# Introduction To Quantitative Genetics 4th Edition

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Parental care includes a wide variety of traits that enhance offspring development and survival. It is taxonomically widespread and is central to the maintenance of biodiversity through its close association with other phenomena such as sexual selection, life-history evolution, sex allocation, sociality, cooperation and conflict, growth and development, genetic architecture, and phenotypic plasticity. This novel book provides a fresh perspective on the study of the evolution of parental care based on contributions from some of the top researchers in the field. It provides evidence that the dynamic nature of family interactions, and particularly the potential for co-evolution among family members, has contributed to the great diversity of forms of parental care and life-histories across as well as within taxa. The Evolution of Parental Care aims to stimulate students and researchers alike to pursue exciting new directions in this fascinating and important area of behavioural and evolutionary biology. It will be of relevance and use to those working in the fields of animal behaviour, ecology, evolution, and genetics, as well as related disciplines such as psychology and sociology.

The genetic information being unlocked by advances in genomic and high throughput technologies is rapidly revolutionizing our understanding of developmental processes in bovine species. This information is allowing researchers unprecedented insight into the genetic basis of key traits. Bovine Genomics is the first book to bring together and synthesize the information learned through the bovine genome sequencing project and look at its practical application to cattle and dairy production. Bovine Genomics opens with foundational chapters on the domestication of cattle and traditional Mendelian genetics. Building on these chapters, coverage rapidly moves to quantitative genetics and the advances of whole genome technologies. Significant coverage is given to such topics as epigenetics, mapping quantitative trail loci, genome-wide association studies and genomic selection in cattle breeding. The book is a valuable synthesis of the field written by a global team of leading researchers. Providing wide-ranging coverage of the topic, Bovine Genomic, is an essential guide to the field. The basic and applied science will be of use to researchers, breeders, and advanced students.

