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Algorithmic Information Dynamics

Biological systems are extensively studied as interactions forming complex networks. Reconstructing causal knowledge from, and principles of, these networks from noisy and incomplete data is a challenge in the field of systems biology. Based on an online course hosted by the Santa Fe Institute Complexity Explorer, this book introduces the field of Algorithmic Information Dynamics, a model-driven approach to the study and manipulation of dynamical systems to solve general inverse problems. It draws tools from network and systems biology as well as information theory, complexity science, and dynamical systems to study natural and artificial phenomena in software space. It consists of a theoretical and methodological framework to guide an exploration and generate computable candidate models able to explain complex phenomena in particular adaptive systems, making the book valuable for graduate students and researchers in a wide number of fields in science from physics to cell biology to cognitive sciences.

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Algorithmic Information Dynamics

A Computational Approach to Causality with Applications to Living Systems

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Preface

This book is based on the Massive Open Online Course (MOOC) on Algorithmic Information Dynamics, supported by the Foundational Questions Institute (FQXi) and hosted by the Complexity Explorer. The course and textbook introduce the field of *Algorithmic Information Dynamics* (AID). AID is a type of model-driven approach to the study and manipulation of dynamical systems. A type of digital calculus that studies dynamical systems in software space.

The material we have elected to cover derives from work undertaken over the last 15 years. Though its arrangement suggests a series of discrete topics, in fact what we attempt here is the exploration of avenues to build bridges between them, mirroring the kinds of research programmes we ourselves have been engaged in.

In Chapter 1, we outline the broader intellectual landscape within which the course is situated. To paraphrase a famous line, 'No book is an island'. The course was conceived and designed to be very different from others covering related topics. On the one hand, both the course and textbook are highly eclectic in nature, being research-orientated and focused largely on topics and questions at the forefront of scientific inquiry from what we believe to be an unconventional angle. For example, some of contemporary science's main challenges arguably involve topics such as causation, the corresponding causal networks, and the network dynamics that effectively produce regularities in data or observations. Questions such as system identification, control, and reprogrammability are therefore germane. These topics can be approached from a generative equation-based (physics) perspective, or a statistical machine-learning perspective driven by the data. Here, we develop a fundamental information-based approach to address these challenges. To this end, we assess the extent to which algorithmic information theory can provide a framework within which to understand regularities in data and observations. In an important sense this reflects our vision of a more horizontal science, which proceeds by cross-pollinating seemingly disparate areas that together push the boundaries of the individual fields involved. On the other hand, our ambition from the outset was to design the course to be self-contained, and this has meant having to include a large preliminary section, with individual chapters that could conceivably be expanded into one or several free-standing courses. However, this has not been our choice, as to do so would in our view disrupt the flow between disparate areas and mask their deep interconnectedness, which is precisely what we think deserves careful investigation. Our course and textbook are thus quite different from others in that they treat emerging areas of interest in depth while both broadening in scope and disrupting

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every one of the established fields drawn upon. In doing so we are able to offer, in return as it were, some new insights into the many concepts and tools lent us by the said fields. This is the case with, for example, graph and network theory, where we make specific contributions by defining native measures of algorithmic complexity, or with dynamical systems, where we provide new tools to characterise systems, and help reconstruct and explore dynamics from disordered data, asking, for example, how informative eigenvalues are in the context of graph spectra. Likewise, with respect to classical Shannon information theory, we contribute a new measure that joins forces with estimations of algorithmic complexity to make each measure stronger than it would be on its own. And finally, to causation, where our mechanistic/algorithmic approach is intended to make its greatest contribution, we bring a fresh and novel viewpoint, moving beyond a solely statistical approach to data analysis towards model inference and program synthesis.

The Introduction will provide the background to the many concepts involved in the study of AID and, in particular, prior approaches to the challenge of causality or causation that we have built upon.

