## Exploring Variability in Individual Growth: Introducing a Hierarchy of Stochastic Models

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#### Talk Abstract

In a scenario involving M individual animals experiencing random environmental fluctuations, a broad class of individual growth models, initially introduced by O. García [1], relies on the stochastic differential equation (SDE)

$$dY_i(t) = \beta(\alpha - Y_i(t))dt + \sigma dW_i(t), \ (i = 1, \dots, M),$$
(1)

where  $X_i(t)$  represents the size of the *i*-th individual (i = 1, ..., M) at age t,  $Y_i = h(X_i)$  is a transformed size via a strictly monotonous  $C^1$  function h,  $\alpha = h(A)$  denotes the transformed value of the asymptotic size  $A, \beta > 0$  is a growth parameter,  $W_i(t)(i = 1, ..., M)$  are independent standard Wiener processes, and  $\sigma \geq 0$  quantifies the strength of environmental fluctuations on growth. In previous work, we have extensively investigated this model for parameter estimation, profit optimization in livestock production, and other related topics. However, there is the possibility of individual variability, wherein different individuals possess distinct parameter values, denoted as  $\alpha_i$ and/or  $\beta_i$  (i = 1, ..., M). This leads to a mixed SDE model, characterized by

$$dY_i(t) = \beta_i(\alpha_i - Y_i(t))dt + \sigma dW_i(t), \ (i = 1, \dots, M),$$
(2)

with  $\alpha_i = \mu + \sigma^* \epsilon_i$ , where  $\epsilon_i$  are i.i.d. standard Gaussian random variables (and/or similarly for  $\beta_i$ ). Parameter estimation for mixed models often requires approximate methods, as demonstrated in [2, 3], where we have developed the delta approximation method and compared it with existing techniques. Moreover, individual parameter values, such as  $\alpha_i$ , may vary

according to specific characteristics (e.g., genetic values) of the individual. Here, we will illustrate with the linear dependence on one genetic value  $g_i$ , so that  $\alpha_i = \mu + cg_i + \sigma^* \varepsilon_i$ . This leads to the formulation of more intricate models and provide more individualized predictions. By employing a hierarchy of models with increasing complexity, we can systematically evaluate the significance of various sources of variability. Here, we will focus on the case of  $\alpha$  varying randomly among animals. Testing a hierarchy of hypotheses related to environmental variability effects ( $\sigma = 0$ ), parameter variability among individuals ( $\sigma^* = 0$ ), and the impact of a specific characteristic (e.g., genetic value) (c = 0) facilitates a comprehensive understanding of the underlying dynamics. We will illustrate statistical methods for detecting significant sources of variability and estimating parameters using real data from a large dataset of bovines from the Mertolengo breed.

**Keywords:** genetic traits, individual growth, mixed models, stochastic differential equations.

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