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The Genetics of Teliospore Production and Microevolution in Rust Fungi, Feb 27 2021

Population Genetics and Microevolutionary Theory Apr 12 2022 The advances

made possible by the development of molecular techniques have in recent years revolutionized quantitative genetics and its relevance for population genetics.

Population Genetics and Microevolutionary Theory takes a modern approach to population genetics, incorporating modern molecular biology, species-level evolutionary biology, and a thorough acknowledgment of quantitative genetics as the theoretical basis for population genetics. Logically organized into three main sections

on population structure and history, genotype-phenotype interactions, and selection/adaptation Extensive use of real examples to illustrate concepts Written in a clear and accessible manner and devoid of complex mathematical equations Includes the author's introduction to background material as well as a conclusion for a handy overview of the field and its modern applications Each chapter ends with a set of review questions and answers Offers helpful general references and Internet links
Dental Genetics and Microevolution in Prehistoric and Living Koniag Eskimo Jul 23 2020

Selection, Genetic Environment, and Adaptive Evolution Sep 17 2022

Comparative Quantitative Genetics of the Pelvis in Four-species of Rodents and the Conservation of Genetic Covariance and Correlation Structure Jan 17 2020

Quantitative genetics is a powerful tool for predicting phenotypic evolution on a microevolutionary scale. This predictive power primarily comes from the Lande equation, a multivariate expansion of the breeder's equation, where phenotypic change is predicted from the genetic covariances and selection. Typically restricted to generational change, evolutionary biologists have proposed that quantitative genetics could bridge micro- and macroevolutionary patterns if predictions were expanded to longer timescales. While mathematically possible, making quantitative genetic

predictions across generations or species is contentiously debated, principally in assuming long-term stability of the G-matrix. Here we tested stability at a macroevolutionary timescale by conducting full-sib breeding programs in two species of sigmodontine rodents from South America, the leaf-eared mice *Phyllotis xanthopygus* and *Phyllotis darwini* and estimated the G-matrices for eight pelvic traits. To expand our phylogenetic breadth, we incorporated two additional G-matrices measured for the same traits from Kohn and Atchley's 1988 study of the murine rodents *Mus musculus* and *Rattus norvegicus*. Using a phylogenetic comparative framework and four separate metrics of matrix divergence or similarity, we found no significant association between evolutionary divergence among species G-matrices and time, supporting the assumption of stability for at least some structures. However, the phylogenetic sample size is necessarily small. We suggest that small fluctuations in covariance structure can occur rapidly, but underlying developmental regulation prevents significant divergence at macroevolutionary scales, analogous to an Ornstein-Uhlenbeck pattern. Expanded taxonomic sampling will be needed to test this suggestion.

Population Genetics of Island Endemics Mar 19 2020 Island archipelagoes are ideal for the study of microevolutionary forces due to their multiple, closely related but

geographically disjunct populations. I used both neutral and major histocompatibility complex (MHC) loci to determine the population genetic structures of bird species endemic to the Galápagos Islands. MHC molecules recognize foreign pathogens in the body, and these loci are known for their high degree of genetic variability maintained by natural selection. Small island populations are predicted to have reduced genetic variability due to the effects of genetic drift; however, selection may be strong enough to prevent the loss of variability at MHC loci. First, I characterized neutral genetic structure in the Galápagos hawk (*Buteo galapagoensis*). Analyses of both neutral nuclear VNTR (Chapter 1) and mitochondrial (Chapter 2) loci showed low within-population variability but high between-population differentiation. In Chapter 3, we found that smaller, more inbred populations had birds with higher louse loads and, in general, lower and less variable natural antibody titres than the larger, more genetically variable hawk populations. Chapter 4 presents MHC work done on the Galápagos penguin (*Spheniscus mendiculus*), a seabird whose breeding colonies experience population bottlenecks associated with El Niño events. Galápagos penguins had low variability, having only three MHC alleles which differed by only a few base pairs. MHC work on the Galápagos hawks (Chapter 5) revealed similarly low variability. Galápagos hawks had fewer and less divergent alleles than the Swainson's hawk, their

closest mainland relative. The MHC diversity in both the Galápagos species was lower than in the mainland species, indicating that genetic drift has had an overwhelming effect. Lastly, in Chapter 6, I characterized the neutral population genetic structure of six Galápagos mockingbird (*Mimus* spp.) populations. Genetic variability increased with island area and we found a pattern of isolation by distance, both indicating the influence of genetic drift. Significant levels of genetic and morphological differentiation existed among all six populations, though morphological distances were smaller between islands of similar area suggesting the influence of natural selection.