Maize is used in an endless list of products that are directly or indirectly related to human nutrition and food security. Maize is grown in producer farms, farmers depend on genetically improved cultivars, and maize breeders develop improved maize cultivars for farmers. Nikolai I. Vavilov defined plant breeding as plant evolution directed by man. Among crops, maize is one of the most successful examples for breeder-directed evolution. Maize is a cross-pollinated species with unique and separate male and female organs allowing techniques from both self and cross-pollinated crops to be utilized. As a consequence, a diverse set of breeding methods can be utilized for the development of various maize cultivar types for all economic conditions (e.g., improved populations, inbred lines, and their hybrids for different types of markets). Maize breeding is the science of maize cultivar development. Public investment in maize breeding from 1865 to 1996 was $3 billion (Crosbie et al., 2004) and the return on investment was $260 billion as a consequence of applied maize breeding, even without full understanding of the genetic basis of heterosis. The principles of quantitative genetics have been successfully applied by maize breeders worldwide to adapt and improve germplasm sources of cultivars for very simple traits (e.g. maize flowering) and very complex ones (e.g., grain yield). For instance, genomic efforts have isolated early-maturing genes and QTL for potential MAS but very simple and low cost phenotypic efforts have caused significant and fast genetic progress across genotypes moving elite tropical and late temperate maize northward with minimal investment. Quantitative genetics has allowed the integration of pre-breeding with cultivar development by characterizing populations genetically, adapting them to places never thought of (e.g., tropical to short-seasons), improving them by all sorts of intra- and inter-population recurrent selection methods, extracting lines with more probability of success, and exploiting inbreeding and heterosis. Quantitative genetics in maize breeding has improved the odds of developing outstanding maize cultivars from genetically broad based improved populations such as B73. The inbred-hybrid concept in maize was a public sector invention 100 years ago and it is still considered one of the greatest achievements in plant breeding. Maize hybrids grown by farmers today are still produced following this methodology and there is still no limit to genetic improvement when most genes are targeted in the breeding process. Heterotic effects are unique for each hybrid and exotic genetic materials (e.g., tropical, early maturing) carry useful alleles for complex traits not present in the B73 genome just sequenced while increasing the genetic diversity of U.S. hybrids. Breeding programs based on classical quantitative genetics and selection methods will be the basis for proving theoretical approaches on breeding plans based on molecular markers. Mating designs still offer large sample sizes when compared to QTL approaches and there is still a need to successful integration of these methods. There is a need to increase the genetic diversity of maize hybrids available in the market (e.g., there is a need to increase the number of early maturing testers in the northern U.S.). Public programs can still develop new and genetically diverse products not available in industry. However, public U.S. maize breeding programs have either been discontinued or are eroding because of decreasing state and federal funding toward basic science. Future significant genetic gains in maize are dependent on the incorporation of useful and unique genetic diversity not available in industry (e.g., NDSU EarlyGEM lines). The integration of pre-breeding methods with cultivar development should enhance future breeding efforts to maintain active public breeding programs not only adapting and improving genetically broad-based germplasm but also developing unique products and training the next generation of maize breeders producing research dissertations directly linked to breeding programs. This is especially important in areas where commercial hybrids are not locally bred. More than ever public and private institutions are encouraged to cooperate in order to share breeding rights, research goals, winter nurseries, managed stress environments, and latest technology for the benefit of producing the best possible hybrids for farmers with the least cost. We have the opportunity to link both classical and modern technology for the benefit of breeding in close cooperation with industry without the need for investing in academic labs and time (e.g., industry labs take a week vs months/years in academic labs for the same work). This volume, as part of the Handbook of Plant Breeding series, aims to increase awareness of the relative value and impact of maize breeding for food, feed, and fuel security. Without breeding programs continuously developing improved germplasm, no technology can develop improved cultivars. Quantitative Genetics in Maize Breeding presents principles and data that can be applied to maximize genetic improvement of germplasm and develop superior genotypes in different crops. The topics included should be of interest of graduate students and breeders conducting research not only on breeding and selection methods but also developing pure lines and hybrid cultivars in crop species. This volume is a unique and permanent contribution to breeders, geneticists, students, policy makers, and land-grant institutions still promoting quality research in applied plant breeding as opposed to promoting grant monies and indirect costs at any short-term cost. The book is dedicated to those who envision the development of the next generation of cultivars with less need of water and inputs, with better nutrition; and with higher percentages of exotic germplasm as well as those that pursue independent research goals before searching for funding. Scientists are encouraged to use all possible breeding methodologies available (e.g., transgenics, classical breeding, MAS, and all possible combinations could be used with specific sound long and short-term goals on mind) once germplasm is chosen making wise decisions with proven and scientifically sound technologies for assisting current breeding efforts depending on the particular trait under selection. Arnel R. Hallauer is C. F. Curtiss Distinguished Professor in Agriculture (Emeritus) at Iowa State University (ISU). Dr. Hallauer has led maize-breeding research for mid-season maturity at ISU since 1958. His work has had a worldwide impact on plant-breeding programs, industry, and students and was named a member of the National Academy of Sciences. Hallauer is a native of Kansas, USA. José B. Miranda Filho is full-professor in the Department of Genetics, Escola Superior de Agricultura Luiz de Queiroz - University of São Paulo located at Piracicaba, Brazil. His research interests have emphasized development of quantitative genetic theory and its application to maize breeding. Miranda Filho is native of Pirassununga,

São Paulo, Brazil. M.J. Carena is professor of plant sciences at North Dakota State University (NDSU). Dr. Carena has led maize-breeding research for short-season maturity at NDSU since 1999. This program is currently one the of the few public U.S. programs left integrating pre-breeding with cultivar development and training in applied maize breeding. He teaches Quantitative Genetics and Crop Breeding Techniques at NDSU. Carena is a native of Buenos Aires, Argentina. http://www.ag.ndsu.nodak.edu/plantsci/faculty/Carena.htm

The main goal of this book is to encourage and formalize the infusion of evolutionary thinking into mainstream conservation biology. It reviews the evolutionary foundations of conservation issues, and unifies conceptual and empirical advances in evolutionary conservation biology. The book can be used either as a primary textbook or as a supplementary reading in an advanced undergraduate or graduate level course - likely to be called Conservation Biology or in some cases Evolutionary Ecology. The focus of chapters is on current concepts in evolution as they pertain to conservation, and the empirical study of these concepts. The balanced treatment avoids exhaustive reviews and overlapping duplication among the chapters. Little background in genetics is assumed of the reader.

