

Falconer And Mackay Quantitative Genetics

Genetical Analysis of Quantitative Traits Introduction to Quantitative Genetics Bioinformatics Data Skills Genetics and Exploitation of Heterosis in Crops Handbook of Statistical Genomics Introduction to Quantitative Genetics Quantitative Genetics Quantitative Genetics in the Wild Evolution and Selection of Quantitative Traits Problems on Quantitative Genetics Quantitative Genetics in Maize Breeding Molecular and Quantitative Animal Genetics Quantitative Genetics in Maize Breeding Quantitative Genetics Principles of Plant Genetics and Breeding Quantitative Genetics and Selection in Plant Breeding Principles of Behavioral Genetics Basic Concepts in Population, Quantitative, and Evolutionary Genetics Evolutionary Theory and Processes: Modern Perspectives Introduction to Quantitative Genetics A Primer of Population Genetics and Genomics Principles of Statistical Genomics New Developments for Embracing Genomic Selection in Breeding Applications Adaptive Genetic Variation in the Wild Mutation and Evolution Biometrical genetics Ex Situ Plant Conservation Domains and Major Transitions of Social Evolution Personality in Nonhuman Animals Genetic Improvement of Farmed Animals Genes and Behaviour Adaptation and Fitness in Animal Populations Microevolution Rate, Pattern, Process Encyclopedia of Evolutionary Biology Handbook of the Biology of Aging Avian Migration Genetics of Populations Encyclopedia of Genetics Animal production and animal science worldwide Anthropological Genetics Dr M Kearsey Douglas Scott Falconer Vince Buffalo J. G. Coors David J. Balding Douglas Scott Falconer Shizhong Xu Anne Charmantier Bruce Walsh Douglas Scott Falconer A. R. Hallauer Hasan Khatib Arnel R. Hallauer Armando Caballero George Acquaah Günter Wricke Robert Rene Henri Anholt James Franklin Crow Solomon P. Wasser Douglas S. Falconer Daniel L. Hartl Shizhong Xu Diego Jarquin Timothy A. Mousseau Ronny C. Woodruff Kenneth Mather Center for Plant Conservation Jacobus J. Boomsma Jennifer Vonk Geoff Simm David J. Hosken Julius van der Werf Andrew P. Hendry Edward J. Masoro Peter Berthold Philip W. Hedrick Eric C.R. Reeve A. Rosati Michael H. Crawford

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Genomics New Developments for Embracing Genomic Selection in Breeding Applications Adaptive Genetic Variation in the Wild Mutation and Evolution Biometrical genetics Ex Situ Plant Conservation Domains and Major Transitions of Social Evolution Personality in Nonhuman Animals Genetic Improvement of Farmed Animals Genes and Behaviour Adaptation and Fitness in Animal Populations Microevolution Rate, Pattern, Process Encyclopedia of Evolutionary Biology Handbook of the Biology of Aging Avian Migration Genetics of Populations Encyclopedia of Genetics Animal production and animal science worldwide Anthropological Genetics *Dr M Kearsey Douglas Scott Falconer Vince Buffalo J. G. Coors David J. Balding Douglas Scott Falconer Shizhong Xu Anne Charmantier Bruce Walsh Douglas Scott Falconer A. R. Hallauer Hasan Khatib Arnel R. Hallauer Armando Caballero George Acquaah Günter Wricke Robert Rene Henri Anholt James Franklin Crow Solomon P. Wasser Douglas S. Falconer Daniel L. Hartl Shizhong Xu Diego Jarquin Timothy A. Mousseau Ronny C. Woodruff Kenneth Mather Center for Plant Conservation Jacobus J. Boomsma Jennifer Vonk Geoff Simm David J. Hosken Julius van der Werf Andrew P. Hendry Edward J. Masoro Peter Berthold Philip W. Hedrick Eric C.R. Reeve A. Rosati Michael H. Crawford*

this text provides a guide to the experimental and analytical methodologies available to study quantitative traits a review of the genetic control of quantitative traits and a discussion of how this knowledge can be applied to breeding problems and evolution

