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Evolution Algebras and their Applications

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To my parents

Bi-Yuan Tian and Yu-Mei Liu

My father, the only person I know who can operate two abaci using his left and right hand simultaneously in his business.

Preface

In this book, we introduce a new type of algebra, which we call evolution algebras. These are algebras in which the multiplication tables are of a special type. They are motivated by evolution laws of genetics. We view alleles (or organelles or cells, etc,) as generators of algebras. Therefore we define the multiplication of two "alleles" G_i and G_j by $G_i \cdot G_j = 0$ if $i \neq j$. However, $G_i \cdot G_i$ is viewed as "self-reproduction," so that $G_i \cdot G_i = \sum_j p_{ij} G_j$, where the summation is taken over all generators G_j. Thus, reproduction in genetics is represented by multiplication in algebra. It seems obvious that this type of algebra is nonassociative, but commutative. When the p_{ij}s form Markovian transition probabilities, the properties of algebras are associated with properties of Markov chains. Markov chains allow us to develop an algebra theory at deeper hierarchical levels than standard algebras. After we introduce several new algebraic concepts, particularly algebraic persistency, algebraic transiency, algebraic periodicity, and their relative versions, we establish hierarchical structures for evolution algebras in Chapter 3. The analysis developed in this book, particularly in Chapter 4, enables us to take a new perspective on Markov process theory and to derive new algebraic properties for Markov chains at the same time. We see that any Markov chain has a dynamical hierarchy and a probabilistic flow that is moving with invariance through this hierarchy. We also see that Markov chains can be classified by the skeleton-shape classification of their evolution algebras. Remarkably, when applied to non-Mendelian genetics, particularly organelle heredity, evolution algebras can explain establishment of homoplasmy from heteroplasmic cell population and the coexistence of mitochondrial triplasmy, and can also predict all possible mechanisms to establish the homoplasmy of cell population. Actually, these mechanisms are hypothetical mechanisms in current mitochondrial disease research. By using evolution algebras, it is easy to identify different genetic patterns from the complexity of the progenies of *Phytophthora infectans* that cause the late blight of potatoes and tomatoes. Evolution algebras have many connections with other fields of mathematics, such as graph theory, group theory, knot theory, 3-manifolds, and Ihara-Selberg zeta functions. Evolution algebras provide a theoretical framework to unify many phenomena. Among the further research topics related to evolution algebras and other fields, the most significant topic perhaps is to develop a continuous evolution algebra theory for continuous time dynamical systems.

The intended audience of this book includes graduate students and researchers with interest in theoretical biology, genetics, Markov processes, graph theory, and nonassociative algebras and their applications.

Professor Jean-Michel Morel gave me a lot of support and encouragement, which enabled me to take the step to publish my research results as a book. Other editors and staff in LNM made efforts to find reviewers and edit my book. Here, I wish to express my great thanks to them.

I thank Professor Michael T. Clegg for his stimulating problems in coalescent theory. From that point, I began to study genetics and stochastic processes. I am greatly indebted to Professor Xiao-Song Lin, my Ph.D advisor, for his valuable advice and long-time guidance. I am thankful to professors Bai-Lian Larry Li, Michel L. Lapidus, and Barry Arnold for their valuable suggestions. It gives me great pleasure to thank Professors Bun Wong, Yat Sun Poon, Shizhong Xu, Keh-Shin Lii, Peter March, Dennis Pearl, Raymond L. Orbach, Murray Bremner, Yuan Lou, and Yang Kuang for their encouragement. I also thank Professor C. William Birky Jr. for his explanation of non-Mendelian genetics through e-mails. I acknowledge Professor Winfried Just for his suggestions of writing style of the book and a formula in Chapter 3. I am grateful to my current mentor, Professor Avner Friedman, for his detailed and cherished suggestions on the research in this book and my other research directions. I thank three reviewers for their suggestions and constructive comments.

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