The book focuses on the principles and practices of tropical maize improvement with special emphasis on early and extra-early maize to feed the increasing population in Sub-Saharan Africa. It highlights the similarities and differences between results obtained in temperate regions of the world and WCA in terms of corroboration or refutation of genetic principles and theory of maize breeding. The book is expected to be of great interest to maize breeders, advanced undergraduates, graduate students, professors and research scientists in the national and international research institutes all over the world, particularly Sub-Saharan Africa. It will also serve as a useful reference for agricultural extension and technology transfer systems, Non-governmental Organizations (NGOs) and Community-Based Organizations (CBOs), seed companies and community-based seed enterprises, policy makers, and all those who are interested in generating wealth from agriculture and alleviating hunger and poverty in Sub-Saharan Africa.

This volume presents some of the most recent dramatic results of molecular, genomic, and organismal evolutionary processes. It represents analyses, experiments, observations, reviews, discussions and forecasts of evolutionary theory comprising both novel methods and results, reanalyzed and reviewed data sets based on comparative, experimental, and theoretical studies utilizing model organisms across phylogeny, including bacteria, fungi, plants, animals and humans. It elucidates the revolution in molecular biology that ushered in our understanding of the evolutionary process over time and space. The topics discussed include major problems of evolutionary theory concerning origins, phylogeny, relative importance of evolutionary forces, structure and function, adaptation and speciation in space and time in changing and stressful environments. A major emerging generalization is the nonrandomness of genome structure highlighting the importance of natural selection as a major organizing evolutionaryforce not only at the phenotypic level, but most importantly at the interlinked genotypic molecular level. The integration between the molecular

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.

An enduring controversy in evolutionary biology is the genetic basis of adaptation. Darwin emphasized "many slight differences" as the ultimate source of variation to be acted upon by natural selection. In the early 1900's, this view was opposed by "Mendelian geneticists", who emphasized the importance of "macromutations" in evolution. The Modern Synthesis resolved this controversy, concluding that mutations in genes of very small effect were responsible for adaptive evolution. A decade ago, Allen Orr and Jerry Coyne reexamined the evidence for this neo-Darwinian view and found that both the theoretical and empirical basis for it were weak. Orr and Coyne encouraged evolutionary biologists to reexamine this neglected question: what is the genetic basis of adaptive evolution? In this volume, a new generation of biologists have taken up this challenge. Using advances in both molecular genetic and statistical techniques, evolutionary geneticists have made considerable progress in this emerging field. In this volume, a diversity of examples from plant and animal studies provides valuable information for those interested in the genetics and evolution of complex traits.

"Animal genetics is a central topic in upper-level animal science programs. Filling a void in existing literature on animal science, Animal Genetics introduces genetic principles and presents their application in production and companion animals. The book details population and quantitative genetics, epigenetics, biotechnology, and breeding among other topics. Useful in upper-level studies, Animal Genetics is an irreplaceable educational resource"--Provided by publisher.

Two of the great mysteries of biology yet to be explored concern the distribution and abundance of genetic variation in natural populations and the genetic architecture of complex traits. These are tied together by their relationship to natural selection and evolutionary history, and some of the keys to disclosing these secrets lie in the study of wild organisms in their natural environments. This book, featuring a superb selection of papers from leading authors, summarizes the state of current understanding about the extent of genetic variation within wild populations and the ways to monitor such variation. It proposes the idea that a fundamental objective of evolutionary ecology is necessary to predict organism, population, community, and ecosystem response to environmental change. In fact, the overall theme of the papers centers around the expression of genetic variation and how it is shaped by the action of natural selection in the natural environment. Patterns of adaptation in the past and the genetic basis of traits likely to be under selection in a dynamically changing environment is discussed along with a wide variety of techniques to test for genetic variation and its consequences, ranging from classical demography to the use of molecular markers. This book is perfect for professionals and graduate students in genetics, biology, ecology, conservation biology, and evolution.