the latest edition of this classic text continues to provide the basis for understanding the genetic principles behind quantitative differences in phenotypes and how they apply to animal and plant improvement and evolution it extends these concepts to the segregation of genes that cause genetic variation in quantitative traits key techniques and methods are also covered

learn the data skills necessary for turning large sequencing datasets into reproducible and robust biological findings with this practical guide you'll learn how to use freely available open source tools to extract meaning from large complex biological data sets at no other point in human history has our ability to understand life's complexities been so dependent on our skills to work with and analyze data this intermediate level book teaches the general computational and data skills you need to analyze biological data if you have experience with a scripting language like python you're ready to get started go from handling small problems with messy scripts to tackling large problems with clever methods and tools process bioinformatics data with powerful unix pipelines and data tools learn how to use exploratory data analysis techniques in the r language use efficient methods to work with genomic range data and range operations work with common genomics data file formats like fasta fastq sam and bam manage your bioinformatics project with the git version control system tackle tedious data processing tasks with with bash scripts and makefiles

explore the momentous contributions of hybrid crop varieties with worldwide experts topics include an overview quantitative genetics genetic

diversity biochemistry and molecular biology methodologies commercial strategies and examples from numerous crops

a timely update of a highly popular handbook on statistical genomics this new two volume edition of a classic text provides a thorough introduction to statistical genomics a vital resource for advanced graduate students early career researchers and new entrants to the field it introduces new and updated information on developments that have occurred since the 3rd edition widely regarded as the reference work in the field it features new chapters focusing on statistical aspects of data generated by new sequencing technologies including sequence based functional assays it expands on previous coverage of the many processes between genotype and phenotype including gene expression and epigenetics as well as metabolomics it also examines population genetics and evolutionary models and inference with new chapters on the multi species coalescent admixture and ancient dna as well as genetic association studies including causal analyses and variant interpretation the handbook of statistical genomics focuses on explaining the main ideas analysis methods and algorithms citing key recent and historic literature for further details and references it also includes a glossary of terms acronyms and abbreviations and features extensive cross referencing between chapters tying the different areas together with heavy use of up to date examples and references to web based resources this continues to be a must have reference in a vital area of research provides much needed timely coverage of new developments in this expanding area of study numerous brand new chapters for example covering bacterial genomics microbiome and metagenomics detailed coverage of application areas with chapters on plant breeding conservation and forensic genetics extensive coverage of human genetic epidemiology including ethical aspects edited by one of the leading experts in the field along with rising stars as his co editors chapter authors are world renowned experts in the field and newly emerging leaders the handbook of statistical genomics is an excellent introductory text for advanced graduate students and early career researchers involved in statistical genetics

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the intended audience of this textbook are plant and animal breeders upper level undergraduate and graduate students in biological and agricultural science majors statisticians who are interested in understanding how statistical methods are applied to genetics and agriculture can benefit substantially by reading this book one characteristic of this textbook is represented by three chapters of technical reviews for mendelian genetics population genetics and preliminary statistics which are prerequisites for studying quantitative genetics numerous examples are provided to illustrate different methods of data analysis and estimation of genetic parameters along with each example of data analyses is the program code of sas statistical analysis system

this book gathers the expertise of 30 evolutionary biologists from around the globe to highlight how applying the field of quantitative genetics the analysis of the genetic basis of complex traits aids in the study of wild populations

quantitative traits be they morphological or physiological characters aspects of behavior or genome level features such as the amount of rna or protein expression for a specific gene usually show considerable variation within and among populations quantitative genetics also referred to as the genetics of complex traits is the study of such characters and is based on mathematical models of evolution in which many genes influence the trait and in which non genetic factors may also be important evolution and selection of quantitative traits presents a holistic treatment of the subject showing the interplay between theory and data with extensive discussions on statistical issues relating to the estimation of the biologically relevant parameters for these models quantitative genetics is viewed as the bridge between complex mathematical models of trait evolution and real world data and the authors have clearly framed their treatment as such this is the second volume in a planned trilogy that summarizes the modern field of quantitative genetics informed by empirical observations from wide ranging fields agriculture evolution ecology and human biology as well as population genetics statistical theory mathematical modeling genetics and genomics whilst volume 1 1998 dealt with the genetics of such traits the main focus of volume 2 is on their evolution with a special emphasis on detecting selection ranging from the use of genomic and historical data through to ecological field data and examining its consequences