We will briefly introduce graphs and networks from the mathematical perspective, as well as in terms of the way in which they serve to represent interactions in biology. Networks will be a fundamental object of study throughout the book.

In Part I, we will have the difficult task of providing a general overview of information theory, computability theory, and algorithmic complexity, the three topics, apart from dynamical systems, which are most essential to an understanding of AID.

We will also walk you through another fundamental area, that of dynamical systems, one of the main disciplines needed to understand algorithmic information dynamics, where we will be able to study the evolution of systems over time.

In Part II, covering theory and methods, we will begin by introducing the measures on which AID directly stands, that is, the so-called Coding Theorem Method or CTM, and the so-called Block Decomposition Method or BDM, as well as the concept of sequence models.

At the end of the second part (Chapter 8), we will introduce Algorithmic Information Dynamics, its associated algorithmic causal calculus, and its direct application to understanding and reconstructing dynamical systems. The seminal concept of reprogrammability will close this part of the book.

While we would have preferred the process of learning and communication to be less sequential, we humans have few options other than to present written material in a consecutive order, even when ontologically unwarranted and pedagogically less than optimal.

However, you may elect not to move sequentially through the book, especially if you are comfortable and knowledgeable in these areas, in which case you can go directly to those topics that are of particular interest to you, even if that means going directly to Part II. Figure 1 should help you understand the dependencies.

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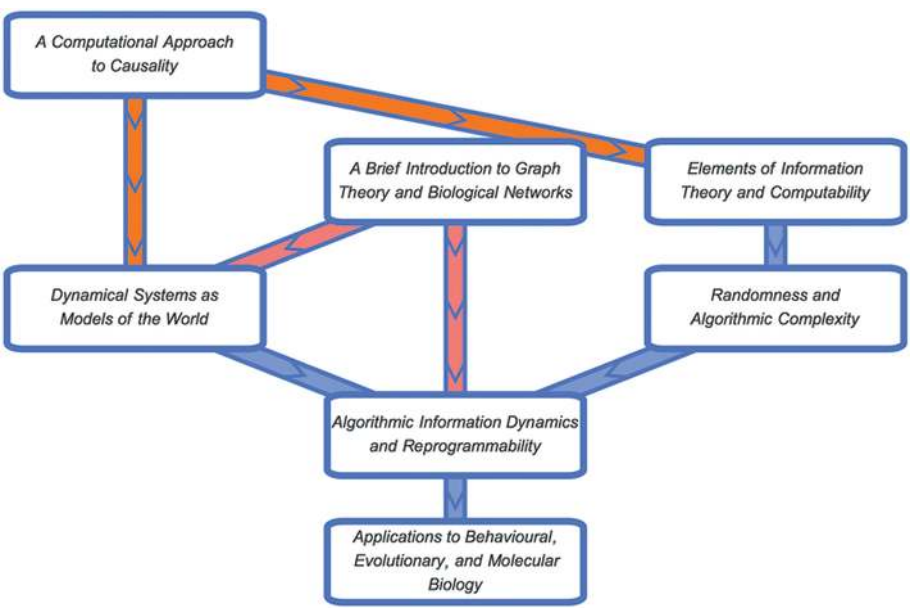

Figure 1 Module dependencies of the course and of the new field of algorithmic information dynamics. Orange links signify conceptual/motivational dependency. Pink links signify weak dependency. Blue links indicate strong dependency.

Part III of the textbook pulls everything together, from networks to evolving systems, from perturbation analysis to complexity and computability, from information theory to causation and applications to genetics, molecular biology, cognition, and evolution. Because of the level of multidisciplinarity of our work, we will include a summary some chapters that explains how an observer from the field under review in that chapter would regard the fields covered in each of the remaining chapters.

Finally, in Chapters 11 and 12 we will explore the various applications of algorithmic information dynamics, in particular to behavioural, evolutionary, and molecular biology, to static and evolving genetic networks, and in the new area of algorithmic machine learning, providing pointers toward future research.

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