependent adoption rate and the probability of a contact which is informative and therefore potentially consequential regarding the event or feature. We have now formulated a general diffusion model on the basis of the postulates for $r(t)$ and $w(t)$, as discussed above.

3.2 Model conclusions

The assumptions (3), (4) and (5) determine a flexible risk function which itself implies a general diffusion equation. The model prerequisites result in the hazard function

$$h(t) = ce^{\delta t} t^{\varepsilon-1} (1 - (1 - F(t))^k). \quad (7)$$

Before looking at the corresponding density function $f(t)$ and thereby the general diffusion equation, it makes sense to discuss briefly the process-theoretical implications of (7). Because $h(t) = r(t)w(t)$, and $w(t)$ increases with the number of the statistically independent contacts k , $h(t)$ increases with k , assuming otherwise identical conditions. If one assumes $0 < F(\cdot) < 1$, then diffusion processes can be differentiated according to the potential of influence of interactions:

Contact-dependent spreading: If k is not very large, then $w(t) < 1$ represents the probability of an informative contact. Thus, apart from the adoption function $r(t)$, this probability influences the hazard rate $h(t)$ and interactions therefore play a rather important role for the spreading process.

Contact-independent spreading: In the case of innumerable contacts per unit of time, we have the opposite result. In the borderline case $k \rightarrow \infty$, $w(t) = 1$, the risk function $h(t)$ is determined exclusively by the adoption function $r(t)$. In this scenario the occurrence of an event is independent of the probability of an informative contact which means that interactions between the system actors play no role in the spreading process.

The distinction between contact-dependent and contact-independent diffusion is of course, also relevant for the density $f(t) = dF(t)/dt$ from (7). This results from combining the definition $h(t) = (dF(t)/dt)/(1 - F(t))$ with the hazard function (7):

$$\frac{dF(t)}{dt} = ce^{\delta t} t^{\varepsilon-1} (1 - (1 - F(t))^k)(1 - F(t)). \quad (8)$$

Like Diekmann's differential equation, this diffusion equation is explicitly solvable only for certain parameter combinations. Table 1 presents a selection according to the diffusion-theoretical interpretation of these special cases: for $k = 1$ infection processes are present; for $k = \gamma/\beta$, a flexible model arises in the sense of a generalised contagion process; and for $k \rightarrow \infty$, we have contact-independent propagation processes. In addition to a brief look at the exponential model and the logistic model, we will take a closer look at the remaining special cases from Table 1 in the following.

Because the latter either exhibit or at least permit a bell-shaped hazard rate curve, this discussion serves also in preparation for the application.

3.2.1 Exponential distribution

One of the process types in Table 1 is based on the assumption of innumerable interactions between system actors ($k \rightarrow \infty$). In this scenario there is always an informative contact concerning the feature per unit of time, so the spreading process occurs independently of the interaction pattern. The diffusion process thus does not take place via contagion as a result of interactions between potential and prior adopters. Rather, it is driven exclusively by the adoption function.

In Table 1, this type of process is, *inter alia*, represented by the exponential model which frequently serves as a reference model in event history analysis. Based on (8), this classical model of a contact-independent spreading process results from the additional assumption of a constant adoption rate (cf., e. g., Coleman, Katz and Menzel 1957). Assuming $c > 0$, $\delta = 0$ and $\varepsilon = 1$:

$$\frac{dF(t)}{dt} = c(1 - F(t)), F(t) = 1 - e^{-ct}, h(t) = c, \quad (9)$$

Table 1:
Special cases of the diffusion model

Logistic model (spreading through infection):

$$k = 1 \text{ as well as } c > 0, \delta = 0 \text{ and } \varepsilon = 1, \text{ so that} \\ w(t) = F(t), r(t) = c \text{ and } h(t) = cF(t)$$