animal genetics is a foundational discipline in the fields of animal science animal breeding and veterinary sciences while genetics underpins the healthy development and breeding of all living organisms this is especially true in domestic animals specifically with respect to breeding for key traits molecular and quantitative animal genetics is a new textbook that takes an innovative approach looking at both quantitative and molecular breeding approaches the book provides a comprehensive introduction to genetic principles and their applications in animal breeding this text provides a useful overview for those new to the field of animal genetics and breeding covering a diverse array of topics ranging from population and quantitative genetics to epigenetics and biotechnology molecular and quantitative animal genetics will be an important and invaluable educational resource for undergraduate and graduate students and animal agriculture professionals divided into six sections pairing fundamental principles with useful applications the book s comprehensive coverage will make it an ideal fit for students studying animal breeding and genetics at any level

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 ag ndsu nodak edu plantsci faculty carena htm

an up to date accessible guide to the main concepts and applications of quantitative genetics

the revised edition of the bestselling textbook covering both classical and molecular plant breeding principles of plant genetics and breeding integrates theory and practice to provide an insightful examination of the fundamental principles and advanced techniques of modern plant breeding combining both classical and molecular tools this comprehensive textbook describes the multidisciplinary strategies used to produce new varieties of

crops and plants particularly in response to the increasing demands to of growing populations illustrated chapters cover a wide range of topics including plant reproductive systems germplasm for breeding molecular breeding the common objectives of plant breeders marketing and societal issues and more now in its third edition this essential textbook contains extensively revised content that reflects recent advances and current practices substantial updates have been made to its molecular genetics and breeding sections including discussions of new breeding techniques such as zinc finger nuclease oligonucleotide directed mutagenesis rna dependent dna methylation reverse breeding genome editing and others a new table enables efficient comparison of an expanded list of molecular markers including allozyme rflps rapd ssr issr damd aflp snps and ests also new and updated industry highlights sections provide examples of the practical application of plant breeding methods to real world problems this new edition organizes topics to reflect the stages of an actual breeding project incorporates the most recent technologies in the field such as crspr genome edition and grafting on gm stock includes numerous illustrations and end of chapter self assessment questions key references suggested readings and links to relevant websites features a companion website containing additional artwork and instructor resources principles of plant genetics and breeding offers researchers and professionals an invaluable resource and remains the ideal textbook for advanced undergraduates and graduates in plant science particularly those studying plant breeding biotechnology and genetics

no detailed description available for quantitative genetics and selection in plant breeding

this book blends classical and modern genetic principles with neurobiological and ecological perspectives to teach students how to find and map genes that affect behaviors as well as how the coordinated expression of ensembles of these genes enables the nervous system to express complex behaviors in response to changes in the environment rinciples of behavioral genetics introduces us to the fascinating science that aims to understand how our genes determine what makes us tick

this volume consists of papers written by evolutionary molecular and organismal biologists geneticists ecologists behavioural ecologists morphologists mathematicians theoreticians and experimentalists in honour of professor eviatar eibi nevo on the occasion of his seventieth birthday the contributors are only a small subset of eibi s many friends collaborators and students not that one can distinguish these categories among eibi s colleagues his widespread influence and activity both in israel and more generally as a leading evolutionary biologist is indicated by his many co authors on books and papers and by his many students integrated in teaching and research 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 evolutionary force not only at the phenotypic level but most importantly at the interlinked genotypic molecular level the integration between the molecular and organismal levels unifies life which is subjected to the mechanism of natural selection as a major orienting evolutionary force

the latest edition of this classic text continues to provide the basis for understanding the genetic principles behind quantitative differences in phenotypes and how they apply to animal and plant improvement and evolution it extends these concepts to the segregation of genes that cause genetic variation in quantitative traits key techniques and methods are also covered

this accessible primer has been completely revised and updated to provide a concise but comprehensive introduction to the basic concepts of population genetics and genomics

statistical genomics is a rapidly developing field with more and more people involved in this area however a lack of synthetic reference books and textbooks in statistical genomics has become a major hurdle on the development of the field although many books have been published recently in bioinformatics most of them emphasize dna sequence analysis under a deterministic approach principles of statistical genomics synthesizes the state of the art statistical methodologies stochastic approaches applied to genome study it facilitates understanding of the statistical models and methods behind the major bioinformatics software packages which will help researchers choose the optimal algorithm to analyze their data and better interpret the results of their analyses understanding existing statistical models and algorithms assists researchers to develop improved statistical methods to extract maximum information from their data resourceful and easy to use principles of statistical genomics is a comprehensive reference for researchers and graduate students studying statistical genomics

