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Modelling Individual Animal Growth in Random Environments

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Abstract: We have considered, as general models for the evolution of animal size in a random environment, stochastic differential equations of the form $dY(t) = b(A - Y(t))dt + \sigma dW(t)$, where $Y(t) = g(X(t))$, $X(t)$ is the size of an animal at time t , g is a strictly increasing function, $A = g(a)$ where a is the asymptotic size, σ measures the effect of random environmental fluctuations on growth, and W_t is the Wiener process. We have considered the stochastic Bertalanffy-Richards model ($g(x) = x^c$ with $c > 0$) and the stochastic Gompertz model ($g(x) = \ln x$). We have studied the problems of parameter estimation for one path and also considered the extension to several paths. We also used bootstrap methods. Results and methods are illustrated using bovine growth data.

Keywords: growth models; stochastic differential equations; estimation; cattle weight.

1 Introduction

The most common models used to describe the growth of an individual animal in terms of its size $X(t)$ at time t have assumed the form of a differential equation $dY(t) = b(A - Y(t))dt$, $Y(t_0) = y_0$, where we made a change of variable $Y(t) = g(X(t))$ with g a strictly increasing function (which we assume known). We have $y_0 = g(x_0)$ and $A = g(a)$, where x_0 is the size at birth and a is the asymptotic size or size at maturity of the animal. The parameter $b > 0$ is a rate of approach to maturity.

The *Bertalanffy-Richards model* (Bertalanffy (1957) and Richards (1959)) corresponds to the choice $g(x) = x^c$ for $c > 0$ (typical choices are $c = 1$ and $c = 1/3$) and the *Gompertz model* corresponds to $g(x) = \ln x$ (can be considered the limiting case of Bertalanffy-Richards model when $c \rightarrow 0$).

If the animal is growing in a randomly fluctuating environment, we can model growth through a *stochastic differential equation* (SDE) of the form

$$dY(t) = b(A - Y(t))dt + \sigma dW(t), \quad (1)$$

where $\sigma > 0$ measures the strength of environmental fluctuations and $W(t)$ is a standard Wiener process. Garcia (1983) applied these type of models to tree growth.

The solution of (1) is a homogeneous diffusion process with drift and diffusion coefficient, respectively, $b(A - y)$ and σ^2 . The solution of this SDE is $Y(t) = A + e^{-bt}(y_0 - A) + \sigma e^{-bt} \int_0^t e^{bs} dW(s)$ (see, for instance, Braumann (2005)). The distribution of $Y(t)$ is Gaussian with mean $A + e^{-bt}(y_0 - A)$ and variance $\frac{\sigma^2}{2b}(1 - e^{-2bt})$ and converges, as $t \rightarrow +\infty$, to a Gaussian distribution with mean A and variance $\frac{\sigma^2}{2b}$.

The data used for illustration is the weight of "mertolengo" cattle of the "rosilho" strand and was provided by Carlos Roquete (ICAM-UE).

2 Parameter estimation

In Filipe et al. (2007), we have considered, for a single path, the statistical problems of parameter estimation and of prediction of future sizes of an animal for model (1). Subsection 2.1 gives a brief summary of the estimation part. Subsection 2.2 presents the extension of the estimation methods to the case of several paths, assumed to be independent. We have also studied bootstrap estimation methods, shown on subsection 2.3.

2.1 Parameter estimation for a single path

Let us assume we observe the evolution of the weight of one animal at times $0 = t_0 < t_1 < \dots < t_n$, and represent the weight of the animal at time t_k ($k = 1, 2, \dots, n$) by $X_k = X(t_k)$. Let $Y_k = g(X_k)$ and $\mathbf{Y} = (Y_0, Y_1, \dots, Y_n)$. We want to estimate $\mathbf{p} = (A, b, \sigma)$. Since we know the transition distributions of $Y(t)$, using the fact that it is a Markov process and given $Y_0 = y_0$, assumed known, we can obtain the log-likelihood function

$$L_{\mathbf{Y}}(\mathbf{p}) = -\frac{n}{2} \ln \left(\frac{2\pi\sigma^2}{2b} \right) - \frac{1}{2} \sum_{k=1}^n \ln (1 - E_k^2) - \frac{b}{\sigma^2} \sum_{k=1}^n \frac{(y_k - A - (y_{k-1} - A) E_k)^2}{1 - E_k^2},$$