Log-logistic model (spreading through infection):

$$k = 1 \text{ as well as } c > 0, \delta = 0 \text{ and } \varepsilon = 0, \text{ so that} \\ w(t) = F(t), r(t) = c/t \text{ and } h(t) = (c/t)F(t)$$

Generalised log-logistic model (spreading through contacts):

$$k = \gamma/\beta > 0 \text{ and } c = \alpha\beta/\gamma > 0, \delta = 0, \varepsilon = 0, \text{ so that} \\ w(t) = 1 - (1 - F(t))^{\gamma/\beta}, r(t) = \alpha\beta/\gamma t \\ \text{and } h(t) = (\alpha\beta/\gamma t)(1 - (1 - F(t))^{\gamma/\beta})$$

Sickle model (contact-independent spreading):

$$k \rightarrow \infty \text{ as well as } c > 0, \delta = -1/\lambda < 0 \text{ and } \varepsilon = 2, \text{ so that} \\ w(t) = 1 \text{ and } r(t) = cte^{-t/\lambda} = h(t)$$

Exponential model (contact-independent spreading):

$$k \rightarrow \infty \text{ as well as } c > 0, \delta = 0 \text{ and } \varepsilon = 1, \text{ so that} \\ w(t) = 1 \text{ and } r(t) = c = h(t)$$

Note: Further model descriptions can be found in textbooks on event history analysis (e.g., Blossfeld, Hamerle and Mayer 1989; Blossfeld and Rohwer 1995; Diekmann and Mitter 1984).

where the integration of the density $f(t) = dF(t)/dt$ yields the distribution function $F(t)$ so that the corresponding hazard rate $h(t) = f(t)/(1 - F(t))$ is determined by the constant c .

3.2.2 Sickle models

In addition to the exponential model, TABLE 1 contains a further model for a spreading process which does not rely on contagion by interactions between prior and potential adopters. The constellation of the contact-independent spreading also characterises the sickle-shaped hazard function of Diekmann and Mitter (1983, 1984a). Using the positive parameters c and λ , the “defective” distribution function $F(t)$ and the hazard rate $h(t)$ of the sickle model are given by

$$F(t) = 1 - e^{\lambda c(\lambda - (t+\lambda)e^{-t/\lambda})}, \quad h(t) = cte^{-t/\lambda}, \quad (10)$$

so that in the long run, “immunity” is present in the sense of $F(\infty) < 1$. The estimated value of λ thereby determines the point in time of the highest transition risk (i. e., the maximum of the rate function with $t_m = \lambda$). Apart from $k \rightarrow \infty$, a diffusion-theoretical explanation for the sickle hypotheses in the sense of (8) requires the parameter specification $c > 0$, $\delta = -1/\lambda$ and $\varepsilon = 2$:

$$\frac{dF(t)}{dt} = cte^{-t/\lambda} (1 - F(t)). \quad (11)$$

If one views the sickle model on this basis, this has two consequences. On the one hand, innumerable interactions per unit of time guarantee that only the adoption rate plays a role in the spreading of the feature, i.e., the adoption function $r(t)$ corresponds to the hazard function $h(t)$. On the other hand, the transition risk exhibits a linearly decreasing elasticity of time $(dr/dt)(t/r(t)) = 1 - (1/\lambda)t$. A one per cent increase in time (passed since the beginning of the process), will result, up to a certain point in time (at $t_m = \lambda$), in a proportional increase in the willingness of adoption. Thereafter, however, there is a proportional decrease. After initial acceleration, the adoption tendency is thus retarded once again, although contacts do not play a role in the spreading process. This contrasts with the logic of infection.

3.2.3 Logistic models

Examples of social contagion processes are easy to find. The spreading of certain modes, the acquisition of new technologies, and also the propagation of rumors can always be understood as consequences of informative interactions. Assuming the validity of (8), infection processes result if one supposes a statistically independent contact per unit of time ($k = 1$) which means that the proportion of adopters determines the probability of a given informative contact.