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

although debated since the time of darwin the evolutionary role of mutation is still controversial in over 40 chapters from leading authorities in mutation and evolutionary biology this book takes a new look at both the theoretical and experimental measurement and significance of new mutation deleterious nearly neutral beneficial and polygenic mutations are considered in their effects on fitness life history traits and the composition of the gene pool mutation is a phenomenon that draws attention from many different disciplines thus the extensive reviews of the literature will be valuable both to established researchers and to those just beginning to study this field through up to date reviews the authors provide an insightful overview of each topic and then share their newest ideas and explore controversial aspects of mutation and the evolutionary process from topics like gonadal mosaicism and mutation clusters to adaptive mutagenesis mutation in cell organelles and the level and distribution of dna molecular changes the foundation is set for continuing the debate about the role of mutation fitness and adaptability it is a debate that will have profound consequences for our understanding of evolution

the properties of continuous variation are basic to the theory of evolution and to the practice of plant and animal improvement yet the genetical study of continuous variation has lagged far behind that of discontinuous variation the reason for this situation is basically methodological mendel gave us not merely his principles of heredity but also a method of experiment by which these principles could be tested over a wider range of living species and extended into the elaborate genetical theory of today the power of this tool is well attested by the speed with which genetics has grown in less than fifty years it has not only developed a theoretical structure which is unique in the biological sciences but has established a union with nuclear cytology so close that the two have become virtually a single science offering us a new approach to problems so diverse as those of evolution development disease cellular chemistry and human welfare much of this progress would have been impossible and all would have been slower without the mendelian method of recognizing and using unit differences in the genetic materials

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

evolutionary change is usually incremental and continuous but some increases in organizational complexity have been radical and divisive evolutionary biologists who refer to such events as major transitions have not always appreciated that these advances were novel forms of pairwise commitment that subjugated previously independent agents inclusive fitness theory convincingly explains cooperation and conflict in societies of animals and free living cells but to deserve its eminent status it should also capture how major transitions originated from prokaryote cells to eukaryote cells via differentiated multicellularity to colonies with specialized queen and worker castes as yet no attempt has been made to apply inclusive fitness principles to the origins of these events domains and major transitions of social evolution develops the idea that major evolutionary transitions involved new levels of informational closure that moved beyond looser partnerships early neo darwinians understood this principle but later social gradient thinking obscured the discontinuity of life s fundamental organizational transitions the author argues that the major transitions required maximal kinship in simple ancestors not conflict reduction in already elaborate societies reviewing more than a century of literature he makes testable predictions proposing that open societies and closed organisms require very different inclusive fitness explanations it appears that only human ancestors lived in societies that were already complex before our major cultural transition occurred we should therefore not impose the trajectory of our own social history on the rest of nature this thought provoking text is suitable for graduate level students taking courses in evolutionary biology behavioural ecology organismal developmental biology and evolutionary genetics as well as professional researchers in these fields it will also appeal to a broader interdisciplinary audience including the social sciences and humanities

this stimulating and comprehensive collection brings together multiple perspectives on the topic of personality in nonhuman animals linking historical perspectives theoretical approaches methods and cutting edge discoveries experts from various fields describe their findings on species ranging from dogs cats chimpanzees and dolphins to sharks snakes and other reptiles chapters not only discuss the evolution of personality but also describe potential applications within the areas of animal human interactions animal ethics and welfare conservation science and other areas a key focus is the role of genetics and the environment in determining animal behavior and personality including related traits such as creativity and boredom these chapters present the study of personality in nonhumans as a means by which we can better understand medical and psychological

issues specific to our own species as well chapters include exploring factor space and other adventures with the hominoid personality questionnaire the quantitative and molecular genetics of individual differences in animal personality personality temperament and individuality in reptile behavior what do we want to know about personality in marine mammals individual differences in nonhuman animals examining boredom curiosity and creativity the interplay between animal personality and foraging ecology taking significant steps in advancing the study of animal personality personality in nonhuman animals will engage personality psychologists comparative psychologists and behavior ecologists as well as conservationists zookeepers livestock managers and all those interested in the brain and behavior of animals

