STUDY OF BONE CELL POPULATION MODELS OF S-SYSTEM TYPE

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INTRODUCTION

This study represents a deterministic and stochastic analysis of the S-System of bone remodelling. We explore this system through its homogeneous coupled ordinary nonlinear differential equations,

$$\frac{du_i}{dx} = \alpha_i \prod_{j=1}^{2} u_j^{g_{ij}} - \beta_i u_i, \quad i = 1, 2, \tag{1}$$

as well as through its probabilistic analogue,

$$\emptyset \xrightarrow{\alpha_i u_i u_j} u_i, \quad u_i \xrightarrow{\beta_i} \emptyset, \quad i = 1, 2, \text{ and } \quad j \neq i, \tag{2}$$

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.

METHODS

Eq. (1) is used to analyse steady state stability, bifurcations and system sensitivity to parameters and initial conditions changes. The analogous probabilistic model (2) cannot be analysed so easily, thus, we turn to simulation. Namely, stochastically simulating the system 1000 times allows us to extract probabilistic distributions of the outcomes, which capture the noisy features of cell division and death, especially in the transition regimes on the beginning and ending of the processes.

RESULTS

Population dynamics are illustrated using time series plots, phase portraits, histograms and bifurcation diagrams. These motivate discussions regarding the model viability and parameter's value range and importance.

DISCUSSION AND CONCLUSIONS

Mathematical models are a great way of cementing biological verbal models. Specifically, they can provide causative mechanisms linking inputs and outputs and they can illuminate underlying assumptions that determine a biological system's dynamics. Finally, 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.

Continuum models (such as (1)) assume that the simulated populations are large enough that a continuum approximation is valid. In such cases the stochastic and deterministic descriptions are equivalent as noise reduces relative to population size. 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 apt. Critically, we see that dynamics that are often present in the deterministic equation, which used to explain a variety of observed experimental dynamics, do not occur in the stochastic model. Thus, we must question biological reality that these equations present.