

# **Likelihood, Bayesian, and MCMC Methods in Quantitative Genetics**

*Daniel Sorensen  
Daniel Gianola*

**Springer**

# Likelihood Bayesian And Mcmc Methods In Genetics

**Benjamin Neale, Manuel Ferreira, Sarah  
Medland, Danielle Posthuma**



## **Likelihood Bayesian And Mcmc Methods In Genetics:**

**Likelihood, Bayesian, and MCMC Methods in Quantitative Genetics** Daniel Sorensen, Daniel Gianola, 2007-03-22 This book suitable for numerate biologists and for applied statisticians provides the foundations of likelihood Bayesian and MCMC methods in the context of genetic analysis of quantitative traits Although a number of excellent texts in these areas have become available in recent years the basic ideas and tools are typically described in a technically demanding style and contain much more detail than necessary Here an effort has been made to relate biological to statistical parameters throughout and the book includes extensive examples that illustrate the developing argument *Computational Methods for Genetics of Complex Traits*, 2010-11-10 The field of genetics is rapidly evolving and new medical breakthroughs are occurring as a result of advances in knowledge gained from genetics research This thematic volume of *Advances in Genetics* looks at Computational Methods for Genetics of Complex traits Explores the latest topics in neural circuits and behavior research in zebrafish drosophila C elegans and mouse models Includes methods for testing with ethical legal and social implications Critically analyzes future prospects Mathematical and Statistical Methods for Genetic Analysis Kenneth Lange, 2012-12-06 During the past decade geneticists have cloned scores of Mendelian disease genes and constructed a rough draft of the entire human genome The unprecedented insights into human disease and evolution offered by mapping cloning and sequencing will transform medicine and agriculture This revolution depends vitally on the contributions of applied mathematicians statisticians and computer scientists Mathematical and Statistical Methods for Genetic Analysis is written to equip students in the mathematical sciences to understand and model the epidemiological and experimental data encountered in genetics research Mathematical statistical and computational principles relevant to this task are developed hand in hand with applications to population genetics gene mapping risk prediction testing of epidemiological hypotheses molecular evolution and DNA sequence analysis Many specialized topics are covered that are currently accessible only in journal articles This second edition expands the original edition by over 100 pages and includes new material on DNA sequence analysis diffusion processes binding domain identification Bayesian estimation of haplotype frequencies case control association studies the gamete competition model QTL mapping and factor analysis the Lander Green Kruglyak algorithm of pedigree analysis and codon and rate variation models in molecular phylogeny Sprinkled throughout the chapters are many new problems **Statistical Learning in Genetics** Daniel Sorensen, 2025-07-26 This book provides an introduction to computer based methods for the analysis of genomic data Breakthroughs in molecular and computational biology have contributed to the emergence of vast data sets where millions of genetic markers for each individual are coupled with medical records generating an unparalleled resource for linking human genetic variation to human biology and disease Similar developments have taken place in animal and plant breeding where genetic marker information is combined with production traits An important task for the statistical geneticist is to adapt construct and implement models that can

extract information from these large scale data An initial step is to understand the methodology that underlies the probability models and to learn the modern computer intensive methods required for fitting these models The objective of this book suitable for readers who wish to develop analytic skills to perform genomic research is to provide guidance to take this first step This book is addressed to numerate biologists who may lack the formal mathematical background of the professional statistician For this reason considerably more detailed explanations and derivations are offered Examples are used profusely and a large proportion involves programming with the open source package R The code needed to solve the exercises is provided and it can be downloaded allowing students to experiment by running the programs on their own computer Part I presents methods of inference and computation that are appropriate for likelihood and Bayesian models Part II discusses prediction for continuous and binary data using both frequentist and Bayesian approaches Some of the models used for prediction are also used for gene discovery The challenge is to find promising genes without incurring a large proportion of false positive results Therefore Part II includes a detour on the False Discovery Rate assuming frequentist and Bayesian perspectives The last chapter of Part II provides an overview of a selected number of non parametric methods Part III consists of exercises and their solutions This second edition has benefited from many clarifications and extensions of themes discussed in the first edition Daniel Sorensen holds PhD and DSc degrees from the University of Edinburgh and is an elected Fellow of the American Statistical Association He was professor of Statistical Genetics at Aarhus University where at present he is professor emeritus

