

laboratory 8 population genetics and evolution

Laboratory 8: Population Genetics and Evolution

laboratory 8 population genetics and evolution delves into the fundamental principles that drive evolutionary change within populations. This exploration examines how allele frequencies shift over time, driven by mechanisms such as mutation, gene flow, genetic drift, and natural selection. Understanding these forces is crucial for comprehending the diversity of life on Earth and predicting future evolutionary trajectories. We will investigate the theoretical underpinnings of population genetics, explore common laboratory exercises designed to illustrate these concepts, and discuss the implications of these processes for conservation, medicine, and agriculture. This comprehensive overview aims to provide a solid foundation for anyone interested in the dynamic field of evolutionary biology.

- Introduction to Population Genetics
- Key Mechanisms of Evolutionary Change
- Hardy-Weinberg Equilibrium: A Baseline for Evolution
- Experimental Approaches in Laboratory 8
- Interpreting Results and Drawing Conclusions
- Applications of Population Genetics and Evolution

Introduction to Population Genetics

Population genetics is the study of genetic variation within populations and the evolutionary forces that alter allele and genotype frequencies. It forms the bedrock of modern evolutionary theory, bridging the gap between Mendelian genetics and Darwinian evolution. By examining the genetic makeup of groups of interbreeding individuals, scientists can track evolutionary processes in action. This field recognizes that evolution occurs at the population level, not at the individual level. The focus is on how the genetic composition of a population changes from one generation to the next.

The core concept in population genetics is the allele, a specific variant of a gene. The collection of all alleles for a particular gene within a population is known as the gene pool. Changes in the frequencies of these alleles over time are the hallmark of evolution. Factors that influence these changes are diverse and often

interact in complex ways, leading to the incredible biodiversity we observe.

Understanding population genetics is essential for fields ranging from conservation biology, where it helps assess the genetic health and viability of endangered species, to human medicine, where it informs our understanding of disease susceptibility and drug resistance. This foundational knowledge allows us to predict how populations will respond to environmental changes and human interventions.

Key Mechanisms of Evolutionary Change

Several primary mechanisms drive the evolution of populations. These forces act on the genetic variation present within a population, leading to shifts in allele frequencies over generations. Each mechanism plays a distinct role, and often they operate concurrently.

Mutation: The Ultimate Source of New Genetic Variation

Mutation is the process by which changes occur in the DNA sequence. These changes can range from small, single-nucleotide alterations to larger chromosomal rearrangements. Mutations are the ultimate source of all new genetic variation. While many mutations are neutral or even deleterious, some can be beneficial, providing the raw material for adaptation. In the context of population genetics, the rate of mutation is a crucial factor, albeit often a slow one, in introducing new alleles into a population's gene pool.

Gene Flow: The Movement of Alleles Between Populations

Gene flow, also known as migration, refers to the movement of alleles from one population to another. This can occur through the dispersal of individuals or their gametes. Gene flow tends to homogenize allele frequencies between populations, reducing genetic differences. It can also introduce new alleles into a recipient population or increase the frequency of existing alleles. The rate of gene flow can significantly impact the genetic structure of populations and their potential for local adaptation.

Genetic Drift: Random Changes in Allele Frequencies

Genetic drift is the change in allele frequencies in a population due to random chance. It is a particularly potent force in small populations, where random fluctuations can have a substantial impact on allele frequencies. Imagine a small population of beetles where, by chance, more individuals with a certain allele reproduce than others in a given generation. This random sampling can lead to the loss of some alleles and

the fixation of others, regardless of their adaptive value. Two important scenarios of genetic drift are the bottleneck effect, where a population's size is drastically reduced, and the founder effect, where a new population is established by a small number of individuals.

Natural Selection: Differential Survival and Reproduction

Natural selection is the process by which individuals with traits that are better suited to their environment tend to survive and reproduce more successfully than those with less advantageous traits. This differential survival and reproduction lead to an increase in the frequency of advantageous alleles and a decrease in the frequency of disadvantageous alleles over time. Natural selection is a non-random process that can lead to adaptation and the evolution of complex traits. The concept of fitness in population genetics refers to an organism's reproductive success in a particular environment.

Hardy-Weinberg Equilibrium: A Baseline for Evolution

The Hardy-Weinberg principle, also known as the Hardy-Weinberg law or theorem, provides a theoretical framework for understanding how allele and genotype frequencies change in a population. It describes a hypothetical population that is not evolving. This null hypothesis serves as a baseline against which real populations can be compared to detect evolutionary forces at work.

