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## Preface

The biology of life is highly complex and dynamic, making it an attractive system for us to study and understand. The life-forms on earth range from single-celled organisms to large multicellular organisms and can sustain themselves in a variety of environmental conditions such as hot thermal vents and cold polar ice caps. Our fascination for this diversity has led us to study them in much detail, and we have come to understand that there is a plethora of patterns occurring in nature. For example the migratory patterns of different species of birds, and the presence of specific codons in DNA that allows a gene to be transcribed and translated into a protein of a specific amino acid sequence. Nature being too complex, these patterns are often not apparent and there is almost always an element of stochasticity. With the increasing influence of computer-based algorithms and statistics in biology, we have successfully come up with methods for modeling such complex and noisy biological systems. Hidden Markov Model (HMM) is one such statistical model widely used in modeling complex systems and in the identification of “hidden” patterns. It was initially used in the field of signal processing and speech recognition but because of its assumptions, its ability to process sequential data, and its tolerance to intrinsic noise it soon became an ideal tool to address many biological questions. By far the most extensively studied field in biology that uses HMM is the sequence analysis of protein and DNA/RNA biomolecules. There are numerous books that substantially cover HMM’s seminal applications in studying biological sequences. But our understanding of biology has changed immensely since the start of this century, and with it the methods used to study them. These changes have enabled HMM to find its way into various new aspects of biological research. This book aims to provide the readers with a perspective of the newer and a broader usage of HMMs in biology. It is roughly structured in the order of the physical size of the biological system under study, ranging from single biomolecule (Chapters 2–7), cellular level (Chapters 8–13) to organism level (Chapters 14 and 15). All the authors in this book are experts in their respective fields with publications related to HMMs in peer-reviewed journals, and they have attempted to give you a good overview of what system they are modeling and how they have adopted HMM to attain their objectives. Therefore each chapter is autonomous and expert readers can get up to speed by reading only the chapters of their interest. For readers with no prior experience in HMM, we have provided you with an easy to read introduction to HMM (Chapter 1) that will aid you in understanding the rest of the chapters in this book. The beauty of HMM is that it is simple to understand and easy to apply to real-world scenarios, and hence the reader need not necessarily rely on equations given in the chapters in order to understand them. We hope that this book helps you in appreciating the impact of HMM in biology and inspire you in your own research.

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