Connecting Microevolutionary Processes with Macroevolutionary Patterns Across Space and Time Jul 03 2021

Whether microevolutionary processes can explain macroevolutionary patterns has long been a matter of contentious debate. The debate has persisted largely because of the challenging task of connecting microevolutionary theory, which examines population-level phenomena on the generation scale, to data collected across larger spatial and temporal scales. My dissertation research broadly examines phenotypic evolution across multiple scales by connecting microevolutionary theory to macroevolutionary phenomena such as speciation and large-scale phenotypic change. In particular, I focus on the so-called "paradox of stasis"; which wrestles with the apparent conflict between frequently-observed cases of rapid evolution on short

timescales and the frequent appearance of stasis in the fossil record. I attempt to link micro and macroevolution by using the theoretical framework of evolutionary quantitative genetics for modeling the effects of drift and selection. My four dissertation chapters examine four different systems (1) connecting quantitative genetic models of sexual selection to speciation (2) connecting microevolutionary and macroevolutionary body size data across scales of time (3) using phylogenetic comparative methods and quantitative genetic models to examine the evolution of a classic example of stasis, mammalian body temperature and (4) finally, using multi-locus phylogeography to understand the evolutionary processes that contribute to the diversification of a widespread snake across broad spatial scales. In chapter 2, I demonstrate that genetic drift combined with sexual selection can promote speciation and diversification of male ornaments. Furthermore, I demonstrate that drift promotes the evolution of elaborate ornaments even when preferences are costly. In chapter 3, I combine data from microevolutionary field studies, the fossil record, and phylogenetic comparative data into a single analytical framework to resolve apparent conflicts between micro and macroevolutionary patterns. To do so, I compiled and analyzed the largest database of phenotypic divergence data in existence. I demonstrate that patterns of stasis persist until a million-year threshold, after which divergence begins to

accumulate in a time-dependent manner. This pattern is best fit with a hierarchical model that describes evolution as occurring in bursts on the million-year timescale, but that allows for rapid, but bounded, evolution on short timescales. In chapter 4, I demonstrate that mammalian body temperature -- which has been previously presented as a classic example of stasis -- does in fact evolve extensively across the mammalian radiation (albeit slowly). Furthermore, I show that mammalian body temperature evolves in response to changing environmental conditions. Finally, I evaluate the role that genetic constraints play in the apparent slowness of body temperature evolution. In chapter 5, I examine a well-studied empirical system of garter snakes in which a strong signature of stabilizing selection has been found for phenotypic traits. Using multiple mitochondrial and nuclear loci, I show that introgression is rampant between species, and dynamic patterns of range expansion, contraction, and introgression among clades have led to a complex pattern of genetic variation. This structure of genetic variation underscores the need to examine range-wide processes for generating phenotypic divergence across clades. Overall, these chapters suggest that apparent disconnects between microevolutionary processes and macroevolutionary patterns could be explained by the scaling of population-level theory over large spatial and temporal scales.

Microevolutionary Patterns in Aboriginal Australia Nov 14 2019 Detailed study of the geographic distribution of genetic traits among Australian Aboriginal populations; theories of racial origin; population structure and movement; population genetics - blood groupings, dentition, morphological, metrical and idicial traits; relation to regional, temporal, environmental and linguistic factors; territorial groupings.

Microevolutionary Processes in Natural Populations of the Waterstrider *Aquarius Remigis* Feb 10 2022

Sketches of Nature Jun 14 2022 This visually appealing book recounts the history of molecular ecology and evolution as seen through the personal lens of one of its most prolific practitioners, who has studied a panorama of creatures ranging from corals, sponges, and other invertebrates to a wide variety of vertebrate animals including numerous birds, mammals, herps, and fishes. The sketches are of two types: evocative drawings of the animals themselves, and more than 230 written abstracts summarizing the author's eclectic research on ecological-genetic topics spanning the microevolutionary to macroevolutionary. With the abstracts arranged by organismal group and placed in chronological order, the chapters in this book lead readers on a fascinating historical journey into the realm of molecular genetics as applied across the past four decades to intriguing questions in ecology, evolution, animal behavior, and

natural history. Encapsulates salient genetic findings on a diverse array of creatures in nature
Recounts the history of technological and conceptual developments in ecological genetics
Includes approximately 80 beautiful line drawings of the animals themselves
Provides context by preceding each abstract with an anecdote or historical backdrop
Concludes each abstract with an addendum that further contextualizes the research findings
Written by a world-leading authority in molecular ecology and evolution

