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Introduction

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Authors for correspondence:
Berta Verd
e-mail: berta.verdfernandez@zoo.ox.ac.uk
Rubén Pérez-Carrasco
e-mail: r.perez-carrasco@imperial.ac.uk

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Interdisciplinary approaches to dynamics in biology

Berta Verd[1] and Rubén Pérez-Carrasco[2]

[1]Department of Zoology, University of Oxford, Oxford, UK
[2]Department of Life Sciences, Imperial College London, London, UK

BV, 0000-0001-9835-009X

1. It is time's time

Biology is dynamic in nature. From ecological systems to embryonic pattern formation: change is at the centre of any biological phenomenon. The last three decades of molecular genetics have been incredibly successful at identifying the components involved in many biological processes, and now we find ourselves at the advent of very exciting times where new methodologies and technologies are, for the first time, allowing us to address the dynamics of these processes directly. Biologists can now quantify the dynamics of biological processes [1–4], analyse [2,5,6] and image them [7–9] in unprecedented resolution. These and other related advances have been shifting the way we represent biological phenomena, away from static representations and towards increasingly more dynamic and therefore realistic accounts.

Biological dynamics are steadily moving to the forefront of many fields in biology. Increasingly more dynamic perspectives and explanations are challenging the validity of static analyses, which although generally more tractable both from a theoretical and an experimental perspective, will have to be justified rather than assumed. The mechanisms underlying biological phenomena will need to address and explain the timing of the processes being investigated as well as their components and spatial distribution. Close interdisciplinary collaborations will be required in order to develop new techniques, methodologies, models, computational tools and conceptual frameworks to address and explain the dynamics that have always characterized biological systems and processes at every level of their organization.

2. Introduction to the theme issue

In the light of these advances in dynamics, and to ensure that this new and growing body of knowledge moves beyond a descriptive level towards mechanistic and causal accounts of biological processes, in February 2020 we hosted a Royal Society Hooke Theo Murphy meeting at Chichely Hall in Buckinghamshire. The meeting, 'Interdisciplinary approaches to dynamics in biology', brought together a highly interdisciplinary cohort of scientists from quantitative biologists working infields as far ranging as cell biology to ecology, to live-imaging experts, mathematical modellers and philosophers of biology. By shifting the focus away from any biological process in particular to the dynamics of biological phenomena more generally, the meeting helped find common ground between fields that would otherwise seldom overlap, and exploited the intersection between them to translate methodologies, tools and perspectives. In this theme issue, our authors present some of the core ideas and main topics that emerged from the many discussions held at the meeting.

2.1. Bridging spatio-temporal scales

A focus on timing draws our attention to the many previously unappreciated mechanisms by which biological systems regulate and tune their dynamics. In their review, Busby & Steventon [10] explore the role of tissue tectonics—the movement of tissues relative to one another—in controlling and regulating developmental timing and evolutionary change. They propose that the dynamics of cell signalling and commitment depend on various kinds of timers across different spatio-temporal scales within the developing embryo and highlight the importance of considering downward causation from the tissue to the single-cell level, to understand developmental dynamics. With a similar focus, in their review, Rayon & Briscoe [11] identify the mechanisms controlling developmental pace and tempo, while arguing for the value and explanatory potential of cross-species comparisons to understand developmental timing across evolutionary time-scales. These papers go on further to illustrate also how understanding developmental timing is critical to advance bio-engineering and translational medicine.

The challenges that arise from the study of the interplay between different dynamical scales is not restricted to molecular and cellular processes. In their paper, Brejcha *et al.* [12] study the coevolutionary process of mimicry, defined by the interaction of two different dynamic processes—prey–prey interactions and predator perception. By formalizing this interaction using an attractor field model, the authors reveal how novel mathematical frameworks are key.

2.2. Dynamical modules

The inherent complexity of including time in our conceptualization of biological processes poses the question of how best to understand biological processes in general and their dynamics in particular. Jaeger & Monk [13] present a thorough review of the different accounts of biological modularity to date, focusing on how biological dynamics can be understood as modular too. Centring their argument on the dynamics of biological processes, the authors propose top-down approaches to decompose systems' dynamics and explain through the use of a wide range of examples from metabolism, and cell and developmental biology, the advantages of adopting such a framework, often in concomitance with more traditional approaches.

Clark's paper explores how the concept of dynamical modules can be applied to understand the evolution of segmentation [14]. By defining and combining different dynamical modules, the author is able to describe the relationship and possible evolutionary transitions between the different modes of segmentation observed in vertebrates and arthropods. This approach illustrates that understanding and insight can be obtained by focusing on dynamics without the need to consider any of the gene regulatory mechanisms that generate them.

To finalize, diFrisco and Jaeger define homology of processes [15] as a conceptual framework from which to address the evolution of biological dynamics. The authors propose a marked departure from previous accounts of homology, which have systematically focused on establishing homology at the level of individual genes, networks and traits, but not at the level of the developmental process. They illustrate through examples of how processes can be homologous without the need for their components to be and present a set of criteria to help determine homology at the level of the process.

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