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Research Note Forecasting technology diffusion with the Richards model

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ABSTRACT

The Richards model has a shape parameter m that allows it to fit any sigmoidal curve. This article demonstrates the ability of a modified Richards model to fit a variety of technology diffusion curvilinear data that would otherwise be fit by Bass, Gompertz, Logistic, and other models. The performance of the Richards model in forecasting was examined by analyzing fragments of data computed from the model itself, where the fragments simulated either an entire diffusion curve but with sparse data points, or only the initial trajectory of a diffusion curve but with dense data points. It was determined that accurate parameter estimates could be obtained when the data was sparse but traced out the curve at least up to the third inflection point (concave down), and when the data was dense and traced out the curve up to the first inflection point (concave up). Rogers' Innovation I, II and III are discussed in the context of the Richards model. Since m is scale independent, the model allows for a typology of diffusion curves and may provide an alternative to Rogers' typology.

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1. Introduction

Technology diffusion is widely accepted as tracing a sigmoidal trajectory that resembles a biotic growth curve [1,2]. Accordingly, empirical growth models are commonly fit to technology diffusion data. Much of the activity surrounding empirical growth models relates to model selection, where for example the Fisher–Pry model [3] is appropriate to technology diffusion in general and the Gompertz [4] as a mortality model is appropriate to cases of technology diffusion involving replacement [5].

The Richards model [6] is an empirical model developed for fitting growth data. Through the use of a shape parameter m that enables the curve to stretch or shrink, the Richards model encompasses the Gompertz, Fisher–Pry and every other imaginable sigmoidal model (Fig. 1). When m = 0, the model approximates the exponential growth function. When m = 0.67, the model behaves like the von Bertalanffy [7]. When m approaches 1, the model behaves like the Gompertz. When m = 2, the model behaves like the Logistic model [8]. Thus one of the advantages of the Richards model is that it, in effect, selects the model for you.

The Richards model has been investigated in at least two white papers as a tool for technology forecasting [9,10], but it has not been reported in the peer-reviewed literature in the context of diffusion of technology diffusion or diffusion forecasting. Neither has its behavior under a variety of data qualities been examined. This article demonstrates the ability of a modified Richards model to fit a variety of technology diffusion curves that would otherwise be fit by the Bass [11], Gompertz, Logistic, and other models.

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Fig. 1. The Richards model at various m-values. W[∞], T^{*}, and k also vary between curves.

2. Methods

The Richards model was introduced in 1959 in the context of plant growth [6]. Richards conceived of the model as an extension to the von Bertalanffy model, but he recognized its ability to emulate the Gompertz and Logistic as well. The model has been modified and reparameterized by several researchers. As modified by Sugden et al. [12], the model is:

$$W_{t} = W^{\infty} \Big[1 - (1 - m) exp \Big[-k \big(t - T^{*} \big) / m^{m/(1-m)} \Big] \Big]^{1/(1-m)}$$

where W_t is the weight or growth at time t, W^{∞} is the asymptotic weight, k is the maximum relative growth rate per unit time, T^* is the maximum rate of growth per unit time, and m is a shape parameter with the property that $m^{1/(1-m)}$ is the relative weight at time T^* .

In terms of technology diffusion, W^{∞} is the asymptotic weight, i.e., the asymptotic or maximum level of diffusion achieved. k is the maximum relative growth rate per unit time; when applied to diffusion data, k signifies the maximum diffusion per unit time relative to the size of the population. As shown in Fig. 2a, the k-value is associated with the lagging effect: the higher the k-value, the longer the lag. T^* is the maximum rate of diffusion per unit time. The m-value is the shape parameter that determines the position of the concave up–concave down inflection point. As shown in Fig. 2b, all other parameters held equal, the relation



Fig. 2. a. Shapes of curves in Table 1, all other parameters held equal. b. Richards model curves for m = 1.3026, but k varies from 0.05 to 0.1.

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