Tracking Microevolution Over Millennia Using Ancient DNA Oct 26 2020

A Companion to Anthropological Genetics Sep 05 2021 Explore the latest research in anthropological genetics and understand the genome's role in cultural and social development
A Companion to Anthropological Genetics illustrates the role of genetic analysis in advancing the modern study of human origins, populations, evolution, and diversity. Broad in scope, this essential reference work establishes and explores the relationship between genetic research and the major questions of anthropological study. Through contributions by leading researchers, this collection explores molecular genetics and evolutionary mechanisms in the context of macro- and microevolution, paleontology, phylogeny, diet, and disease, with detailed explanations of quantitative methods, including coalescent and approximate Bayesian computation. With an

emphasis on contextualizing new and developing genetic research within anthropological frameworks, this text offers critical perspective on the conditions of molecular evolution that accompany cultural and social transformation, while also addressing critical disciplinary questions, such as the ethical issues surrounding ancestry testing and community-based genetic research. Acts as an essential reference on the contributions of genetic science to the field of anthropology Features new work by leading researchers of the field Explores the evolution of immunity, including the genetics and epigenetics of pathogens, chronic illness, and disease resistance Provides in-depth examination of mutation and dietary adaptation, including AMY1, lactase persistence, and sensory polymorphisms Explains essential quantitative and phylogenetic methods for aligning genomic analysis with evolution and migration time scales Offering thorough coverage on leading questions and developing research, A Companion to Anthropological Genetics is a comprehensive resource for students and scholars.

Microevolution Rate, Pattern, Process Jul 15 2022 From guppies to Galapagos finches and from adaptive landscapes to haldanes, this compilation of contributed works provides reviews, perspectives, theoretical models, statistical developments, and empirical demonstrations exploring the tempo and mode of microevolution on

contemporary to geological time scales. New developments, and reviews, of classic and novel empirical systems demonstrate the strength and diversity of evolutionary processes producing biodiversity within species. Perspectives and theoretical insights expand these empirical observations to explore patterns and mechanisms of microevolution, methods for its quantification, and implications for the evolution of biodiversity on other scales. This diverse assemblage of manuscripts is aimed at professionals, graduate students, and advanced undergraduates who desire a timely synthesis of current knowledge, an illustration of exciting new directions, and a springboard for future investigations in the study of microevolution in the wild.

A Simulation Approach to Studying the Relationship Between Landscape Features and Social System on the Genetic Structure of a Tamarin Primate Population

Feb 16 2020 Landscape genetics is an emerging field that seeks to understand how specific landscape features and microevolutionary processes such as gene flow, genetic drift, and selection interact to shape the amount and spatial distribution of genetic variation. This study explores, through agent based simulations, how the specific mating and social system of tamarin primates (genus *Saguinus*) influences population genetic structure and patterns of relatedness within and among groups of this primate species, which might affect the ability of landscape genetic

studies to detect the effects of fragmentation on gene flow. I use a spatially-explicit agent-based population genetics simulation model (GENESYS) configured to reflect the particular social system of tamarin monkeys (i.e. small group size, limited numbers of breeders per group, frequent twin births, and short dispersal distances) to assess whether the isolation by distance model of genetic differentiation expected in an unfragmented landscape can be distinguished from the isolation by barrier model expected in a fragmented landscape. GENESYS allows a user to explore the effects of social structure and landscape features on the population genetic structure of social animals, such as primates. I simulated two different landscapes containing an otherwise equivalent population of tamarins. In the first setup I simulated a homogeneous landscape unconstrained by any barriers to gene flow, while for the second setup, a barrier to gene flow restricted dispersal from one half of the landscape to the other. I found that the particular mating system of tamarin results in the rapid genetic differentiation of its social groups and consequently its populations. Social groups in the continuous landscape indeed revealed an isolation by distance pattern, while social groups on the fragmented landscape yielded instead an isolation by barrier model, where the barrier rather than geographic distance per se influenced the spatial genetic structure of the population. The results from this study suggest that features of the

tamarin social system influence population genetic structure, which could affect the ability of landscape genetic studies to detect the effects of fragmentation on gene flow. To more fully address that issue, future studies should focus on a range of different primate social systems.