A complete background to concepts and principles of behavioral genetics, Neurobehavioral Genetics: Methods and Applications, Second Edition features a broad spectrum of the most current techniques in neurobehavioral genetics in a single source. International researchers incorporate several new developments in the field, including: De

Across these fields, there is increasing appreciation of the need to quantify the genetic - rather than just the phenotypic - basis and diversity of key traits, the genetic basis of the associations between traits, and the interaction between these genetic effects and

the environment. This research activity has been fuelled by methodological advances in both molecular genetics and statistics, as well as by exciting results emerging from laboratory studies of evolutionary quantitative genetics, and the increasing availability of suitable long-term datasets collected in natural populations, especially in animals. Quantitative Genetics in the Wild is the first book to synthesize the current level of knowledge in this exciting and rapidly-expanding area.

Evolutionary Behavioral Ecology presents a comprehensive treatment of theevolutionary and ecological processes shaping behavior across a wide array of organisms and a diverse set of behaviors and is suitable as a graduate-level text and as a sourcebook for professional scientists.

Quantitative methods are needed in conservation biology more than ever as an increasing number of threatened species find their way onto international and national "red lists. " Objective evaluation of population decline and extinction probability are required for sound decision making. Yet, as our colleague Selina Heppell points out, population viability analysis and other forms of formal risk assessment are underused in policy formation because of data uncertainty and a lack of standardized methodologies and unambiguous criteria (i. e. , "rules of thumb"). Models used in conservation biology range from those that are purely heuristic to some that are highly predictive. Model selection should be dependent on the questions being asked and the data that are available. We need to develop a toolbox of quantitative methods that can help scientists and managers with a wide range of systems and that are subject to varying levels of data uncertainty and environmental variability. The methods outlined in the following chapters represent many of the tools needed to fill that toolbox. When used in conjunction with adaptive management, they should provide information for improved monitoring, risk assessment, and evaluation of management alternatives. The first two chapters describe the application of methods for detecting trends and extinctions from sighting data. Presence/absence data are used in general linear and additive models in Chapters 3 and 4 to predict the extinction proneness of birds and to build habitat models for plants.

Modern plant breeding is considered a discipline originating from the science of genetics. It is a complex subject, involving the use of many interdisciplinary modern sciences and technologies that became art, science and business. Revolutionary developments in plant genetics and genomics and coupling plant "omics" achievements with advances on computer science and informatics, as well as laboratory robotics further resulted in unprecedented developments in modern plant breeding, enriching the traditional breeding practices with precise, fast, efficient and cost-effective breeding tools and approaches. The objective of this Plant Breeding book is to present some of the recent advances of 21st century plant breeding, exemplifying novel views, approaches, research efforts, achievements, challenges and perspectives in breeding of some crop species. The book chapters have presented the latest advances and comprehensive information on selected topics that will enhance the reader's knowledge of contemporary plant breeding.

The new edition of Introducing Genetics is a clear, concise, and accessible guide to inheritance and variation in individuals and populations. It first establishes the principles of Mendelian inheritance and the nature of chromosomes, before tackling quantitative and population genetics. The final three chapters introduce the molecular mechanisms t

