A subordinated stochastic process model

Ana Paula Palacios[1], J. Miguel Marín[2], Michael P. Wiper[2]

Second Bayesian Young Statisticians Meeting (BAYSM 2014)
Vienna, September 18–19, 2014

---

[1] Plymouth University, School of Computing and Mathematics, UK
`ana.palacios@plymouth.ac.uk`

[2] Universidad Carlos III de Madrid, Departament of Statistics, Spain
`<jmmarin,m.wiper>@est-econ.uc3m.es`

Abstract

We introduce a new stochastic model for non-decreasing processes which can be used to include stochastic variability into any deterministic growth function via subordination. This model is useful in many applications such as growth curves (children's height, fish length, diameter of trees, etc) and degradation processes (crack size, wheel degradation, laser light, etc). One advantage of our approach is to be able to easily deal with data that are irregularly spaced in time or different curves that are observed at different moments of time. With the use of simulations and applications, we examine two approaches to Bayesian inference for our model: the first based on a Gibbs sampler and the second based on approximate Bayesian computation.

Keywords: growth models; Bayesian inference; time change.

1 Introduction

Growth processes are usually described using discrete time models where the mean function is deterministic and a stochastic element is introduced via an additive, random noise component. An alternative approach is to consider continuous time modelling. In the literature some stochastic growth models are proposed using stochastic differential equations to model the variations ([1], [2]). However, the solution of these equations are not monotonically increasing and therefore can fail to model non-decreasing growth processes like, for example, children's height, fish size or crack length. We introduce a new stochastic model for non-decreasing processes which can be used to include stochastic variability into any deterministic growth function via subordination.

2 The model

Consider a birth-death process (BDP), $\{U_t : t \geq 0\}$, that is a continuous, time homogeneous, Markov process with finite state space, such that if, at time t, the process is in state i, after an exponential amount of time, then it moves to either of the neighbouring states $i \rightarrow i+1$ or $i \rightarrow i-1$. The process U_t is uniquely determined by the generator matrix, $\mathbf{Q}$, and the initial distribution of the process, $\boldsymbol{\nu}_0$.

The transition rate matrix $\mathbf{Q}$ is a tri-diagonal matrix with parameters $\alpha > 0$, the instantaneous birth rate and $\beta > 0$, the instantaneous death rate. Let $\mathcal{S} = \{a + ib; i = 0, \dots, k\}$ be the state space, where $a \geq 0$ is the minimum state value, b is a jump size and $k + 1$ is the number of states.

Now we define a continuous state process, $\{V_t : t \geq 0\}$, such that

$$V_t = J \int_0^t U_s ds, \tag{1}$$

where $J > 0$. This is a non-decreasing, continuous time process. Realizations of V_t are the path integrals of a simple stochastic process and their trajectories are piece-wise linear.

Finally, we will consider a simple time change of the process V_t governed by any deterministic non-decreasing function (see figure 1). Therefore, we define our stochastic growth process, $\{Y_t : t \geq 0\}$ to be the continuous time stochastic process with continuous state space, defined as

$$Y_t = V_{G(t)}, \tag{2}$$

where V_t as defined in (1) is a *subordinator* and $G(t)$ is a deterministic non-decreasing function.

