

# Guidelines for publishing papers containing theory and modeling

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The use of quantitative approaches in cell biology, including modeling and theory, has been increasing steadily in the past decade. A number of seminal works that combine experiments and modeling have made a significant impact on the field (see Hill and Kirschner, 1982; Peskin *et al.*, 1993; Barkai and Leibler, 1997, to name but a few). Mathematical modeling can help when our intuition fails or misleads us. It can provide a precise language for understanding complex cell biological phenomena. Modeling represents a new addition to our repertoire of strategies to understand biological systems.

Like other journals in molecular and cellular biology, *Molecular Biology of the Cell* (MBoC) has thus far published a limited repertoire of papers that include modeling. Roughly speaking, there are two types of modeling/theoretical papers: one that is purely theoretical and another in which a quantitative model complements and extends experimental approaches. Furthermore, there are several different kinds of modeling, including deterministic or stochastic modeling, geometrical modeling, such as model convolution, and network (or database) modeling. Recognizing that modeling is becoming an indispensable tool, MBoC welcomes modeling and theoretical papers. This article is intended to help authors understand what MBoC is looking for in a modeling paper through advice and guidelines.

1. A paper should clearly and convincingly advance the understanding of a cell biological phenomenon of wide interest for the biological (rather than modeling) community.
2. A model should not be “window dressing” to make an experimental paper trendier. If a mathematical or quantitative model is used, there should be a clear demonstration of its usefulness.
3. Typical applications of modeling include (but are not restricted to) the following: (1) demonstrating that a qualitative hypothesis

cannot work as suggested; (2) calculating important quantities or hidden variables that are hard to measure experimentally, based on those that are observed; (3) discriminating between competing hypotheses; (4) supporting a qualitative hypothesis by showing that (simulated) computational results fit the experimental data; (5) reverse engineering a biological system, that is, using fits to observed data to deduce values of important rates or parameters; and (6) extracting quantitative information from quantitative data.

4. In the main text, the model should be described in lay terms understandable by the wider scientific community. Mathematical/computer/physical jargon is to be avoided. The explanation in the main text should highlight the key assumptions and strategy used in deriving the appropriate model and should carefully explain the gist of the model. This could be done by including schematic (“flowchart” or “network”) diagrams and putting the more technical details in the supplemental material. However, supplemental material should be informative enough that a qualified reviewer can appraise the relevance and formulation of the model.
5. Because biologists may be unfamiliar with mathematical or physical terms, these should be carefully defined and used appropriately.
6. Figures reporting modeling results should be as clear and well-explained as the rest of the paper.
7. In the theoretical supplemental material (written and edited as carefully as the main text), equations, model parameters (see next point), and other technical details should be included. Ideally, a reader should not have to guess how any part of calculations/simulations is done. The modeling results have to be as reproducible as the experimental results. We recommend including a list of assumptions either in the main text or in supplemental material.
8. All model parameter values (with relevant units) should be listed and defined in a supplemental table. Each value should be explained by citing published sources (when available), giving the basis for the calculation or estimate of the value or indicating that the value is unknown/fitted. We recommend some discussion of which parameters are crucial for predicted behaviors and which are less important.
9. MBoC recommends that authors voluntarily submit (well annotated) computational codes that could be used to reproduce the modeling result, either as a part of the supplemental material or on the Web. This submission is not currently a formal requirement, but discussions are under way about making this part of the MBoC policy.
10. MBoC welcomes purely theoretical papers that provide an especially novel conceptual model or discussion of a fundamental biological question.

Examples of papers with well-presented links between theory and experiment include (but are not restricted to) the following: Meinhardt, 1999—a purely theoretical conceptual model that started

DOI: 10.1091/mbc.E11-01-0088

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the modern modeling of eukaryotic cell chemotaxis; Marshall and Rosenbaum, 2001—a mathematical model summarizing experimental data; Chen *et al.*, 2004—reverse engineering a complex biological system; Lomakin *et al.*, 2009—a model that complements experiment by examining aspects that cannot be addressed experimentally; Odell and Foe, 2008—modeling used to discriminate between competing hypotheses; and Vogel *et al.*, 2009—a model that guides experiments and proves correctness of qualitative conclusions from the data.

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