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

provides a broad snapshot of recent findings showing how the environment and genes influence behavior the great debate of nature versus nurture rages on but our understanding of the genetic basis of many behaviors has expanded over the last decade and there is now very good evidence showing that seemingly complex behaviours can have relatively simple genetic underpinnings but also that most behaviours have very complicated genetic and environmental architecture studies have also clearly shown that behaviors and other traits are influenced not just by genes and the environment but also by the statistical interaction between the two this book aims to end the nature versus nurture argument by showing that behaviors are nature and nurture and the interaction between the two and by illustrating how single genes can explain some of the variation in behaviors even when they are seemingly complex genes and behaviour beyond nature nurture puts to rest the nature versus nurture dichotomy providing an up to date synopsis of where we are how far we ve come and where we are headed it considers the effects of a dual inheritance of genes and culture and genes and social environment and highlights how indirect genetic effects can affect the evolution of behavior it also examines the effect of non self genes on the behavior of hosts shines a light on the nature and nurturing of animal minds and invites us to embrace all the complexity nature and nurture generates and more explores exciting new findings about behavior and where we go from here features contributions by top scholars of the subject seeks to end the nature versus nurture debate forever genes and behaviour beyond nature nurture is a unique and eye opening read that will appeal to ph d students post doctoral fellows and researchers in evolution and behavior additionally the book will also be of interest to geneticists sociologists and philosophers

fitness and adaptation are fundamental characteristics of plant and animal species enabling them to survive in their environment and to adapt to the inevitable changes in this environment this is true for both the genetic resources of natural ecosystems as well as those used in agricultural production extensive genetic variation exists between varieties breeds in a species and amongst individuals within breeds this variation has developed

over very long periods of time a major ongoing challenge is how to best utilize this variation to meet short term demands whilst also conserving it for longer term possible use many animal breeding programs have led to increased performance for production traits but this has often been accompanied by reduced fitness in addition the global use of genetic resources prompts the question whether introduced genotypes are adapted to local production systems understanding the genetic nature of fitness and adaptation will enable us to better manage genetic resources allowing us to make efficient and sustainable decisions for the improvement or breeding of these resources this book had an ambitious goal in bringing together a sample of the world s leading scientists in animal breeding and evolutionary genetics to exchange knowledge to advance our understanding of these vital issues

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

encyclopedia of evolutionary biology four volume set is the definitive go to reference in the field of evolutionary biology it provides a fully comprehensive review of the field in an easy to search structure under the collective leadership of fifteen distinguished section editors it is comprised of articles written by leading experts in the field providing a full review of the current status of each topic the articles are up to date and fully illustrated with in text references that allow readers to easily access primary literature while all entries are authoritative and valuable to those with advanced understanding of evolutionary biology they are also intended to be accessible to both advanced undergraduate and graduate students broad topics include the history of evolutionary biology population genetics quantitative genetics speciation life history evolution evolution of sex and mating systems evolutionary biogeography evolutionary developmental biology molecular and genome evolution coevolution phylogenetic methods microbial evolution diversification of plants and fungi diversification of animals and applied evolution presents fully comprehensive content allowing easy access to fundamental information and links to primary research contains concise articles by leading experts in the field that ensures current coverage of each topic provides ancillary learning tools like tables illustrations and multimedia features to assist with the comprehension process

the handbook of the biology of aging sixth edition provides a comprehensive overview of the latest research findings in the biology of aging intended