For a population to be in Hardy-Weinberg equilibrium, it must meet five strict conditions:

- No mutation
- No gene flow
- Random mating
- No genetic drift (i.e., a very large population size)
- No natural selection

If a population is in Hardy-Weinberg equilibrium, the allele frequencies (represented by 'p' for one allele and 'q' for the other) and genotype frequencies (represented by p^2 , $2pq$, and q^2) will remain constant from generation to generation. The equation for allele frequencies is $p + q = 1$, and for genotype frequencies is $p^2 + 2pq + q^2 = 1$. Deviations from these expected frequencies in a real population indicate that one or more of the Hardy-Weinberg conditions are not being met, implying that evolution is occurring.

Experimental Approaches in Laboratory 8

Laboratory 8 typically involves hands-on activities designed to illustrate the principles of population genetics and evolution. These experiments often utilize simulation methods or observable biological systems to demonstrate the impact of evolutionary forces.

Simulating Genetic Drift with Beads or Dice

A common simulation involves using colored beads or dice to represent alleles in a population. Students repeatedly draw samples of these "alleles" to mimic reproduction. By performing this process over multiple generations, especially with small sample sizes, the random fluctuations in allele frequencies characteristic of genetic drift become apparent. This exercise helps visualize how chance events can lead to the loss or fixation of alleles, particularly in small populations.

Investigating Natural Selection with Controlled Environments

Another approach may involve observing natural selection in action using organisms with short generation times, such as fruit flies or bacteria. Different environmental conditions or selective pressures can be applied to replicate populations. For instance, introducing a predator or a specific antibiotic can lead to differential survival and reproduction of individuals with particular traits, thus altering allele frequencies over time. Measuring the changes in these frequencies allows for the direct observation of selection's power.

Modeling Gene Flow Through Population Mixing

Experiments can also simulate gene flow by combining individuals (or their representative alleles) from distinct populations with differing allele frequencies. This mixing demonstrates how the introduction of new genetic material can alter the genetic landscape of a population, leading to a reduction in genetic differentiation between populations.

Using Computer Simulations

Modern laboratories often employ computer simulations to model complex evolutionary scenarios. These simulations can incorporate multiple evolutionary forces simultaneously, allowing students to explore how factors like mutation rates, migration rates, population sizes, and selection pressures interact to shape

evolutionary outcomes. Students can manipulate variables and observe the resulting changes in allele and genotype frequencies.

Interpreting Results and Drawing Conclusions

The interpretation of data from laboratory exercises in population genetics and evolution is crucial for understanding the underlying biological processes. This involves comparing observed outcomes with theoretical predictions and identifying the likely evolutionary forces at play.

Comparing Observed Frequencies to Hardy-Weinberg Predictions

A primary goal is often to compare the observed genotype and allele frequencies in a simulated or experimental population with the frequencies predicted by the Hardy-Weinberg principle. Statistical tests, such as chi-square tests, are commonly used to determine if any observed deviations are statistically significant or likely due to random chance. A significant deviation suggests that evolutionary forces are acting on the population.

Identifying the Dominant Evolutionary Forces

Based on the observed patterns of allele frequency change, students must infer which evolutionary mechanisms were most influential. For example, rapid and unpredictable shifts in allele frequencies in small simulated populations strongly indicate genetic drift. Conversely, consistent increases in the frequency of specific traits under defined environmental conditions point towards natural selection. If allele frequencies converge between previously distinct groups, gene flow is likely the cause.

Discussing the Implications of Experimental Outcomes

The conclusions drawn from these experiments have significant implications. For instance, demonstrating the impact of genetic drift on small populations highlights the vulnerability of endangered species to extinction due to loss of genetic diversity. Observing the effects of natural selection can illuminate the mechanisms behind adaptation and the evolution of antibiotic resistance in bacteria.

Relating Lab Findings to Real-World Biological Systems

A critical step is to connect the simplified models and controlled experiments in the lab to the complexities of natural populations. This involves considering how the assumptions made in the lab (e.g., discrete generations, specific selection pressures) might differ in the wild and how these differences could influence evolutionary outcomes. This comparative analysis reinforces the relevance of population genetics principles to understanding biodiversity and ecological dynamics.

Applications of Population Genetics and Evolution

The principles studied in laboratory 8 population genetics and evolution have profound and far-reaching applications across numerous scientific and societal domains. Understanding how populations evolve is not merely an academic pursuit; it provides practical tools and insights for addressing critical real-world challenges.

