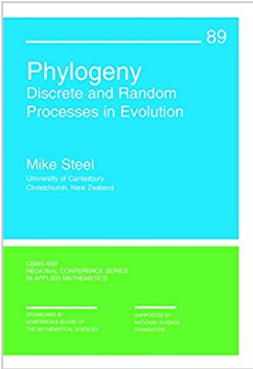

Phylogeny: Discrete and Random Processes in Evolution (CBMS-NSF Regional Conference Series)

By Mike Steel

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Phylogenetics is a topical and growing area of research. Phylogenies (phylogenetic trees and networks) allow biologists to study and graph evolutionary relationships between different species. These are also used to investigate other evolutionary processes - for example, how languages developed or how different strains of a virus (such as HIV or influenza) are related to each other.

This self-contained book addresses the underlying mathematical theory behind the reconstruction and analysis of phylogenies. The theory is grounded in classical concepts from discrete mathematics and probability theory as well as techniques from other branches of mathematics (algebra, topology, differential equations). The biological relevance of the results is highlighted throughout.

In *Phylogeny: Discrete and Random Processes in Evolution*, the author supplies proofs of key classical theorems and includes results not covered in existing books, emphasizes relevant mathematical results derived over the past 20 years, and provides numerous exercises, examples, and figures.

Audience: This book is intended for applied mathematicians, biomathematicians, discrete mathematicians, systematic biologists, computer scientists specializing in algorithms and bioinformatics, statisticians specializing in stochastic processes, researchers working in probability theory, and scholars studying the philosophy of biology.

Contents: Preface; Acknowledgements; Commonly Used Symbols; Chapter 1: Phylogeny; Chapter 2: Basic combinatorics of discrete phylogenies; Chapter 3: Tree shape and random discrete phylogenies; Chapter 4: Pulling trees apart and putting trees together; Chapter 5: Phylogenies based on discrete characters; Chapter 6: Continuous phylogenies and distance-based tree reconstruction;

Chapter 7: Evolution on a tree: Part one; Chapter 8: Evolution on a tree: Part two; Chapter 9: Evolution of trees; Chapter 10: Introduction to phylogenetic networks; Bibliography; Index.

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Editorial Review

About the Author
Mike Steel is a Professor in the School of Mathematics and Statistics at University of Canterbury and Director of its Biomathematics Research Centre. He is an elected fellow of the Royal Society of New Zealand and a recipient of the NZ Mathematical Society's annual Research Award. His research interests include combinatorics and random processes and their applications to questions in evolutionary biology and related areas of sciences, which in biology have mainly concerned phylogenetic theory and methods. Additional research interests include autocatalytic networks in origin of life, inverting random functions in mathematical statistics, and questions in the philosophy of science concerning causality and information loss. He has published approximately 240 academic papers, co-authored two books on phylogenetics, and served as associate editor of various journals, including *Bulletin of Mathematical Biology* and *Systematic Biology*.

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