Principles of Behavioral Genetics provides an introduction to the fascinating science that aims to understand how our genes determine what makes us tick. It presents a comprehensive overview of the relationship between genes, brain, and behavior. Introductory chapters give clear explanations of basic processes of the nervous system and fundamental principles of genetics of complex traits without excessive statistical jargon. Individual chapters describe the genetics of social interactions, olfaction and taste, memory and learning, circadian behavior, locomotion, sleep, and addiction, as well as the evolution of behavior. Whereas the focus is on genetics, neurobiological and ecological aspects are also included to provide intellectual breadth. The book uses examples that span the gamut from classical model organisms to non-model systems and human biology, and include both laboratory and field studies. Samples of historical information accentuate the text to provide the reader with an appreciation of the history of the field. This book will be a valuable resource for future generations of scientists who focus on the field of behavioral genetics. Defines the emerging science of behavioral genetics Engagingly written by two leading experts in behavioral genetics Clear explanations of basic quantitative genetic, neurogenetic and genomic applications to the study of behavior Numerous examples ranging from model organisms to non-model systems and humans Concise overviews and summaries for each chapter

Recent advances in plant genomics and molecular biology have revolutionized our understanding of plant genetics, providing new opportunities for more efficient and controllable plant breeding. Successful techniques require a solid understanding of the underlying molecular biology as well as experience in applied plant breeding. Bridging the gap between developments in biotechnology and its applications in plant improvement, Molecular Plant Breeding provides an integrative overview of issues from basic theories to their applications to crop improvement including molecular marker technology, gene mapping, genetic transformation, quantitative genetics, and breeding methodology.

An up-to-date, accessible guide to the main concepts and applications of quantitative genetics.

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Sequencing of the maize genome has opened up new opportunities in maize breeding, genetics and genomics research. This book highlights modern trends in development of hybrids, analysis of genetic diversity, molecular breeding, comparative and functional genomics, epigenomicsand proteomics in maize. The use of maize in biofuels, phytoremediation and

Quinoa is an invaluable crop, highlighted by the Food and Agriculture Organization of the United Nations (FAO) as one of the world's main crops for future food security. The first comprehensive review of quinoa, this book includes four sections covering the history of the crop, phylogeny and systematics, botany and agrotechnology, and the qualitative aspects, economics and marketing of quinoa, making it a vital resource for students and researchers of crop science.

Plant Breeding Reviews is an ongoing series presenting state-of-the art review articles on research in plant genetics, especially the breeding of commercially important crops. Articles perform the valuable function of collecting, comparing, and contrasting the primary journal literature in order to form an overview of the topic. This detailed analysis bridges the gap between the specialized researcher and the broader community of plant scientists.

In the short time since the publication of the Handbook of Positive Psychology esearch results on the psychology of human strengths have proliferated. However, no major volume has documented the methods and theory used to achieve these results. Oxford Handbook of Methods in Positive Psychology fills this need, providing a broad overview of diverse contemporary methods in positive psychology. With contributions from both leading scholars and promising young investigators, the handbook serves to illuminate and, at times, challenge traditional approaches. Incorporating multiple levels of analysis, from biology to culture, the contributors present state-of-the art techniques, including those for estimating variability and change at the level of the individual, identifying reliability of measurements within and across

individuals, and separating individual differences in growth from aspects of phenomena that exhibit shorter-term variability over time. The volume covers such topics as wisdom, health, hope, resilience, religion, relationships, emotions, well-being, character strengths, and laughter. It enhances our understanding of the balance between human deficits and strengths and demonstrates their connections to other problems. Oxford Handbook of Methods in Positive Psychology will be the essential reference for methods in positive psychology.

This book brings out the central role of evolutionary genetics in all aspects of its connection to evolutionary biology. A comprehensive analysis of the genetic, ecological and phylogenetic aspects of social behaviour, by experts in the field. Foreword by Phillip V. Tobias The introduction of rhesus macaques to Cayo Santiago, Puerto Rico in 1938, and the subsequent development of the CPRC for biomedical research, continues its long history of stimulating studies in physical anthropology. The CPRC monkey colonies, and the precise demographic data on the derived skeletal collection in the Center's Laboratory of Primate Morphology and Genetics (LPMG), provide rare opportunities for morphological, developmental, functional, genetic, and behavioral studies across the life span of rhesus macaques as a species, and as a primate model for humans. The book grows out of a symposium Wang is organizing for the 78th annual meeting of the American Association of Physical Anthropologists to be held in April 2009. This symposium will highlight recent and ongoing research in, or related to, physical anthropology, and reveal the numerous research opportunities that still exist at this unusual rhesus facility. Following an initial historical review of CPRC and its research activities, this book will emphasize recent and current researches on growth, function, genetics, pathology, aging, and behavior, and the impact of these researches on our understanding of rhesus and human morphology, development, genetics, and behavior. Fourteen researchers will present recent and current studies on morphology, genetics, and behavior, with relevance to primate and human growth, health, and evolution. The book will include not only papers presented in the symposium, but also papers from individuals who could not present their work at the meeting due to limitations in the maximum number (14) of permitted speakers.