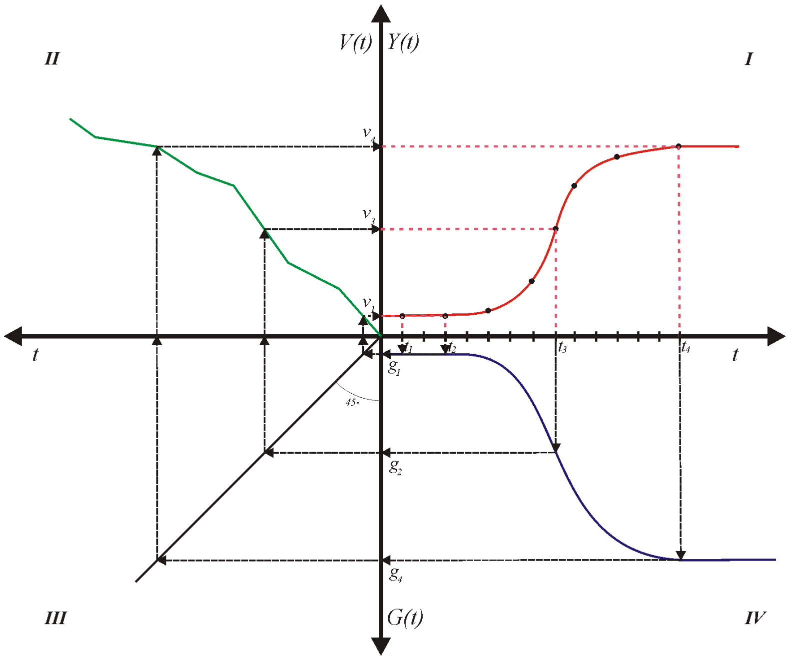
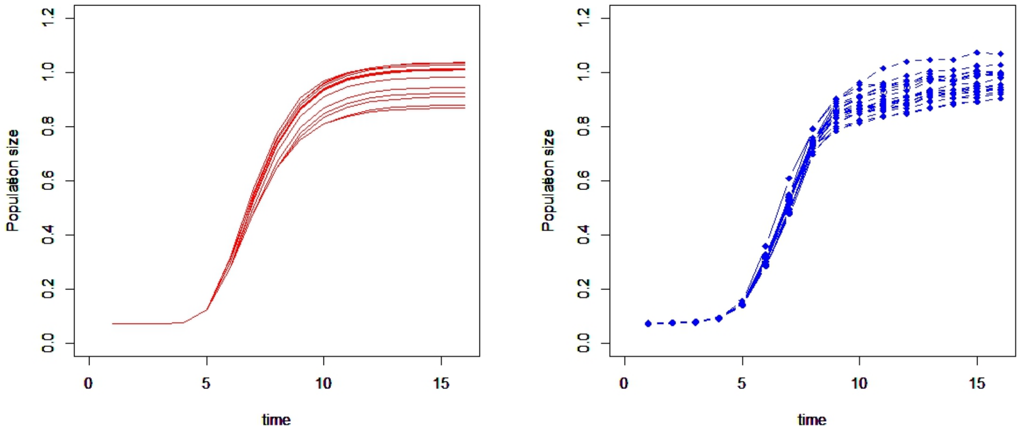


Figure 1: Time change

We show that assuming stationary state of the Markov process, then the mean function of the process Y_t is proportional to the function G: $E[Y_t] = E(U_t)JG(t)$. This means that if $J = 1/E[U_t]$ then the expected value of the process is exactly the deterministic function governing the time change. This fact suggests to use any standard parametric functions commonly used to model the particular kind of the process to drive the time change. For example, for growth curves a logistic or Gompertz function could be used, for fish size the von Bertalanffy growth function could be used, etc.

The variance of the process is increasing with time and its magnitude depends on the instantaneous intensity rates of the Markov process. Illustrative applications and



(a) Several realizations

(b) Replications

Figure 2: Simulated realizations and real bacterial growth curves

simulations are performed via Bayesian inference. See figure 2 for an application to bacterial growth.

The aim of our work was to propose a new stochastic process suitable to model growth process. Thus, the model developed shows two nice features: the growth paths are non-decreasing and the mean function of the process is equal to the parametric function governing the time change.

References

[1] Donnet, S., Foulley, J. and Samson, A. (2010). “Bayesian Analysis of Growth Curves Using Mixed Models Definied by Stochastic Differential Equations.” *Biometrics*, **66**, 733–741.

[2] Rensaw, E. (2011). *Stochastic Population processes: Analysis, Approximations, Simulations*. Oxford University Press, Oxford.