The logistic model indicated in Table 1, offers the classical description of infec-

tion-like diffusion processes (e. g., Coleman, Katz and Menzel 1957). It results from (8) if one additionally assumes a constant adoption rate and thus $c > 0$, $\delta = 0$ and $\varepsilon = 1$:

$$\frac{dF(t)}{dt} = cF(t)(1 - F(t)), F(t) = \frac{F(0)e^{ct}}{1 - (1 - e^{ct})F(0)}, h(t) = cF(t). \quad (12)$$

With $F(0)$, we assume a positive initial value of the S-shaped distribution function $F(\cdot)$. Because the adoption rate is determined by the constant c , the hazard function $h(t)$ represents only a parallel shift in the distribution function. Thus the hazard rate of the logistic model also indicates an S-shaped process, i. e., the risk of adoption rises with the process duration. However, there are also infection processes that are accompanied by an entirely different course of risk.

3.2.4 Log-logistic models

Age-dependent taking up of illegal activities as a result of “bad” contacts or the beginning of regular drug consumption due to interactions with friends who already take drugs could be contact-dependent spreading processes with bell-shaped hazard functions. If one concentrates first on pure infection processes ($k = 1$), and makes the corollary assumption that the adoption function $r(t) = c/t$ is constantly decreasing, then the log-logistic standard model proves to be an example of a pure contagion process which can be accompanied by a bell-shaped hazard function.

As Brüderl and Diekmann (1995) show, the log-logistic model can be generalised by introducing an additional parameter β . If we use the positive parameters α , β and γ , the distribution function $F(t)$ and the hazard function $h(t)$, the generalised log-logistic model is:

$$F(t) = 1 - (1 + (\gamma t)^\alpha)^{\beta/\gamma}, h(t) = \frac{\alpha\beta(\gamma t)^{\alpha-1}}{1 + (\gamma t)^\alpha}, \quad (13)$$

which results in the log-logistic standard model for $\beta = \gamma > 0$. For $\alpha > 1$, we have a bell-shaped curve for $h(t)$, while $\alpha \leq 1$ implies a constantly decreasing hazard rate $h(t)$.

Because the generalised log-logistic model contains the log-logistic standard model as a special case, and the latter is infection-theoretically explicable, the generalised model should be interpretable as a generalised contagion process. In fact, (8) does permit this interpretation of the generalised log-logistic model. If one combines the assumption $k = \gamma/\beta > 0$ in (8), with the specifications $c = \alpha\beta/\gamma > 0$, $\delta = 0$, and $\varepsilon = 0$, then the density of the generalised log-logistic model can be written as a generalised infection process:

$$\frac{dF(t)}{dt} = \frac{\beta}{\gamma} \frac{\alpha}{t} ((1 - F(t)) - (1 - F(t))^{\gamma/\beta} + F(t) (1 - F(t))^{\gamma/\beta}). \quad (14)$$

So the generalised log-logistic model illustrates a further type of process in Table 1. As a flexible model of a contact-dependent diffusion, it is situated between

pure infection processes and contact-independent spreading processes. The estimation results for the generalised log-logistic model thus facilitate the choice between bell-shaped hazard rate models that are based on different process-theoretical foundations. In particular, they make it possible for us to test the infection hypothesis which justifies the log-logistic standard model: The more $\beta = \gamma$ is fulfilled, the more appropriate is an interpretation of a bell-shaped risk process in the sense of a pure contagion process. This reflects the fact that the infection-theoretical interpretation of the log-logistic model for $k = 1$ results directly from (14), whereby a constant time elasticity of -1 is assumed for the adoption rate $r(t)$. In addition to the possible contagion-theoretical interpretation, it is thus characteristic for log-logistic models that a one per cent increase in time (passed since beginning of the process) will lead to a one per cent reduction in adoption willingness. These process-theoretical differences between the log-logistic models and the similarly shaped sickle model serve to help in the selection of the suitable statistical model. We will now show this with an investigation of duration data concerning “divorce”.