Conservation Biology and Biodiversity

Population genetics is indispensable for conservation efforts. By assessing the genetic diversity within endangered species, conservationists can identify populations at risk of inbreeding depression and reduced adaptive potential. Understanding gene flow patterns helps design effective wildlife corridors and translocation strategies to maintain genetic connectivity. Studying evolutionary history can also inform taxonomic classifications and highlight unique lineages worthy of protection.

Medicine and Human Health

In human medicine, population genetics helps unravel the genetic basis of diseases. By studying allele frequencies of disease-related genes in different human populations, researchers can identify genetic predispositions to certain conditions and understand patterns of disease prevalence. This field is also crucial for tracking the evolution of pathogens, such as viruses and bacteria, enabling the development of vaccines and antimicrobial therapies to combat drug resistance.

Agriculture and Animal Husbandry

The principles of population genetics are applied in breeding programs for crops and livestock. By selecting

for desirable traits and managing gene flow, breeders can enhance yield, disease resistance, and nutritional content. Understanding genetic variation within agricultural populations helps maintain long-term productivity and adaptability in the face of changing environmental conditions and pest pressures.

Forensics and Evolutionary Studies

DNA fingerprinting, a cornerstone of forensic science, relies heavily on population genetics. By analyzing variations in DNA markers, forensic experts can identify individuals and establish relationships, often by comparing crime scene DNA to databases of known population allele frequencies. Furthermore, population genetics provides the empirical data for reconstructing evolutionary histories and understanding phylogenetic relationships among species.

Frequently Asked Questions

What is the primary goal of a population genetics lab focusing on evolution?

The primary goal is to understand the genetic basis of evolutionary change within populations, often by examining allele and genotype frequencies and how they change over time due to evolutionary forces.

What are the key evolutionary forces often investigated in population genetics labs?

Commonly investigated forces include natural selection, genetic drift, gene flow (migration), and mutation.

How is allele frequency calculated in a population genetics lab?

Allele frequency is calculated by summing the number of copies of a specific allele and dividing by the total number of gene copies in the population (which is twice the number of individuals for diploid organisms).

What is the Hardy-Weinberg equilibrium and why is it important in population genetics labs?

The Hardy-Weinberg equilibrium describes a theoretical state where allele and genotype frequencies remain constant across generations in the absence of evolutionary forces. It serves as a null hypothesis to detect and measure evolutionary change.

How can genetic drift be demonstrated or simulated in a laboratory setting?

Genetic drift is often demonstrated through simulations using coin flips, beads of different colors, or computer programs that model random fluctuations in allele frequencies, especially in small populations.

What types of molecular data are commonly used in population genetics labs?

Commonly used molecular data include DNA sequences (e.g., mitochondrial DNA, nuclear genes), microsatellites, and single nucleotide polymorphisms (SNPs).

How does gene flow impact genetic variation within and between populations?

Gene flow (migration) tends to increase genetic variation within a population by introducing new alleles and decrease genetic differences between populations by homogenizing allele frequencies.

What is the concept of 'fitness' in the context of natural selection within a population genetics lab?

Fitness refers to an organism's reproductive success, specifically its ability to survive and reproduce in a given environment. In population genetics, it's often quantified as a relative measure of offspring production.

How can population genetics labs help in understanding adaptation?

By studying changes in allele frequencies related to specific environmental pressures (e.g., antibiotic resistance in bacteria, pesticide resistance in insects), labs can infer adaptive evolutionary processes.

What are common statistical methods used to analyze population genetics data in a lab setting?

Common statistical methods include chi-square tests for HWE, F-statistics (F_{st} , F_{is} , F_{it}) to measure genetic differentiation and inbreeding, principal component analysis (PCA) for population structure, and phylogenetic analyses.

Additional Resources

Here is a numbered list of 9 book titles related to laboratory 8, population genetics, and evolution, with short descriptions:

1. *Principles of Population Genetics*

This foundational textbook delves deeply into the theoretical underpinnings of population genetics. It meticulously explains concepts like genetic drift, gene flow, mutation, and natural selection, providing the mathematical frameworks essential for understanding evolutionary change within populations. Students will find comprehensive coverage of key models and experimental approaches.

2. *Evolutionary Genetics: From Molecules to Organisms*

This engaging text bridges the gap between molecular mechanisms and macroevolutionary patterns. It explores how genetic variation arises and is maintained, and how these processes drive adaptation and speciation. The book uses a blend of theoretical discussions, case studies, and experimental evidence to illustrate fundamental evolutionary principles.