Human Biology of Afro-Caribbean Populations Aug 04 2021 A comprehensive study of the microevolution of Caribbean populations of African descent, this 2006 book reviews the conditions endured by the slaves during their passage and in the plantations and how these conditions may have affected their own health and that of their descendants. Providing an evolutionary framework for understanding the epidemiology of common modern-day diseases such as obesity, hypertension and diabetes, it also looks at infectious diseases and their effect on the genetic make-up of Afro-Caribbean populations. Also covered are population genetics studies that have been used to understand the microevolutionary pathways for various populations, and demographic characteristics including the relationships between migration, family type and fertility. Ending with a case study of the Afro-Caribbean population of Limón, Costa Rica, this book is an essential resource for researchers working in biological anthropology, demography, and epidemiology, and for those interested in the African diaspora in the New World.

Human Variation and Human Microevolution Dec 16 2019

Population Genetics of a Vertebrate Metacommunity Jan 29 2021 Population genetic structure is widespread in many organisms and can be found at small spatial scales. Population genetic differentiation is an evolutionary precursor to speciation and can have a significant impact on the microevolutionary dynamics of a region. Levels of divergence, in turn, are determined by numerous ecological and evolutionary factors operating on multiple spatial and temporal scales, including spatial heterogeneity, population size and dispersal. My dissertation uses microsatellite markers to investigate the population genetic structure of three vertebrate species that coexist on a common landscape and share ecological predator-prey and competition interactions. I then identify ecological and evolutionary processes important in shaping the observed patterns within a comparative framework. Finally, I explore evolutionary processes that shape adaptive divergence in one of the species, by comparing levels of population differentiation at quantitative traits and neutral molecular markers among ecotypes.

Connecting Micro and Macroevolution Through Quantitative Genetics Jan 09 2022 Do genetic and developmental constraints play a significant role in shaping the morphological diversity of living organisms? This decades-old question remains as relevant today as it was when it was first formulated, and the debate has mainly

persisted due to the difficulties in connecting population-level processes to phenomena occurring at much broader temporal and spatial scales. Quantitative genetics has long been considered a possible theoretical framework in which to generate testable hypotheses capable of disentangling the relative contribution of evolutionary processes and genetic/developmental constraints in shaping morphological evolution. Therefore, my dissertation examines patterns of skull variation and evolution across multiple scales, and attempts to connect microevolutionary processes to macroevolutionary patterns through quantitative genetic theory. The results presented here emphasize that the variational properties of organisms have a significant impact over macroevolutionary diversification patterns, and that these properties are, therefore, an important but underappreciated contribution of quantitative genetic theory to studies of morphological evolution.

Genetics, Growth, and Microevolution Oct 06 2021

A Theoretical Analysis of Population Genetics of Plants on Restored Habitats Dec 28 2020 Seed and propagules used for habitat restoration are not likely to be closely adapted to local site conditions. Rapid changes of genotypes frequencies on local microsites and/or microevolution would allow plants to become better adapted to a site. These same factors would help to maintain genetic diversity and ensure the survival of

small endangered populations. The authors used population genetics models to examine the selection of genotypes during establishment on restored sites. Vegetative spread was shown to affect selection and significantly reduce genetic diversity. To study general microevolution, the authors linked a model of resource usage with a genetics model and analyzed competition between genotypes. A complex suite of feasible ecogenetic states was shown to result. The state actually resulting would depend strongly on initial conditions. This analysis indicated that genetic structure can vary locally and can produce overall genetic variability that is not simply the result of microsite adaptations. For restoration activities, the implication is that small differences in seed source could lead to large differences in local genetic structure after selection.

Macroevolution Oct 14 2019 This book is divided in two parts, the first of which shows how, beyond paleontology and systematics, macroevolutionary theories apply key insights from ecology and biogeography, developmental biology, biophysics, molecular phylogenetics and even the sociocultural sciences to explain evolution in deep time. In the second part, the phenomenon of macroevolution is examined with the help of real life-history case studies on the evolution of eukaryotic sex, the formation of anatomical form and body-plans, extinction and speciation events of marine invertebrates, hominin evolution and species conservation ethics. The book brings together leading experts,

who explain pivotal concepts such as Punctuated Equilibria, Stasis, Developmental Constraints, Adaptive Radiations, Habitat Tracking, Turnovers, (Mass) Extinctions, Species Sorting, Major Transitions, Trends and Hierarchies – key premises that allow macroevolutionary epistemic frameworks to transcend microevolutionary theories that focus on genetic variation, selection, migration and fitness. Along the way, the contributing authors review ongoing debates and current scientific challenges; detail new and fascinating scientific tools and techniques that allow us to cross the classic borders between disciplines; demonstrate how their theories make it possible to extend the Modern Synthesis; present guidelines on how the macroevolutionary field could be further developed; and provide a rich view of just how it was that life evolved across time and space. In short, this book is a must-read for active scholars and because the technical aspects are fully explained, it is also accessible for non-specialists. Understanding evolution requires a solid grasp of above-population phenomena. Species are real biological individuals and abiotic factors impact the future course of evolution. Beyond observation, when the explanation of macroevolution is the goal, we need both evidence and theory that enable us to explain and interpret how life evolves at the grand scale.