4 An illustration: divorces

One can hardly view divorce as the consequence of social contagion processes. An analysis of divorce data might therefore show whether our suggested approach of connecting diffusion research and event history analysis leads to plausible results. Our starting point is the well-known fact that divorce data can be adequately described by a bell-shaped risk or hazard rate function (cf., e. g., Diekmann and Engelhardt 1999; Brüderl, Diekmann and Engelhardt 1999). In the following, we take a look at the sickle model and the generalised log-logistic model, two parametric models that can illustrate such a shape for the transition rate although they are based on different process-theoretical considerations. Although we orient ourselves throughout to the traditional procedure for the employment of event-analytic methods in divorce research, the substantive findings of the data analysis are neglected to a large extent.¹⁵ Our objective is to prove that the process-theoretical considerations discussed above can be of use when choosing between competitive hazard rate models. After a brief description of the data and covariates, we will also deal briefly with the statistical procedures that are usually employed in model selection.

4.1 Data and variables

This study is based on the German Family Survey from 2000 which was administered by the German Youth Institute (DJI). The DJI study is a random sample of the entire East and West German residential population between the ages of 18 and

¹⁵ Detailed interpretations of the content of similar estimation results can be found in Brüderl, Diekmann and Engelhardt (1997), as well as in Diekmann and Engelhardt (1999).

55 living in private households. A total of 10,093 people participated in personal interviews in which detailed information on their partnership history was collected. 2,002 of the respondents in West Germany were interviewed already a third time in a panel starting in 1988, and 8091 persons were randomly selected. Due to high panel mortality we focus on the cross-sectional survey. Although the response rate was relatively low in the cross-sectional sample (52%), comparisons of the distributions of socio-demographic variables with official statistics show that deviations are no greater than in other national surveys. Women and persons not in the labour force are somewhat overrepresented, while family and household type both correspond to official statistics (Infratest 2000). For the following analyses we consider only first marriages of both partners in West Germany, excluding persons born abroad, “Aussiedler” (ethnic German repatriates, coming mainly from Russia), and migrants from East to West who were over age 20 at the time of migration. There are 3,844 first marriages in the data of which 17,9% had ended in divorce by the time of inquiry. Apart from the central variable “marriage duration”, the data set allows us to control for numerous characteristics of the respondents and the couples which are considered to be central divorce determinants (cf., e. g., Engelhardt 2002). These characteristics can thus be included in the analysis as covariates.

4.2 Estimation and testing procedures

For estimation purposes, covariates are generally included in the respective hazard rate model, with an exponential link function through selected process parameters. In the sickle model the parameters c and λ are usually defined as follows (e. g., Diekmann and Engelhardt 1999):

$$c = b_{c_0} \prod_{j=1}^q b_{c_j}^{x_j}, \lambda = b_{\lambda_0}, \quad (15)$$

where b_{c_0} and b_{λ_0} represent coefficients to be estimated, and the coefficient of the j th covariate which enters the model through the process parameter c . Employing the same notational logic, we follow the recommendation of Brüderl and Diekmann (1995) and define for the generalised log-logistic model accordingly:

$$\alpha = b_{\alpha_0}, \beta = b_{\beta_0} \prod_{j=1}^q b_{\beta_j}^{x_j}, \gamma = b_{\gamma_0}, \quad (16)$$

Thus covariates are included in the model through the process parameter β . Independently of whether we view the sickle model or the generalised log-logistic model, the estimated coefficients of the covariates indicate the “relative risks”. The proportional rate effect of the j th covariate is given by $100(b_{\beta_j} - 1)\%$.