as a summary for researchers it is also adopted as a high level textbook for graduate and upper level undergraduate courses the sixth edition is 20% larger than the fifth edition with 21 chapters summarizing the latest findings in research on the biology of aging the content of the work is virtually 100% new though a selected few topics are similar to the fifth edition these chapters are authored by new contributors with new information the majority of the chapters are completely new in both content and authorship the sixth edition places greater emphasis and coverage on competing and complementary theories of aging broadening the discussion of conceptual issues greater coverage of techniques used to study biological issues of aging include computer modeling gene profiling and demographic analyses coverage of research on *Drosophila* is expanded from one chapter to four new chapters on mammalian models discuss aging in relation to skeletal muscles body fat and carbohydrate metabolism growth hormone and the human female reproductive system additional new chapters summarize exciting research on stem cells and cancer dietary restriction and whether age related diseases are an integral part of aging the handbook of the biology of aging sixth edition is part of the handbooks on aging series including handbook of the psychology of aging and handbook of aging and the social sciences also in their 6th editions

Berthold and Gwinner Bird migration is an intriguing aspect of the living world so much so that it has been investigated for as long and as thoroughly as almost any other natural phenomenon Aristotle who can count as the founder of scientific ornithology paid very close attention to the migrations of the birds he observed but it was not until the reign of Friedrich II in the first half of the 13th century that reliable data began to be obtained from then on the data base grew rapidly systematic studies of bird migration were introduced when the Vogelwarte Rossitten was founded as the first ornithological biological observation station in the world see first chapter in Memory of Vogelwarte Rossitten this area later received enormous impetus when experimental research on the subject was begun the large scale bird ringing experiment initiated in Rossitten in 1903 by Johannes Thienemann who was inspired by the pioneering studies of C. C. M. Mortensen the experiments on photoperiodicity carried out by William Rowan in the 1920s in Canada and retention and release experiments performed by Thienemann in the 1930s in Rossitten the first experimental study on the orientation of migratory birds after the second world war migration research while continuing in the previous areas also expanded into new directions such as radar ornithology ecophysiology and hormonal control mechanisms studies of evolution genetics telemetry and others

genetics and evolution

The encyclopedia includes 125 entries beginning with the origins of genetics including historical background on the work of Gregor Mendel and Charles Darwin and progressing to the structure of DNA and modern theories such as selfish genes all branches of genetics are covered including the genetics of bacteria viruses insects animals and plants as well as humans important topical issues such as the human genome project bioethics the law and genetics genetic disorders GM crops and the use of transgenic animals for food and pharmaceutical products are fully surveyed a section on

techniques and biotechnology includes modern methods of analysis from dna fingerprinting to the new science of bioinformatics the articles all written by specialists are largely non mathematical and progress from general concepts to deeper understanding each essay is fully referenced with suggestions for further reading the text is supplemented by extensive illustrations tables and a color plate section the encyclopedia of genetics will be a valuable companion for all those working or studying in the various fields of genetical research and a fascinating reference for all readers with a basic background in biology also includes color inserts

after the experience of the first volume the world association for animal production waap continues the publication of the book of the year series for the benefit of animal scientists and policy makers in the field of livestock systems the waap asked the best known and significant animal scientists in the world to contribute to the preparation of this book following the success of the first volume of the series the waap book of the year 2003 many authors from the six continents are contributing to this 2nd volume the importance of this publication is to have already established a worldwide reference for the animal science and production sectors there are the usual four sections that raised much interest in the previous volume of the series the first section has six articles describing the changing conditions of livestock systems in each of the six continents the second section has more than twenty papers describing the development of the many sectors in which the animal science field has been divided the third section dealing with contemporary issues is declared by our readers to be the most interesting it allows participating authors to describe current and significant issues important in these last years for the animal science and production sectors the statistics produced in the previous volume are updated and enhanced with new figures in this book to form the fourth section the papers included in this book speak clearly of the development in the last twelve months in the livestock systems worldwide major space is also devoted to the list of references from where every author can start to deepen his knowledge this book is essential for libraries that want their readers to be easily updated also scientists policy makers and scientific writers who need to enhance their competence to have the most practical way of knowing what is going on in the world in the field of livestock science and production will find this book of great value

volume detailing the effects of the molecular revolution on anthropological genetics and how it redefined the field

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Understanding the External Rate of Return (ERR)

The External Rate of Return (ERR), also known as the modified internal rate of return (MIRR), is a crucial financial metric used to evaluate the attractiveness of capital investment projects. Unlike the Internal Rate of Return (IRR), which suffers from certain limitations, the ERR addresses these shortcomings by providing a more realistic and reliable assessment of profitability, especially in scenarios with multiple cash flows and varying reinvestment rates. This article aims to provide a comprehensive understanding of the ERR, outlining its calculation, advantages, limitations, and practical applications.

