Editorial: Do individuals matter? – Individual-based versus population-based models applied to biology and health

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Editorial on the Research Topic
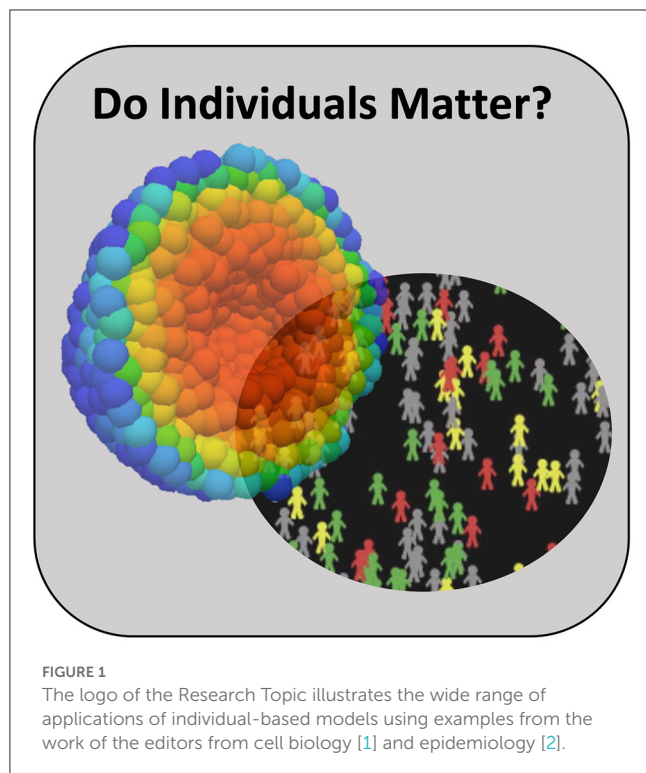Do individuals matter? - Individual-based versus population-based models applied to biology and health

"Do individuals matter?"—if we look at the foundations of various scientific disciplines, the answer to this question is clearly a passionate "Nothing else matters!". Scientific disciplines usually relate their aims to specific fundamental units.

- In the case of physics and chemistry, these are the building blocks of matter, atoms and molecules.
- For biology, it is the cell, the basic building block of life.
- In psychology, sociology, or economics, the fundamental unit is the individual, sometimes also called the agent.

This shows that at the heart of most scientific disciplines we find discrete entities such as particles, cells, or agents, each with their own individual states, in continuous interaction with each other. However, when we look at the scientific practice, we rarely see explicit representations of individuals. Physicists are happy to summarize particles as continuous densities (fluid dynamics) or probability distributions (statistical mechanics); similarly, in chemistry, molecules are aggregated to concentrations and in models of ecology (or, similarly, epidemiology), rather than modeling individuals, population number—individuals are often described as populations of individuals that neglect inter-individual differences. Thus, although the theory is individual-based, the practice is population-based. Recently, as an alternative to population-based approaches, individual-based models have been developed within all areas of Mathematical Biology. The logo for this Research Topic (Figure 1) shows just two examples from applications by the editors, from cell biology [1] and epidemiology [2], respectively.

Musters et al. observe that also in ecology, many questions are phrased in a way so that they become detached from individual agents within an ecosystem—despite the fact that ecology is usually defined as the study of the interactions of organisms both with each other as well as with their environment. This is caused by the introduction of a hierarchy which they call organism-species-community-based ecology (OSCE) where organisms are summarized as populations, populations of various species form communities, and communities form meta-communities. In contrast to this step-wise hierarchical process

FIGURE 1
The logo of the Research Topic illustrates the wide range of applications of individual-based models using examples from the work of the editors from cell biology [1] and epidemiology [2].

which consists of aggregation at each level, Musters et al. propose an alternative approach that they refer to as organism-based ecology (OE). The underlying idea is to investigate not only populations but also the higher levels of the species-community-meta-community hierarchy in terms of organisms. For this purpose, the authors suggest to combine existing frameworks—trait-based ecology (TE), individual-based modeling [for which they use the interchangeable notion of agent-based modeling (ABM)], and maximum entropy theory of ecology (METE). In OE, the role of trait-based ecology is to statistically investigate how traits vary between individuals. By following an individual-based modeling approach, the effect of these heterogeneities between individuals can then be investigated. Finally, METE enables the modeler to validate their IBM and iteratively refine it if necessary. The authors argue that their OE approach will increase the predictive power of ecological studies by representing aspects that are neglected in OSCE.

This proposal of OE as an alternative to OCSE demonstrates that individual-based modeling is not an aim in itself. Two important considerations are as follows:

- Does an IBM enable us to investigate questions that cannot be asked with a population-based approach?
- Is an IBM expected to produce results that are qualitatively different than a population-based model?

These two aspects are beautifully illustrated in the article by Lu et al.. The authors investigate the competition between the invasive species *Melaleuca quinquenervia* and a native tree species in Florida. The individual-based approach enables the authors to represent the mean seedling dispersal distance and, in particular, the effect of standing dead wood on the outcome of competition which would be difficult to achieve using a classical mathematical model such as the Lotka-Volterra competition model. Interestingly,

similar to population-based models, coexistence is difficult to achieve and depending on the model parameters, either the invader or the native species drives the other to extinction. However, the model shows interesting spatio-temporal dynamics which the authors refer to as the "phalanx effect."

As computational power becomes ever more available, IBMs are becoming increasingly used to understand developmental processes. This is exemplified in the article by Müller et al., where the authors present a method for simulating collective cell migration when there are multiple stimuli. In the study, the authors present three different approaches to responding to multiple stimuli and compare these against expected behavior. They find that collective cell migration is robust and qualitatively the same under each approach. The study also highlights the role of IBMs for understanding collective phenomena at the tissue scale that emerge from interactions between cells.

So, have IBMs superseded population-based approaches? Are these models just relics from a time when computers would have crumbled under the computational demands of highly detailed IBMs which represent a large number of states? Instead of regarding IBMs and population-based models as competing approaches, as both frameworks further develop, it is more useful to explore how IBMs and population-based models complement each other. A nice example is the article by Kynaston et al. from a group which has already developed several rigorous methods for combining individual-based and population-based representations in the same model. For this Research Topic, the authors consider chemical reaction networks. When modeling chemical reactions involving a large number of particles, a deterministic model based on mass action kinetics is usually sufficient, whilst for small numbers of particles, a stochastic approach based on Markov jump processes is more accurate. Kynaston et al. present a hybrid model that combines an individual-based Markov process for reactions involving a small number of particles with mass action kinetics for reactions between large populations of particles.

So, do individuals *really* matter? Rather than calling for a primarily individual-based or population-based framework, the articles of this Research Topic support a more nuanced view. The future will most likely be a synthesis that explores new ways of taking advantage of the strengths of both individual-based and population-based descriptions.

Author contributions

Acknowledgments

Conflict of interest

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References

1. Mirams GR, Arthurs CJ, Bernabeu MO, Bordas R, Cooper J, Corrias A, et al. Chaste: An open source C++ library for computational physiology and biology. *PLoS Comput Biol.* (2013) 9:e1002970. doi: 10.1371/journal.pcbi.1002970

2. Siekmann I. Bifurcation analysis of individual-based models in population dynamics. *Ecol Complex.* (2015) 21:177–84. doi: 10.1016/j.ecocom.2014.06.002