If the vector of covariates x_i and the marriage duration t_i are known for each individual i , then the b -coefficients can be estimated, taking censored observations into account consistently and they can be (asymptotically) normally distributed by means of the maximum-likelihood method which enables us to employ inference-statistical

testing methods (cf., eg., Blossfeld, Hamerle and Mayer 1989). The log-likelihood function

$$\ln L(b; t, x) = \sum_{i=1}^N \left(d_i \ln h(t_i | x_i, b) - \int_0^{t_i} h(v | x_i, b) dv \right), \quad (17)$$

which depends on the hazard function $h(\cdot)$ selected, is maximised with respect to the vector of coefficients b . N defines the number of cases and d_i is a binary variable which takes on the value 1 for uncensored observations. We obtain the maximum likelihood estimations using Rohwer's program TDA, although we used the episode-splitting technique for the time-varying covariates (cf., e. g., Blossfeld and Rohwer 1995).

To evaluate the degree of improvement in the estimation ensuing from the addition of further parameters or covariates, the Likelihood Ratio test is usually used. It compares the maximised likelihood of the interesting (or unrestricted) model L_U , with the maximised likelihood of the reference (restricted) model, L_R . The Likelihood Ratio test statistic $LR = 2(\ln L_U - \ln L_R)$ is asymptotically χ^2 -distributed, with the difference in parameters or covariates of the models under consideration as degrees of freedom. If LR exceeds the relevant critical parameter, then the restrictions can be rejected. Roughly speaking, the interesting model turns out to offer a significant improvement in the estimation.

In addition, the likelihood ratio statistic offers the basis for a comparison of non-nested models (e. g., the sickle model and the generalised log-logistic model) using the Bayesian Information Criterion BIC (Raftery 1995). Therefore, one calculates for each model:

$$BIC = \ln(n)z - LR$$

where z indicates the number of additional parameters in comparison to the selected reference model (e. g., exponential distribution). Usually one considers the model with the smallest BIC value to be the relatively "best" model. In the context of a selection to be undertaken on the basis of statistical criteria, this model would be selected.

4.3 Results and model selection

We now compare the sickle model and the generalised log-logistic model on this basis. We first consider the results of an estimation of both models without taking covariates into account (Table 2). The estimation results from the sickle model indicate that the maximum divorce risk occurs at approximately nine years ($\lambda = 8.884$), while the generalised log-logistic model fixes this point at somewhat over seven years.¹⁶

¹⁶ According to Brüderl and Diekmann (1995), in the case of the generalised log-logistic model, the timing of the maximal divorce risk is at $t_m = (1/\gamma)(\alpha - 1)^{1/\alpha}$. When using the estimated results, one gets $t_m = 7.109$.

Table 2:
Maximum likelihood estimations of the divorce risk for three models without covariates

Parameters and test statistics	Sickle model	log-logistic model	Generalised log-logistic model
c	0.005***	–	–
λ	8.884***	–	–
α	–	0.012***	1.924***
β	–	–	0.015***
γ	–	1.232***	0.135*
– Log-likelihood	2899.702	2917.391	2897.492
LR	61.535	26.159	65.957
df	1	1	2
BIC	-53.477	-18.101	-49.841

Notes: * significant for $p \leq .05$, *** significant for $p \leq .001$. LR is the likelihood-ratio statistic with df degrees of freedom. BIC is the Bayesian Information Criterion with the exponential model without covariates as reference model (Log-Likelihood = -2930.47). $N = 3159$.

In addition to the estimated values for the process parameters, TABLE 2 also includes information about the test statistics and 'goodness-of-fit' measures we have discussed. The exponential distribution without covariates serves in all cases as the reference model.¹⁷ If one uses the Bayesian Information Criterion BIC for model selection, then the sickle model is to be preferred to the log-logistic model and to the generalised log-logistic model, judging from the estimated results for the scenario without covariates.

If one includes the covariates in the analysis, this result remains stable, as can be seen in Table 3. Regardless of whether one carries out the comparison with the exponential model with or without covariates, the sickle model presents itself as the "better" model, due to the smaller BIC value for the analysis of the divorce data under consideration. So if one chooses among parametric hazard rate models on the basis of statistical criteria, then the inclusion (or exclusion) of certain covariates obviously plays a substantial role in the decision-making process.