Human Population Genetics Jan 21 2023 Introductory guide to human population

genetics and microevolutionary theory Providing an introduction to mathematical population genetics, Human Population Genetics gives basic background on the mechanisms of human microevolution. This text combines mathematics, biology, and anthropology and is best suited for advanced undergraduate and graduate study. Thorough and accessible, Human Population Genetics presents concepts and methods of population genetics specific to human population study, utilizing uncomplicated mathematics like high school algebra and basic concepts of probability to explain theories central to the field. By describing changes in the frequency of genetic variants from one generation to the next, this book hones in on the mathematical basis of evolutionary theory. Human Population Genetics includes: Helpful formulae for learning ease Graphs and analogies that make basic points and relate the evolutionary process to mathematical ideas Glossary terms marked in boldface within the book the first time they appear In-text citations that act as reference points for further research Exemplary case studies Topics such as Hardy-Weinberg equilibrium, inbreeding, mutation, genetic drift, natural selection, and gene flow Human Population Genetics solidifies knowledge learned in introductory biological anthropology or biology courses and makes it applicable to genetic study. NOTE: errata for the first edition can be found at the author's website: <http://employees.oneonta.edu/relethjh/HPG/errata.pdf>

From DNA to Diversity Dec 20 2022 In this landmark work, the author team led by Dr. Sean Carroll presents the general principles of the genetic basis of morphological change through a synthesis of evolutionary biology with genetics and embryology. In this extensively revised second edition, the authors delve into the latest discoveries, incorporating new coverage of comparative genomics, molecular evolution of regulatory proteins and elements, and microevolution of animal development. An accessible text, focusing on the most well-known genes, developmental processes and taxa. Builds logically from developmental genetics and regulatory mechanisms to evolution at different genetic morphological levels. Adds major insights from recent genome studies, new evo-devo biology research findings, and a new chapter on models of variation and divergence among closely related species. Provides in-depth focus on key concepts through well-developed case studies. Features clear, 4-color illustrations and photographs, chapter summaries, references and a glossary. Presents the research of Dr. Carroll, a pioneer in the field and the past president of the Society for Developmental Biology.

Human Biologists in the Archives May 01 2021 Many physical anthropologists study populations using data that come primarily from the historical record. For this volume's authors, the classic anthropological 'field' is not the glamour of an exotic locale, but the

sometimes tedium of the dusty back rooms of libraries, archives and museum collections. This book tells of the way in which archival data inform anthropological questions about human biology and health. The authors present a diverse array of human biological evidence from a variety of sources including the archaeological record, medical collections, church records, contemporary health and growth data and genetic information from the descendants of historical populations. The papers demonstrate how the analysis of historical documents expands the horizons of research in human biology, extends the longitudinal analysis of microevolutionary and social processes into the present and enhances our understanding of the human condition.

Microevolution Nov 07 2021 Anthropological study of Northeastern India.

Molecular Markers, Natural History and Evolution Aug 24 2020 Molecular approaches have opened new windows on a host of ecological and evolutionary disciplines, ranging from population genetics and behavioral ecology to conservation biology and systematics. **Molecular Markers, Natural History and Evolution** summarizes the multi-faceted discoveries about organisms in nature that have stemmed from analyses of genetic markers provided by polymorphic proteins and DNAs. The first part of the book introduces rationales for the use of molecular markers, provides a history of molecular phylogenetics, and describes a wide variety of laboratory methods

and interpretative tools in the field. The second and major portion of the book provides a cornucopia of biological applications for molecular markers, organized along a scale from micro-evolutionary topics (such as forensics, parentage, kinship, population structure, and intra-specific phylogeny) to macro-evolutionary themes (including species relationships and the deeper phylogenetic structure in the tree of life). Unlike most prior books in molecular evolution, the focus is on organismal natural history and evolution, with the macromolecules being the means rather than the ends of scientific inquiry. Written as an intellectual stimulus for the advanced undergraduate, graduate student, or the practicing biologist desiring a wellspring of research ideas at the interface of molecular and organismal biology, this book presents material in a manner that is both technically straightforward, yet rich with concepts and with empirical examples from the world of nature.