3. *Population Genetics: A Concise Course*

Designed for a focused study, this book offers a streamlined introduction to the core concepts of population genetics. It emphasizes practical applications and problem-solving, making it an ideal resource for laboratory courses. The text efficiently covers the essential theoretical frameworks needed to analyze genetic variation in natural populations.

4. *The Extended Evolutionary Synthesis: An Anthology*

This collection of essays explores the ongoing debates and expansions of traditional evolutionary theory. It examines how new discoveries in fields like epigenetics, developmental biology, and ecology are reshaping our understanding of evolutionary mechanisms. The book encourages critical thinking about the nature of evolution beyond a purely gene-centric view.

5. *Molecular Evolution: A Primer*

This accessible primer introduces the fundamental principles of molecular evolution, focusing on DNA and protein sequence data. It explains how to use molecular data to infer evolutionary relationships, estimate divergence times, and understand the forces that shape genomes. The book is an excellent starting point for those interested in the genetic basis of evolution.

6. *Speciation: The Origin of Species*

This comprehensive treatise tackles the complex question of how new species arise. It reviews the various mechanisms of reproductive isolation, the role of natural selection and genetic drift in divergence, and the impact of geographic factors. The book synthesizes a vast amount of research into a coherent narrative of species formation.

7. *Genetics and Evolution: A Laboratory Manual*

This practical manual provides hands-on experiments designed to teach the principles of genetics and

evolutionary biology. It includes detailed protocols for analyzing genetic variation, simulating evolutionary processes, and interpreting real-world data. The exercises are structured to reinforce theoretical concepts learned in lectures and labs.

8. *The Selfish Gene*

While not a textbook, this seminal work by Richard Dawkins offers a thought-provoking perspective on evolution through the lens of the gene. It vividly explains how natural selection acts on individual genes, shaping organisms as vehicles for their propagation. The book's accessible prose and compelling arguments make complex evolutionary ideas understandable and engaging.

9. *Population Genomics: Modern Methods and Applications*

This advanced text explores the latest techniques and applications in population genomics. It details how large-scale genomic datasets are used to study population structure, adaptive evolution, and conservation genetics. The book highlights the power of high-throughput sequencing and bioinformatics in unraveling evolutionary histories.

Laboratory 8 Population Genetics And Evolution

Laboratory 8: Population Genetics and Evolution

Ebook Chapter Author: Dr. Evelyn Reed, PhD (Genetics)

Chapter Outline:

Introduction: Defining Population Genetics and its connection to Evolution.

Chapter 1: Hardy-Weinberg Equilibrium: Principles, Calculations, and Deviations.

Chapter 2: Mechanisms of Evolution: Natural Selection, Genetic Drift, Gene Flow, and Mutation.

Chapter 3: Measuring Genetic Variation: Techniques and Applications.

Chapter 4: Speciation and Phylogenetics: The Formation of New Species and Evolutionary Relationships.

Chapter 5: Human Population Genetics: Applications and Ethical Considerations.

Conclusion: Synthesis and Future Directions in Population Genetics.

Laboratory 8: Population Genetics and Evolution

Introduction: Understanding the Foundation of Life's Diversity

Population genetics, the study of genetic variation within and between populations, forms the bedrock of evolutionary biology. It bridges the gap between Mendelian genetics, focusing on individual inheritance, and the grand sweep of evolutionary change across generations. Understanding population genetics is crucial for comprehending how life's incredible diversity has arisen and continues to evolve. This chapter delves into the core principles of population genetics, exploring how genetic variation arises, is maintained, and ultimately shapes the evolutionary trajectory of species. We will examine both theoretical frameworks, such as the Hardy-Weinberg principle, and real-world mechanisms that drive evolutionary change, such as natural selection and genetic drift. The applications of population genetics extend far beyond theoretical understanding, impacting fields from conservation biology to human health and disease.

Chapter 1: Hardy-Weinberg Equilibrium: A Null Hypothesis for Evolution

The Hardy-Weinberg principle serves as a fundamental null hypothesis in population genetics. It states that in the absence of disturbing factors, allele and genotype frequencies in a population remain constant from generation to generation. This equilibrium is maintained under five specific conditions:

No Mutation: The rate of mutation must be negligible.

Random Mating: Individuals must mate randomly, without any preference for certain genotypes.

No Gene Flow: There should be no migration of individuals into or out of the population.

No Genetic Drift: The population must be large enough to avoid random fluctuations in allele frequencies.

No Natural Selection: All genotypes must have equal survival and reproductive rates.