with $E_k = e^{-b(t_k - t_{k-1})}$. In terms of X the log-likelihood function is $L_{\mathbf{X}}(\mathbf{p}) = L_{\mathbf{Y}}(\mathbf{p}) + \sum_{k=1}^n \ln \left(\frac{dY}{dX} \Big|_{x=x_k} \right)$. The *maximum likelihood estimator* (MLE), $\hat{\mathbf{p}}$, is obtained by maximization of $L_{\mathbf{Y}}$ (equivalent to maximization of $L_{\mathbf{X}}$). Using the properties of MLE and $Y(t)$ we can obtain the Fisher information matrix and construct approximate confidence intervals for the parameters. In Filipe et al. (2007), we used data of the weight in kg of a single animal for which we had 79 observations. We have applied model (1) for the particular cases $g(x) = x^c$ ($c > 0$) and $g(x) = \ln x$ ($c = 0$) (Table 1). Some choices of c were considered and the models which turned out to be the best choices were correspondent to $c = 0$ and $c = 1/3$.

TABLE 1. Maximum likelihood estimates, log-likelihood value and approximate 95% confidence intervals (data from one animal).

	a	b	σ	L_X
$c = 0(\text{Gompertz})$	407.1 ± 60.5	1.472 ± 0.354	0.226 ± 0.036	-338.12
$c = 1/3$	422.4 ± 81.6	1.096 ± 0.525	0.525 ± 0.083	-337.88

2.2 Parameter estimation for several paths

Assume we have data on m animals. The weight of animal number j ($j = 1, 2, \dots, m$) is observed at times $0 = t_{j,0} < t_{j,1} < \dots < t_{j,n_j}$, and is, respectively, $X_{j,0} = X(t_{j,0})$, $X_{j,1} = X(t_{j,1})$, \dots , $X_{j,n_j} = X(t_{j,n_j})$. Let $Y_{j,k} = Y(t_{j,k}) = g(X_{j,k})$ ($j = 1, 2, \dots, m$; $k = 1, 2, \dots, n_j$) and $\mathbf{Y}_j = (Y_{j,0}, Y_{j,1}, \dots, Y_{j,n_j})$.

For animal number j we can obtain the log-likelihood $L_{\mathbf{Y}_j}$ by proceeding as in the case of a single path. From independence, the overall log-likelihood for the m animals is $L_{\mathbf{Y}_1, \mathbf{Y}_2, \dots, \mathbf{Y}_m}(\mathbf{p}) = \sum_{j=1}^m L_{\mathbf{Y}_j}(\mathbf{p})$. The MLE $\hat{\mathbf{p}}$ is obtained, now, by maximization of $L_{\mathbf{Y}_1, \mathbf{Y}_2, \dots, \mathbf{Y}_m}$.

In Filipe and Braumann (2007), we have applied the procedure for the stochastic Bertalanffy-Richards model, for the cases $c = 0$ and $c = 1/3$, to the data of $m = 5$ animals of the same strand raised under similar conditions. In Figure 1 we can see the observed weights for these 5 animals. For one animal we have 79 observations and the other four have 38 observations each. Table 2 shows the results obtained.

TABLE 2. Maximum likelihood estimates, log-likelihood value and approximate 95% confidence intervals (data from 5 animals).

	a	b	σ	L_{X_1, \dots, X_5}
$c = 0$	352.4 ± 28.3	1.708 ± 0.193	0.253 ± 0.023	-958.84
$c = 1/3$	384.1 ± 46.2	1.147 ± 0.211	0.506 ± 0.047	-941.85

2.3 Bootstrap methods

The asymptotic confidence intervals obtained from the Fisher information matrix may be quite unreliable for small sample sizes. In such case, bootstrap methods are recommended.

In Efron and Tibshirani (1993) we can find two types of bootstrap procedure, respectively, *parametric bootstrap* (PB) and *nonparametric bootstrap* (NPB). We have applied these two bootstrap methods for the cases $c = 0$ and $c = 1/3$.

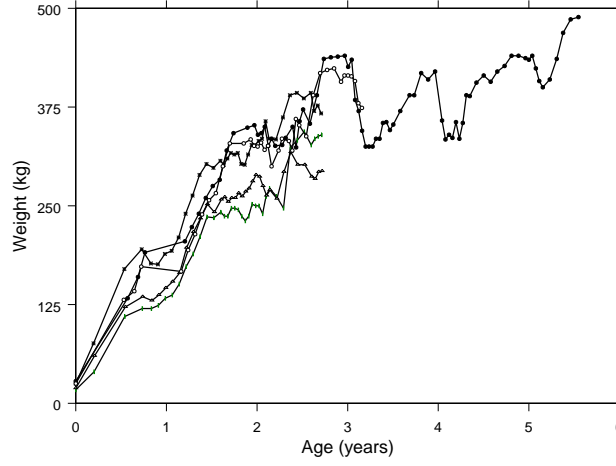


FIGURE 1. Observed growth curves for the 5 animals.