Migration and Colonization in Human Microevolution Dec 08 2021 An integrative approach linking the causes of migration to genetic consequences for human evolution. *Readings in Evolutionary Theory, Genetics, and the Origins of Modern Human Morphology* Jun 02 2021 *Readings in Evolutionary Theory, Genetics, and the Origins of Modern Human Morphology* provides students with a collection of readings that explore critical concepts in biological anthropology and human evolution. The text is

divided into 10 distinct sections that feature an introduction, relevant readings, and post-reading questions. Opening sections explore creationism versus evolution, the history of evolutionary thought, population genetics and microevolution, and heritability. Students read about natural selection in action, primate behavior, evolutionary systematics, and human evolution and the origins of bipedalism. The final sections examine Neanderthals, the origins of modern humans, and what it is to be human. Concise and accessible, *Readings in Evolutionary Theory, Genetics, and the Origins of Modern Human Morphology* is an ideal resource for courses in anthropology and human evolution.

Natural History and Evolution of a Color Polymorphism in *Rana Pipiens*, the Northern Leopard Frog Sep 24 2020 A primary goal of population genetics is to identify the role of microevolutionary forces in producing observed patterns of molecular and phenotypic variation. I conducted four studies in the northern leopard frog, *Rana pipiens*, to determine just how mutation, migration, genetic drift, and selection influenced, genetic structure of mitochondrial DNA (mtDNA), nuclear DNA, and a single locus polymorphism that determines dorsal coloration. In the first study, I surveyed the literature concerning color and pattern polymorphisms in anurans. I conclude that anuran polymorphisms remain a rich but largely unexploited system for

studying the evolution of phenotypic variation in nature. In the second study, I compared mitochondrial DNA variation from 35 populations distributed across the species' range. A phylogenetic analysis indicated *R. pipiens* is split into two deeply divergent mtDNA groups, a western group and an eastern group. Phylogeographic and demographic analyses indicated that although restricted gene flow with isolation by distance explained the majority of the processes influencing current genetic structure, population bottlenecks and expansions also played an important role. In the third study, I investigated mtDNA and microsatellite variation in Pacific Northwest populations of *R. pipiens*, where a recent range contraction had occurred. I found that peripheral populations had reduced levels of genetic variation compared to more interior populations. Moreover, I found that historic samples from peripheral population already had reduced levels of genetic variation. Therefore, low diversity in the remnant populations could not be ascribed to the recent range contraction. In the fourth study, I compared genetic structure from a suite of putatively neutral molecular markers with that derived from the color polymorphism locus. Genetic structure at the color locus, assessed both spatially and temporally, was indistinguishable from structure at neutral loci. This study exemplifies the importance of investigating for evidence of selective maintenance before studies attempt to measure the selective mechanisms maintaining a

polymorphism. Overall, my research helps to elucidate how biogeographic and microevolutionary forces influence a wide-spread North American species, *R. pipiens*.

Microevolutionary Processes in *Euglena Pisciformis* Nov 26 2020

Population Genetics and Microevolutionary Theory Feb 22 2023 *Population Genetics and Microevolutionary Theory* Explore the fundamentals of the biological implications of population genetic theory In the newly revised Second Edition of *Population Genetics and Microevolutionary Theory*, accomplished researcher and author Alan R. Templeton delivers a fulsome discussion of population genetics with coverage of exciting new developments in the field, including new discoveries in epigenetics and genome-wide studies. The book prepares students to successfully apply population genetics analytical tools by providing a solid foundation in microevolutionary theory. The book emphasizes that population structure forms the underlying template upon which quantitative genetics and natural selection operate and is a must-read for future population and evolutionary geneticists and those who wish to work in genetic epidemiology or conservation biology. You'll learn about a wide array of topics, including quantitative genetics, the interactions of natural selection with other evolutionary forces, and selection in heterogeneous environments and age-structured populations. Appendices that cover genetic survey techniques and probability and

statistics conclude the book. Readers will also benefit from the inclusion of: A thorough introduction to population genetics, including the scope of the subject, its premises, and the Hardy-Weinberg Model of Microevolution An exploration of systems of mating, including a treatment of the use of runs of homozygosity to show pedigree inbreeding in distant ancestors A practical discussion of genetic drift, including the use of effective sizes in conservation biology (with a discussion of African rhinos as an example) A concise examination of coalescence, including a treatment of the infinite sites model Perfect for graduate students in genetics and evolutionary biology programs and advanced undergraduate biology majors, Population Genetics and Microevolutionary Theory will also earn a place in the libraries of students taking courses in conservation biology, human genetics, bioinformatics, and genomics.

