Deterministic and stochastic parameter analysis of the bone cell population model

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Abstract

Mathematical models are a great way of cementing biological verbal models. Specifically, they can provide causative mechanisms linking inputs and outputs and illuminating underlying assumptions that determine a biological system's dynamics. Further, they offer a means of predicting new outcomes, as well as highlighting the most sensitive modelled components, resulting in the construction of new experimental hypotheses and reducing experimental waste. This study represents a deterministic and stochastic analysis of bone cell population model. We explore this system through its homogeneous coupled ordinary nonlinear differential equations of generalized S-System type as well as through its probabilistic analogue, to investigate whether the model can capture the essential autocrine, paracrine and synergistic characteristics of bone cell communication processes, both in targeted and random remodeling processes. Continuum deterministic models assume that the simulated populations are large enough that a continuum approximation is valid. However, in the bone creation-degradation application, which these equations describe, cell population numbers often fall below 10 cells. Thus, the stochastic description is more appropriate. Critically, we see dynamics that are often present in the deterministic equation, which are used to explain a variety of observed experimental dynamics, do not occur in the stochastic model. Additionally, we are in a good position to comment and put insights onto parameter ranges according to the constraints from the specific bone multicellular unit (BMU) activity cycle detected in the histopathological screening and 3D in-vitro experiments. Thus, we are able to correlate the biological reality that these equations.

Keywords: bone remodeling, bone cell population model, S-System type, stochastic vs. deterministic computational modeling

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