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Strong inference in mathematical modelling: a new twist to an old idea

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While there are many opinions on what mathematical modelling in biology is, in essence, modelling is a mathematical tool which allows consequences to logically follow from a set of assumptions. Only when this tool is applied appropriately, it may allow to understand importance of specific mechanisms/assumptions in biological processes. Mathematical modelling can be less useful or even misleading if used inappropriately, for example, by creating a false impression of a good understanding of biological processes. It has been argued that the best use of mathematical models is not when a model is used to confirm a hypothesis but rather when a study shows inconsistency of the model (defined by a specific set of assumptions) and data. Following the principle of strong inference for experimental sciences proposed by Platt, I suggest “strong inference in mathematical modelling” as an effective and robust way of using mathematical modelling to understand mechanisms driving dynamics of biological systems. The major steps of strong inference in mathematical modelling are 1) to develop multiple alternative models for the phenomenon in question; 2) to compare the models with available experimental data and to determine which of the models are not consistent with the data; 3) to determine reasons why rejected models failed to explain the data, and 4) to suggest experiments which would allow to discriminate between remaining alternative models. The use of strong inference is likely to provide better robustness of predictions of mathematical models and it should be strongly encouraged in mathematical modelling-based publications in the 21st century.

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