Principles of Evolutionary Genetics Apr 19 2020 Evolutionary genetics studies new mutations that still occur within a species. It derives its primary principles from evolutionary milestones that have been highlighted by the theory of natural selection. There are multiple micro-evolutionary changes that occur within the various groups of a species and they manifest as macro-evolutionary patterns across a period of time, resulting in varying individual and social behavioral actions. Evolutionary genetics has

been applied in sub-fields such as ecological genetics, population genetics and quantitative genetics. This book strives to provide a fair idea about this discipline and to help develop a better understanding of the latest advances within this field. It will serve as a reference to a broad spectrum of readers.

Nature in Silico Oct 18 2022 Dramatic advances in computing power enable simulation of DNA sequences generated by complex microevolutionary scenarios that include mutation, population structure, natural selection, meiotic recombination, demographic change, and explicit spatial geographies. Although retrospective, coalescent simulation is computationally efficient—and covered here—the primary focus of this book is forward-in-time simulation, which frees us to simulate a wider variety of realistic microevolutionary models. The book walks the reader through the development of a forward-in-time evolutionary simulator dubbed FORward Time simUlation Application (FORTUNA). The capacity of FORTUNA grows with each chapter through the addition of a new evolutionary factor to its code. Each chapter also reviews the relevant theory and links simulation results to key evolutionary insights. The book addresses visualization of results through development of R code and reference to more than 100 figures. All code discussed in the book is freely available, which the reader may use directly or modify to better suit his or her own research needs. Advanced

undergraduate students, graduate students, and professional researchers will all benefit from this introduction to the increasingly important skill of population genetic simulation.

Tinkering Nov 19 2022 Much recent research in evolutionary developmental biology has focused on the origin of new body plans. However, most evolutionary change at the population and species level consists of tinkering: small-scale alterations in developmental pathways within a single body plan. Such microevolutionary events have been well studied on a population genetic level and from the perspective of adaptive phenotypic evolution, but their developmental mechanisms remain poorly studied. This book explores both theoretical and practical issues of tinkering. It features a wide range of perspectives to address several fundamental questions. How does tinkering occur developmentally, and how is it manifested phenotypically? Are the developmental mechanisms by which tinkering occur different from those that underlie larger evolutionary changes? What are the developmental constraints on tinkering? And how do we test hypotheses about microevolutionary shifts in development from the fossil record? With contributions from experts in a range of fields, this fascinating book makes exciting reading for anyone studying evolution, developmental biology or genetics.

A Primer of Molecular Population Genetics Aug 16 2022 What are the genomic signatures of adaptations in DNA? How often does natural selection dictate changes to DNA? How does the ebb and flow in the abundance of individuals over time get marked onto chromosomes to record genetic history? Molecular population genetics seeks to answer such questions by explaining genetic variation and molecular evolution from micro-evolutionary principles. It provides a way to learn about how evolution works and how it shapes species by incorporating molecular details of DNA as the heritable material. It enables us to understand the logic of how mutations originate, change in abundance in populations, and become fixed as DNA sequence divergence between species. With the revolutionary advances in genomic data acquisition, understanding molecular population genetics is now a fundamental requirement for today's life scientists. These concepts apply in analysis of personal genomics, genome-wide association studies, landscape and conservation genetics, forensics, molecular anthropology, and selection scans. This book introduces, in an accessible way, the bare essentials of the theory and practice of molecular population genetics.

Genetics Mar 11 2022 Genetic gone through a breakthrough in the discovery that DNA would be the fundamental structure carrying the genetic information. Among the various work with this molecule, he stood out to Watson, Crick, Wilkins, and Franklin

in 1953, which demonstrated the structure of the DNA double helix. After the discovery of DNA structure, several other studies have been conducted to understand who was responsible for producing the proteins. The idea that DNA would be responsible for the synthesis of RNA and that this, in turn, would be responsible for producing proteins was postulated by Crick in 1958 and became known as Molecular Biology of the Central Dogma.