¹⁷ The estimated value of the constant hazard rate in the exponential model is 0.011. In comparison to this basic model with constant rate, the relative likelihood improvement achieved with the estimation from the Sickle model, the log-logistic model and the generalised log-logistic model is small in each case. When using McFadden's Pseudo- $R^2 = (\ln L_R - \ln L_U) / \ln L_R$ as a conservative measure for the relative likelihood improvement, one gets the value 0.01 for the sickle and the generalised log-logistic model and 0.04 for the log-logistic model. If one considers also the covariates mentioned, this results in a Pseudo- R^2 of about 0.012 for the sickle model and the generalised log-logistic model and 0.02 for the log-logistic model.

Table 3:
Maximum likelihood estimations of the divorce risk for three models with covariates

Covariates, parameters and test statistics	Sickle model	log-logistic model	Generalised log-logistic model
Constant	0.060***	0.170***	0.002
Married 1971–80 (=1, 0 else)	1.292+	1.322**	2.671**
Married 1981–90 (=1, 0 else)	2.285***	2.108***	13.867***
Married 1991–2000 (=1, 0 else)	2.870***	2.283***	19.627***
Catholic couple (=1, 0 else)	0.694**	0.776**	0.425**
Non religious couple (=1, 0 else)	0.742	0.805	2.281***
Mix of religions (=1, 0 else)	1.124	1.078	1.325
Mix of nationalities (=1, 0 else)	0.990	0.934	0.894
Years of cohabitation	0.968	0.982	0.930
Child before marriage (=1, 0 else)	0.968***	0.545***	0.160***
First child (time dependent) (=1, 0 else)	0.438***	0.377***	0.160***
Husband: age at marriage	0.990	0.992	0.978
Wife: age at marriage	0.944**	0.958**	0.873**
Wife is 2+ years older (=1, 0 else)	1.129	1.155	1.341
Husband: years of education	0.954	0.972	1.061
Wife: Years of education	1.025	1.019	0.894
Marriage in church (=1, 0 else)	0.488***	0.581***	0.181***
No siblings (=1, 0 else)	1.028	1.058	1.080
Father: Abitur (=1, 0 else)	1.224	1.152	1.519**
Grown up without parents (=1, 0 else)	1.775+	1.490	1.607**
Grown up with widowed parent (=1, 0 else)	0.970	0.945	0.904
Grown up with divorces parents (=1, 0 else)	2.416***	1.831***	7.909***
Grown up with single parent (=1, 0 else)	1.841+	1.431	4.098+
Mating: strong ties (=1, 0 else)	0.831+	0.865+	0.647+
Mating: weak ties (=1, 0 else)	0.736*	0.788**	0.489*
<i>c</i>	par.	–	–
<i>λ</i>	12.449	–	–
<i>α</i>	–	1.579***	1.424***
<i>β</i>	–	–	1.670
<i>γ</i>		par.	par.
– Log-likelihood	2534.209	2536.612	2548.363
<i>LR</i>	92.745	87.9406	64.435
<i>df</i>	1	1	2
<i>BIC</i>	-184.251	-79.928	-48.411

Notes: + significant for $p \leq .1$, * significant for $p \leq .05$, ** significant for $p \leq .01$, *** significant for $p \leq .001$. Reported are the b-coefficients of the covariates which determine the “par.”-marked process parameters. Reference categories: marriage cohort 1971–80, Protestant couple, same nationalities, no child before marriage, no first child, wife is not 2+ more years older, not married in church, siblings, father has no Abitur, lived with both parents up to age 15, mating: no ties. *LR* is the likelihood-ratio statistic with *df* degrees of freedom. *BIC* is the Bayesian Information Criterion with the exponential model with covariates as reference model (Log-likelihood = -2580.582). A comparison with the exponential model without covariates yields *LR (BIC) = 384.552 (-184.251)* for the sickle model, *LR (BIC) = 379.746 (-179.446)* for the log-logistic model, and *LR (BIC) = 356.241 (-147.928)* for the generalised log-logistic model. N = 3017; number of splits = 5161.