The Hardy-Weinberg equation, $p^2 + 2pq + q^2 = 1$, allows us to calculate allele and genotype frequencies. 'p' represents the frequency of one allele, and 'q' represents the frequency of the alternative allele ($p + q = 1$). p^2 represents the frequency of homozygous individuals for the 'p' allele, $2pq$ represents the frequency of heterozygous individuals, and q^2 represents the frequency of homozygous individuals for the 'q' allele.

Deviations from Hardy-Weinberg equilibrium indicate that evolutionary forces are at play. By comparing observed genotype frequencies to those expected under Hardy-Weinberg, we can identify the specific mechanisms driving evolutionary change.

Chapter 2: Mechanisms of Evolution: The Driving Forces of Change

Several mechanisms can disrupt Hardy-Weinberg equilibrium and drive evolutionary change:

Natural Selection: This is the differential survival and reproduction of individuals based on their heritable traits. Beneficial traits become more common over time, leading to adaptation. Different types of natural selection exist, including directional, stabilizing, and disruptive selection.

Genetic Drift: Random fluctuations in allele frequencies, particularly pronounced in small populations. Bottleneck effects (population reduction due to catastrophic events) and founder effects (establishment of a new population by a small number of individuals) are examples of genetic drift.

Gene Flow: The movement of genes between populations through migration. Gene flow can introduce new alleles into a population, increasing genetic diversity and potentially preventing divergence.

Mutation: Changes in the DNA sequence that can introduce new alleles into a population. While mutations are typically rare, they provide the raw material for evolution.

Chapter 3: Measuring Genetic Variation: Tools for Understanding Diversity

Understanding the extent and nature of genetic variation within and between populations is critical for studying evolution. Several techniques are used to measure genetic variation:

Allozyme electrophoresis: This technique separates protein variants based on their charge, revealing variations in enzyme activity.

DNA sequencing: This highly accurate method directly determines the DNA sequence, identifying variations at the nucleotide level.

Microsatellite analysis: This technique examines short, repetitive DNA sequences, which vary greatly among individuals.

SNP analysis: Single Nucleotide Polymorphisms (SNPs) are variations in a single nucleotide base pair. Their high frequency in the genome makes them valuable for population genetic studies.

These techniques provide valuable data for estimating allele frequencies, identifying patterns of genetic variation, and reconstructing evolutionary relationships.

Chapter 4: Speciation and Phylogenetics: The Tree of Life

Speciation, the formation of new and distinct species, is a fundamental process in evolution. Several mechanisms can lead to speciation, including:

Allopatric speciation: Geographic isolation prevents gene flow between populations, leading to independent evolution and eventual divergence.

Sympatric speciation: Speciation occurs within the same geographic area, often driven by mechanisms like sexual selection or habitat differentiation.

Phylogenetics is the study of evolutionary relationships between organisms. Phylogenetic trees, also known as cladograms, visually represent these relationships, providing insights into the evolutionary history of life. Phylogenetic analysis relies heavily on molecular data, such as DNA sequences, to infer evolutionary relationships.

Chapter 5: Human Population Genetics: Applications and Ethical Considerations

Human population genetics has many applications, including:

Disease Mapping: Identifying genetic variants associated with increased risk of disease.

Forensic Science: Using genetic markers for individual identification and paternity testing.

Pharmacogenomics: Understanding how genetic variations affect drug response.

Conservation Genetics: Assessing genetic diversity and developing strategies for species conservation.

However, the application of human population genetics also raises ethical considerations, particularly regarding privacy, discrimination, and informed consent.

Conclusion: A Dynamic Field with Ongoing Discoveries

Population genetics is a dynamic and rapidly evolving field. Technological advances in genomics and computational biology continue to refine our understanding of evolutionary processes and their impact on biodiversity. The principles of population genetics are essential for addressing critical challenges facing humanity, including the conservation of endangered species, the development of new medical treatments, and the understanding of human origins and migration patterns. Further research into the interplay of genetic variation, environmental factors, and evolutionary forces will continue to illuminate the intricacies of life on Earth.