Microsatellites as a Tool for the Study of Microevolutionary Process in Native Forest Trees Mar 31 2021 The main aim of this work is an attempt to help researchers that use microsatellite markers to analyze microevolutionary forces in natural populations of native forest species. This kind of studies drives the researchers to make decisions regarding management or conservation of such species. This chapter pays attention to the entire process—from development of microsatellite markers, going through data analysis and ending with interpretation of these results. This work helps to researchers that are not familiarizing with methods and population genetics theories to analyze nuclear and chloroplast microsatellite data. These methods allow quantification of genetic variation and genetic structure in native forest species, and theoretical content allows knowledge about the past and the present genetic states of populations for making inferences about the future of these populations.

Microevolution, Local Adaptation, and Demography in Wild Populations of Pacific Salmon Jun 21 2020 There is increasing scientific interest in empirically linking evolution to ecology, particularly in wild populations. Although evolutionary change is often thought to proceed slowly, the microevolutionary forces of selection, gene flow, genetic drift and inbreeding can have pronounced effects on genetic variation even on short time scales. These genetic changes may then influence local adaptation and demography. The overarching aim of this dissertation was to estimate levels of gene flow and selection in wild populations, and to assess how microevolutionary change might affect local adaptation and population dynamics within these populations. Pacific salmon (*Oncorhynchus* spp.) are an ideal model organism for studying natural patterns of microevolution and local adaptation. First there is high phenotypic variation within the species, and spawning fish can be sampled comprehensively by capturing adults when they return to freshwater from the ocean. Second, salmon form reproductively isolated spawning populations due to natal homing, but these populations can be genetically and demographically connected via straying. Third, salmon are of ecological and commercial interest, making our findings relevant to population management. This dissertation investigated ecology and evolution in salmon as follows. In Chapter 1, we examined patterns of genetic and phenotypic differentiation

between adjacent populations of beach and stream spawning ecotypes of sockeye salmon, and assessed potential levels of gene flow between ecotypes. The objective of Chapter 2 was to determine whether small populations of Chinook and chum salmon occurring in the Wood River system are reproductively isolated, self-sustaining populations, population sinks that produce returning adults but receive immigration, or strays from other systems that do not produce returning adults. In Chapter 3 we reconstructed pedigrees for two wild populations of sockeye salmon to estimate natural selection and heritability for several phenotypic traits. For Chapter 4, we used empirical results from the first three chapters to develop a stochastic, individual-based model that we used to study effects of gene flow and selection on local adaptation and population dynamics in interconnected salmon populations. Taken together, these studies showed how gene flow and selection affect local adaptation and demography in wild salmon populations.

Spatio-temporal Genetic Variation in Brown Trout (*Salmo Trutta*) May 13 2022

Natural Selection May 21 2020 This book contests the general view that natural selection constitutes the explanatory core of evolutionary biology. It invites the reader to consider an alternative view which favors a more complete and multidimensional interpretation. It is common to present the 1930-1960 period as characterized by the

rise of the Modern Synthesis, an event structured around two main explanatory commitments: (1) Gradual evolution is explained by small genetic changes (variations) oriented by natural selection, a process leading to adaptation; (2) Evolutionary trends and speciation events are macroevolutionary phenomena that can be accounted for solely in terms of the extension of processes and mechanisms occurring at the previous microevolutionary level. On this view, natural selection holds a central explanatory role in evolutionary theory - one that presumably reaches back to Charles Darwin's *Origin of Species* - a view also accompanied by the belief that the field of evolutionary biology is organized around a profound divide: theories relying on strong selective factors and those appealing only to weak ones. If one reads the new analyses presented in this volume by biologists, historians and philosophers, this divide seems to be collapsing at a rapid pace, opening an era dedicated to the search for a new paradigm for the development of evolutionary biology. Contrary to popular belief, scholars' position on natural selection is not in itself a significant discriminatory factor between most evolutionists. In fact, the intellectual space is quite limited, if not non-existent, between, on the one hand, "Darwinists", who play down the central role of natural selection in evolutionary explanations, and, on the other hand, "non-Darwinists", who use it in a list of other evolutionary mechanisms. The "mechanism-centered" approach

to evolutionary biology is too incomplete to fully make sense of its development. In this book the labels created under the traditional historiography - "Darwinian Revolution", "Eclipse of Darwinism", "Modern Synthesis", "Post-Synthetic Developments" - are thus re-evaluated. This book will not only appeal to researchers working in evolutionary biology, but also to historians and philosophers."

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