Faced with widespread and devastating loss of biodiversity in wild habitats, scientists have developed innovative strategies for studying and protecting targeted plant and animal species in "off-site" facilities such as botanic gardens and zoos. Such ex situ work is an increasingly important component of conservation and restoration efforts. Ex Situ Plant Conservation, edited by Edward O. Guerrant Jr., Kayri Havens, and Mike Maunder, is the first book to address integrated plant conservation strategies and to examine the scientific, technical, and strategic bases of the ex situ approach. The book examines where and how ex situ investment can best support in situ conservation. Ex Situ Plant Conservation outlines the role, value, and limits of ex situ conservation as well as updating best management practices for the field, and is an invaluable resource for plant conservation practitioners at botanic gardens, zoos, and other conservation organizations; students and faculty in conservation biology and related fields; managers of protected areas and other public and private lands; and policymakers and members of the international community concerned with species conservation.

Plant Breeding Reviews, Volume 24, Part 1 presents state-of-the-art reviews on plant genetics and the breeding of all types of crops by both traditional means and molecular methods. The emphasis of the series is on methodology, a practical understanding of crop genetics, and applications to major crops.

The Handbook for Statistical Genetics is widely regarded as the reference work in the field. However, the field has developed considerably over the past three years. In particular the modeling of genetic networks has advanced considerably via the evolution of microarray analysis. As a consequence the 3rd edition of the handbook contains a much expanded section on Network Modeling, including 5 new chapters covering metabolic networks, graphical modeling and inference and simulation of pedigrees and genealogies. Other chapters new to the 3rd edition include Human Population Genetics, Genome-wide Association Studies, Family-based Association Studies, Pharmacogenetics, Epigenetics, Ethic and Insurance. As with the second Edition, the Handbook includes a glossary of terms, acronyms and abbreviations, and features extensive cross-referencing between the chapters, tying the different areas together. With heavy use of up-to-date examples, real-life case studies and references to web-based resources, this continues to be must-have reference in a vital area of research. Edited by the leading international authorities in the field. David Balding - Department of Epidemiology & Public Health, Imperial College An advisor for our Probability & Statistics series, Professor Balding is also a previous Wiley author, having written Weight-of-Evidence for Forensic DNA Profiles, as well as having edited the two previous editions of HSG. With over 20 years teaching experience, he's also had dozens of articles published in numerous international journals. Martin Bishop – Head of the Bioinformatics Division at the HGMP Resource Centre As well as the first two editions of HSG, Dr Bishop has edited a number of introductory books on the application of informatics to molecular biology and genetics. He is the Associate Editor of the journal Bioinformatics and Managing Editor of Briefings in Bioinformatics. Chris Cannings – Division of Genomic Medicine, University of Sheffield With over 40 years teaching in the area, Professor Cannings has published over 100 papers and is on the editorial board of many related journals. Co-editor of the two previous editions of HSG, he also authored a book on this topic.

Genetic Improvement of Farmed Animals provides a thorough grounding in the basic sciences underpinning farmed animal breeding. Relating science to practical application, it covers all the major farmed animal species: cattle, sheep, goats, poultry, pigs and aquaculture species.