FAQs:

1. What is the difference between microevolution and macroevolution? Microevolution refers to small-scale evolutionary changes within a population, while macroevolution refers to large-scale evolutionary changes above the species level.
2. How does genetic drift affect small populations? Genetic drift has a more significant impact on small populations, leading to greater fluctuations in allele frequencies and a potential loss of genetic diversity.
3. What is the significance of the Hardy-Weinberg principle? It provides a baseline for understanding evolutionary change by defining the conditions under which allele frequencies remain constant.
4. How is natural selection different from artificial selection? Natural selection is driven by environmental pressures, while artificial selection is driven by human intervention.
5. What are some examples of adaptive traits? Camouflage, antibiotic resistance, and the ability to digest lactose are examples of adaptive traits.
6. How do we use phylogenetic trees? Phylogenetic trees are used to represent evolutionary relationships among organisms, aiding in understanding their evolutionary history and diversification.
7. What are some ethical considerations in human population genetics? Ethical concerns include privacy, potential for discrimination based on genetic information, and informed consent for genetic testing.
8. What is the role of mutation in evolution? Mutations introduce new genetic variation, providing the raw material upon which natural selection acts.
9. How does gene flow affect genetic diversity? Gene flow can increase genetic diversity by introducing new alleles into a population, reducing the risk of inbreeding.

Related Articles:

1. The Bottleneck Effect and Genetic Diversity: Explains how population bottlenecks reduce genetic variation.
2. Founder Effect and its Evolutionary Consequences: Describes how the founding individuals of a new population shape its genetic makeup.
3. Adaptive Radiation and Speciation: Explores the rapid diversification of a lineage into multiple species.
4. Molecular Clocks and Evolutionary Time: Discusses methods for estimating the time of divergence between species.
5. Neutral Theory of Molecular Evolution: Presents the idea that much molecular evolution is driven by random drift rather than selection.
6. Coevolution and Arms Races: Examines the reciprocal evolutionary adaptations between interacting species.
7. Human Migration Patterns and Genetic Diversity: Details how human migrations have shaped global genetic variation.
8. Conservation Genetics and Endangered Species: Discusses the use of genetics to manage and

conserve endangered populations.

9. The Evolution of Drug Resistance: Explains the mechanisms by which pathogens develop resistance to antibiotics and other drugs.

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foundation of population biology, life history evolution and demography, density and frequency dependent selection, recent advances in quantitative genetics and bioinformatics, evolutionary case history of model organisms focusing on polymorphisms and selection, mating system evolution and evolution in the hybrid zones, and applied population biology including conservation, infectious diseases and human diversity. This is the third of three volumes published in honour of Richard Lewontin.

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E. Holsinger, 2014-11-08 Lecture Notes in Population Genetics By Kent E. Holsinger

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many popular books on such topics as human evolution, race and racism, equality, and human destiny. In this, the first book devoted to an analysis of the historical, scientific, and cultural dimensions of Dobzhansky's life and thought, an international group of historians, biologists, and philosophers addresses the full span of his career in Russia and the United States. Beginning with the reminiscences of his daughter, Sophia Dobzhansky Coe, these essays cover Dobzhansky's Russian roots (Nikolai L. Krementsov, Daniel A. Alexandrov, Mikhail B. Konashev), the Morgan Lab (Garland E. Allen, William B. Provine, Robert E. Kohler, Richard M. Burian), his scientific legacy (Scott F. Gilbert, Bruce Wallace, Charles E. Taylor), and his social, political, philosophical, and religious thought (Costas B. Krimbas, John Beatty, Diane B. Paul, Michael Ruse). Originally published in 1994. The Princeton Legacy Library uses the latest print-on-demand technology to again make available previously out-of-print books from the distinguished backlist of Princeton University Press. These editions preserve the original texts of these important books while presenting them in durable paperback and hardcover editions. The goal of the Princeton Legacy Library is to vastly increase access to the rich scholarly heritage found in the thousands of books published by Princeton University Press since its founding in 1905.

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mathematical aspects of population genetics with an emphasis on evolutionary theory. This volume draws heavily from the author's 1979 classic, but it has been revised and expanded to include recent topics which follow naturally from the treatment in the earlier edition, such as the theory of molecular population genetics.

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Microsatellites are short stretches of repeated DNA, found in most genomes, that show exceptional variability in humans and most other species. This variability has made microsatellites the genetic marker of choice for most applications, including genetic mapping and studies of the evolutionary connections between species and populations. This book brings together an international group of scientists currently working in microsatellites. Their contributions provide a detailed description of microsatellite biology, focusing on their mutation properties, generation, decay, and possible functional roles. They introduce the theoretical models that underpin the most popular methods for analysing the information that microsatellites can yield, including methods for estimating coalescent times, population divergences, and migration. Finally, the book describes the various ways in which the potential of microsatellites is being harnessed in a range of applications including medical genetics, forensics, genetic mapping, the analysis of human evolution, and conservation genetics.

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