For PB, we have considered the Gaussian distribution of Y_k , mentioned on section 1, and, using the MLE $\hat{\mathbf{p}}$ to approximate \mathbf{p} , generated 1000 independent "samples", $\mathbf{y}^{*i} = (y_0^{*i}, y_1^{*i}, \dots, y_n^{*i})$ ($i = 1, \dots, 1000$). For each one of these "samples" we have computed the estimates $\hat{\mathbf{p}}^{*i}$ ($i = 1, \dots, 1000$) (following the procedure described in subsection 2.1), and consequently, by calculating the mean, obtained the bootstrap estimate $\hat{\mathbf{p}}^*$.

Extending this procedure to m animals, we have generated $\mathbf{y}_j^{*i} = (y_{j,0}^{*i}, y_{j,1}^{*i}, \dots, y_{j,n_j}^{*i})$ ($i = 1, \dots, 1000$; $j = 1, \dots, m$) using as an approximation of \mathbf{p} the overall MLE, $\hat{\mathbf{p}}$, presented in subsection 2.2. We have obtained, for each $i = 1, \dots, 1000$, the maximum likelihood estimates $\hat{\mathbf{p}}^{*i}$ as in subsection 2.2. From the 1000 replicates $\hat{\mathbf{p}}^{*i}$ ($i = 1, \dots, 1000$), to obtain $\hat{\mathbf{p}}^*$ the procedure is similar to the one presented for a single animal.

For the NPB method we can find in Efron and Tibshirani (1993) how to approach the problem of dependency between observations, which must be considered in our case. We can see that

$$e_k = (e^{t_k} Y_k - e^{t_{k-1}} Y_{k-1} - A(e^{t_k} - e^{t_{k-1}})) / \sqrt{\frac{\sigma^2(e^{2t_k} - e^{2t_{k-1}})}{2b}}, \quad (2)$$

for $k = 1, \dots, n$, are i.i.d with standard Gaussian distribution. We have obtained 1000 independent replicates, $\mathbf{e}^{*i} = (e_0^{*i}, e_1^{*i}, \dots, e_n^{*i})$ ($i = 1, \dots, 1000$) where the e_k^{*i} ($k = 1, \dots, n$; $i = 1, \dots, 1000$) are obtained by sampling with

replacement the empirical distribution of the observed values of e_1, \dots, e_n . For each $i=1, \dots, 1000$, we have used \mathbf{e}^{*i} to reconstruct, using the inverted expression of (2), a vector of n observations \mathbf{y}^{*i} . We can, then, obtain the bootstrap estimates of the parameters in the same way as in PB.

In case we have m animals, in a similar way we must consider e_{jk} , i.i.d with standard Gaussian distribution. For each path we proceed as described above for a single animal.

For both PB and NPB, the standard bootstrap confidence intervals are obtained using normality and the sample standard deviation of the 1000 replicates of the estimates. We can also obtain bootstrap confidence intervals using the empirical quantiles, which, in our example, gives very similar results.

Although our data has a reasonably large sample size, for illustration purposes we still obtained the bootstrap estimates and 95% confidence intervals for both PB and NPB (see Table 3).

TABLE 3. Bootstrap estimates and 95% confidence intervals

		a	b	σ
1 animal (PB)	$c = 0$	405.3 ± 59.5	1.517 ± 0.376	0.222 ± 0.036
	$c = 1/3$	418.3 ± 84.1	1.180 ± 0.466	0.516 ± 0.085
1 animal (NPB)	$c = 0$	404.8 ± 59.5	1.519 ± 0.371	0.223 ± 0.043
	$c = 1/3$	419.1 ± 80.3	1.179 ± 0.453	0.518 ± 0.097
5 animals (PB)	$c = 0$	352.4 ± 31.4	1.714 ± 0.184	0.252 ± 0.024
	$c = 1/3$	384.9 ± 46.7	1.159 ± 0.210	0.504 ± 0.047
5 animals (NPB)	$c = 0$	362.2 ± 31.4	1.630 ± 0.189	0.250 ± 0.031
	$c = 1/3$	392.5 ± 50.8	1.094 ± 0.201	0.501 ± 0.057

3 Conclusions

Stochastic differential equations models for the growth of individual animals where considered and parameter estimation were developed for the case of several animals. In progress is the study of nonparametric estimation of the drift and diffusion coefficients, with the goal of finding a more general growth model. We have also considered the more realistic case in which we have different asymptotic expected size for different animals (to appear).

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