Understanding the Limitations of IRR

Before diving into the ERR, it's essential to understand why a modified approach is necessary. The IRR assumes that all intermediate cash flows are reinvested at the same rate as the project's IRR. This assumption is often unrealistic. In reality, funds generated by a project may be reinvested at the company's cost of capital or at a prevailing market rate, which is likely different from the project's IRR. This discrepancy can lead to an overestimation or underestimation of the project's true profitability when using IRR alone.

Calculating the External Rate of Return

The ERR calculation involves two key steps: 1. Determining the Future Value of Cash Inflows: This step involves calculating the future value of all positive cash inflows (receipts) at the project's reinvestment rate (typically the cost of capital or a predetermined hurdle rate). This rate reflects the return the company can achieve on its funds. 2. Calculating the ERR: Once the future value of the cash inflows is determined, the ERR is calculated by finding the discount rate that equates the present value of the initial investment (outflow) to the future value of the positive cash inflows. This can be solved using financial calculators, spreadsheet software (like Excel's `IRR` or `MIRR` function), or iterative numerical methods. Example: Let's consider

a project with an initial investment of \$10,000 and the following cash flows: Year 1: -\$2,000 (negative as it's an expense) Year 2: \$5,000 Year 3: \$8,000 Assume a reinvestment rate of 8%. Step 1: Future Value of Cash Inflows: Year 2 inflow: \$5,000 $(1 + 0.08) = \$5,400$ Year 3 inflow: \$8,000 Total Future Value: $\$5,400 + \$8,000 = \$13,400$ Step 2: Calculating ERR: We need to find the discount rate that makes the present value of \$13,400 equal to \$10,000 (initial investment). Using Excel's `RATE` function or a financial calculator, we find the ERR to be approximately 11.7%.

Advantages of Using ERR

Realistic Reinvestment Assumption: The ERR assumes a more realistic reinvestment rate, usually the company's cost of capital, providing a more accurate reflection of project profitability. **Improved Decision Making:** By providing a more accurate picture of profitability, ERR improves the decision-making process regarding project selection and capital budgeting. **Avoids Multiple IRRs:** Unlike the IRR, the ERR avoids the problem of multiple IRRs (which can occur with unconventional cash flows), providing a single, unambiguous result.

Limitations of ERR

Sensitivity to the Reinvestment Rate: The choice of reinvestment rate significantly impacts the calculated ERR. An inappropriate rate can lead to inaccurate conclusions. **Complexity:** The ERR calculation is slightly more complex than the IRR, requiring more steps and potentially specialized software.

Conclusion

The External Rate of Return provides a significant improvement over the traditional IRR by addressing the unrealistic reinvestment rate assumption. By using a more appropriate reinvestment rate (typically the cost of capital), ERR offers a more accurate and reliable measure of project profitability, leading to better investment decisions. While slightly more complex to calculate, the benefits of a more realistic assessment often outweigh the increased computational effort.

FAQs

1. What is the difference between IRR and ERR? The IRR assumes reinvestment at the IRR itself, while ERR uses a more realistic reinvestment rate, typically the cost of capital. 2. Which is better, IRR or ERR? ERR is generally preferred due to its more realistic reinvestment assumption, leading to a more accurate assessment of project profitability. 3. How do I choose the reinvestment rate for ERR? The reinvestment rate should reflect the return the company can realistically achieve on its funds, often the cost of capital or a hurdle rate. 4. Can ERR be negative? Yes, a negative ERR indicates that the project is expected to generate a return lower than the reinvestment rate, suggesting it is not a worthwhile investment. 5. What software can calculate ERR? Spreadsheet software like Microsoft Excel (using the `MIRR` function) and dedicated financial calculators can easily compute the ERR.

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