Preface

Modern biology is awash in data. This situation, the result of a technical revolution in high-throughput genomics, promises rapid scientific advances. However, analyzing the data poses unique challenges. Unlike in physics, there is usually no quantitative biological model that can guide investigation and generate precise predictions; often, we do not even know what the relevant quantities are that could capture the essential behavior of the biological system.

In response to the flood of data, the use of clustering algorithms and dimensionality reduction procedures is now ubiquitous. These families of techniques can be regarded as efforts to describe the *shape* of the data set. Although there have been noted successes, such methods provide only crude descriptions of this shape. The power of these tools, as well as their evident limitations, makes it clear that there would be substantial scientific benefit from richer and more robust methods for understanding geometric structure in data.

Algebraic topology is a well-established branch of pure mathematics that studies qualitative descriptors of the shape of geometric objects. Roughly speaking, the goal of algebraic topology is to reduce questions about comparing shapes to questions about comparing algebraic invariants (e.g., numbers), which are typically easier to solve. Moreover, algebraic topology has had a long tradition of employing combinatorial models of geometric objects, *simplicial complexes*, that are well suited to algorithmic computation.

Topological data analysis is a rapidly developing subfield that leverages the tools and outlook of algebraic topology to provide a methodology for analyzing the shape of data sets. The basic strategy is to assign a family of simplicial complexes to a data set; invariants of the complexes integrate information about the shape of the data across different feature scales.

Our aim in this book is to provide a concise introduction to the central ideas and techniques of topological data analysis and to explain in detail a number of specific

applications to biology. We imagine as our idealized readers a modern quantitative biologist or a graduate student in mathematics with a background in topology or geometry and an interest in applied problems. We have three central goals:

1. to equip the modern quantitative biologist with techniques from topological data analysis,
2. to direct mathematicians with training in geometry and topology towards problems of interest to biologists, and
3. to make it easier for mathematicians and biologists to communicate and collaborate.

These goals pose an expositional challenge, as we expect two quite different audiences with different backgrounds. To address this, we have attempted as much as possible to provide a self-contained introduction to the relevant topics along with abundant and detailed references. We assume that the reader has some familiarity with calculus, linear algebra, elementary probability, and basic statistics.

The first part of this book presents the mathematical background necessary to understand topological data analysis and then provides an overview of techniques in the area. These chapters are intended to be read in order, as each one builds on the previous chapters. The second part of this book consists of a collection of distinct biological applications; each chapter can be read independently.

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