Family demographers are now particularly interested in the effects of covariates. One could take a pragmatic point of view and point out that the effects of covariates are practically identical at least in the sickle and in the log-logistic model. In the three-parametric generalised-log-logistic model, the estimated coefficients differ substantially. From this perspective, the question of model selection between the two-parametric models appears irrelevant in the case that the list of the covariates is fixed. However, this line of argumentation is not entirely convincing. The covariates can be compatible sooner with a certain type of the propagation than with another type. The covariates from Table 3 refer to individual and couple-specific characteristics but not to relations with other persons and their characteristics. In this application, interactions with unmarried or already divorced actors should therefore not be crucial components of the propagation process which is determined by the choice of the estimate model. Given the list of covariates, the assumption of a contact-independent propagation process seems appropriate for this example.

Furthermore, covariate effects are frequently interpreted with the help of theories that refer, more or less explicitly, to the individual decision behaviour concerning the event under consideration (e. g., divorce). For reasons of consistency, this theoretically founded micro-interpretation of covariate effects should not collide with the macro-process which is specified by the choice of parametric event model. Even if the covariates are fixed, for an adequate interpretation of their effects a process model has to be estimated that is compatible with the initial theoretical considerations.

Therefore, it seems useful to consider the process-theoretical implications discussed above when choosing the model. It is well known that the generalised log-logistic model illustrates a generalised infection process which is reduced to a pure infection scenario (log-logistic model), given a certain parameter constellation ($k = \gamma/\beta = 1$). It thus offers a test for whether the application under consideration can be interpreted as being a case of social infection. The estimated values of the β and γ for the scenario without covariates in Table 2 then exclude an infection-theoretical interpretation of the divorce data ($k \approx 15$).

Instead, these values indicate, as expected, that the divorce risk depends less on interactions with third persons than on the adoption function which is substantially determined by individual characteristics of the spouses and intra-couple processes. Moreover, if one considers the estimated results from Table 3, most covariates exhibit significant and more or less strong effects on the risk of divorce. In all models, this risk increases in comparison to the reference category (see Section 4.1) if the interviewed person grew up in a broken home, with a single parent, or without parents. Furthermore, the risk of divorce increases for younger marriage cohorts. In contrast, the affiliation of both husband and wife to the Catholic Church, church marriage and the birth of the first conjugal child decrease the risk. The risk is also reduced for couples who met incidentally without a social network (e. g., friends or relatives) involved.

Overall, these results are in agreement with the basic intuition that divorces result

mainly from characteristics of the couple and intra-couple processes. With increasing time spent together, one acquires additional information about positive and negative characteristics of one's partner and conflicts, boredom or indifference can come about; factors that manifest themselves in an increasing inclination on the part of at least one of the partners to separate. These considerations are in keeping with existing theories of divorce research which form the basis of interpretations of the covariate effects. For example, according to Becker's economic theory of divorce (1991) it is the information about one's spouse acquired in the course of time which increases the likelihood of divorce. A general sense of disillusionment about one's spouse can arise as a result of additional experiences, or a mismatch can be diagnosed, so that an end to the relationship ultimately appears as the lesser evil.

In the analysis of divorce data, the effects of covariates are frequently interpreted in the sense of Becker's family economics. From a process-theoretical perspective, such an interpretation is most likely compatible with the assumption of a contact-independent propagation. Accordingly, if one considers the event "divorce", it makes sense to use the sickle model. If the underlying logic of spreading is unclear in some other application with bell-shaped rate process, such doubts might well be eliminated by the estimation of the generalised log-logistic model. Indeed, according to the model for connecting diffusion research and event analysis presented here, process-theoretical considerations facilitate the choice among competitive hazard rate models, if statistical criteria do not offer us a clear basis for decision.

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