To respond to the increasing need to feed the world's population as well as an ever greater demand for a balanced and healthy diet there is a continuing need to produce improved new cultivars or varieties of plants, particularly crop plants. The strategies used to produce these are increasingly based on our knowledge of relevant science, particularly genetics, but involves a multidisciplinary understanding that optimizes the approaches taken. Principles of Plant Genetics and Breeding, 2nd Edition introduces both classical and molecular tools for plant breeding. Topics such as biotechnology in plant breeding, intellectual property, risks, emerging concepts (decentralized breeding, organic breeding), and more are addressed in the new, updated edition of this text. Industry highlight boxes are included throughout the text to

contextualize the information given through the professional experiences of plant breeders. The final chapters provide a useful reference on breeding the largest and most common crops. Up-to-date edition of this bestselling book incorporating the most recent technologies in the field Combines both theory and practice in modern plant breeding Updated industry highlights help to illustrate the concepts outlined in the text Self assessment questions at the end of each chapter aid student learning Accompanying website with artwork from the book available to instructors

Over the last two decades, research into epistasis has seen explosive growth and has moved the focus of research in evolutionary genetics from a traditional additive approach. We now know the effects of genes are rarely independent, and to reach a fuller understanding of the process of evolution we need to look at gene interactions as well as gene-environment interactions. This book is an overview of non-additive evolutionary genetics, integrating all work to date on all levels of evolutionary investigation of the importance of epistasis in the evolutionary process in general. It includes a historical perspective on this emerging field, in-depth discussion of terminology, discussions of the effects of epistasis at several different levels of biological organization and combinations of theoretical and experimental approaches to analysis.

Across the globe, populations of plants and animals live in clusters, but maintain a connectivity a population of populations. There are naturally occurring metapopulations, such as clusters of groupers spread across coral reefs, and there are metapopulations humans have helped create by fragmenting landscapes: stands of trees separated by roads, prairies separated by agricultural farms. As the dynamics of landscape change have accelerated, and understanding of how metapopulations functions has played a critical role in ecology and evolutionary biology. Adaptation in Metapopulations synthesizes the role of genetic interactions in adaptive evolution and their influence on the effectiveness of different types of selection. Drawing on extensive field work and lab experiments, cohered with a strong conceptual arc, the work also integrates molecular and organismal biology, as Wade explores adaptation at multiple scales, and shows how evolutionary dynamics scale from the gene to the metapopulation. "

Statistical Genetics is an advanced textbook focusing on conducting genome-wide linkage and association analysis in order to identify the genes responsible for complex behaviors and diseases. Starting with an introductory section on statistics and quantitative genetics, it covers both established and new methodologies, providing the genetic and statistical theory on which they are based. Each chapter is written by leading researchers, who give the reader the benefit of their experience with worked examples, study design, and sources of error. The text can be used in conjunction with an associated website (www.genemapping.org) that provides supplementary material and links to downloadable software.

Evolutionary maternal effects occur whenever a mother's phenotypic traits directly affect her offspring's phenotype, independent of the offspring's genotype. Some of the phenotypic traits that result in maternal effects have a genetic basis, whereas others are environmentally determined. For example, the size of a litter produced by a mammalian mother—a trait with a strong genetic basis—can affect the growth rate of her offspring, while a mother's dominance rank—an environmentally determined trait—can affect the dominance rank of her offspring. The first volume published on the subject in more than a decade, Maternal Effects in Mammals reflects advances in genomic, ecological, and behavioral research, as well new understandings of the evolutionary interplay between mothers and their offspring. Dario Maestripieri and Jill M. Mateo bring together a learned group of contributors to synthesize the vast literature on a range of species, highlight evolutionary processes that were previously overlooked, and propose new avenues of research. Maternal Effects in Mammals will serve as the most comprehensive compendium on and stimulus for interdisciplinary treatments of mammalian maternal effects.

Written for plant breeders, researchers and post-graduate students, this excellent new book provides a comprehensive review of the methods and underlying theoretical foundations used for selection in plant breeding programs. The authors review basic elements of population and quantitative genetic theory, moving on to consider in a unique way the tackling of the problems presented by soil heterogeneity and intergenotypic competition when selecting quantitative characters.