**Statistical Genetics** Benjamin Neale,Manuel Ferreira,Sarah Medland,Danielle Posthuma,2007-11-30 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](http://www.genemapping.org) that provides supplementary material and links to downloadable software

*Quantitative Genetics in the Wild* Anne Charmantier,Dany Garant,Loeske E. B. Kruuk,2014-04-03 Although the field of quantitative genetics the study of the genetic basis of variation in quantitative characteristics such as body size or reproductive success is almost 100 years old its application to the study of evolutionary processes in wild populations has expanded greatly over the last few decades During this time the use of wild quantitative genetics has provided insights into a range of important questions in evolutionary ecology ranging from studies conducting research in well established fields such as life history theory behavioural ecology and sexual selection to others addressing relatively new issues such as populations responses to climate change or the process of senescence in natural environments 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 This comprehensive volume also offers exciting perspectives for future studies in emerging areas including the application of quantitative genetics to plants or arthropods unraveling the molecular basis of variation in quantitative traits or estimating non additive genetic variance Since this book deals with many fundamental questions in evolutionary ecology it should be of interest to graduate post graduate students and academics from a wide array of fields such as animal behaviour ecology evolution and genetics

**Brenner's Encyclopedia of Genetics** Stanley Maloy,Kelly Hughes,2013-03-03 The explosion of the field of genetics over the last decade with the new technologies that have stimulated research suggests that a new sort of reference work is needed to keep pace with such a fast moving and interdisciplinary field Brenner s Encyclopedia of Genetics Second Edition Seven Volume Set builds on the foundation of the first edition by addressing many of the key subfields of genetics that were just in their infancy when the first edition was published The currency and accessibility of this foundational content will be unrivalled making this work useful for scientists and non scientists alike Featuring relatively short entries on genetics topics written by experts in that topic Brenner s Encyclopedia of Genetics Second Edition Seven Volume Set provides an effective way to quickly learn about any aspect of genetics from Abortive Transduction to Zygotes Adding to its utility the work provides short entries that briefly define key terms and a guide to additional reading and relevant websites for further study Many of the entries include figures to explain difficult concepts Key terms in related areas such as biochemistry cell and molecular biology are also included and there are entries that describe historical figures in genetics providing insights into their careers and discoveries This 7 volume set represents a 25% expansion from the first edition with over 1600 articles encompassing this burgeoning field Thoroughly up to date with many new topics and subfields covered that were in their infancy or not in existence at the time of the first edition Timely coverage of emergent areas such as epigenetics personalized genomic medicine pharmacogenetics and genetic enhancement technologies Interdisciplinary and global in its outlook as befits the field of genetics Brief articles written by experts in the field which not only discuss define and explain key elements of the field but also provide definition of key terms suggestions for further reading and biographical sketches of the key people in the history of genetics

**Statistical Monitoring of Clinical Trials** Michael A. Proschan,K. K. Gordon Lan,Janet Turk Witten,2006-12-31 The approach taken in this book is to studies monitored over time what the Central Limit Theorem is to studies with only one analysis Just as the Central Limit Theorem shows that test statistics involving very different types of clinical trial outcomes are asymptotically normal this book shows that the joint distribution of the test statistics at different

analysis times is asymptotically multivariate normal with the correlation structure of Brownian motion the B value irrespective of the test statistic Thus this book offers statisticians an accessible incremental approach to understanding Brownian motion as related to clinical trials

**The Evaluation of Surrogate Endpoints** Geert Molenberghs, Tomasz Burzykowski, Marc Buyse, 2005-02-28 Covers the latest research on a sensitive and controversial topic in a professional and well researched manner Provides practical outlook as well as model guidelines and software tools that should be of interest to people who use the software tools described and those who do not Related title by Co author Geert Molenbergh has sold more than 3500 copies world wide Provides dual viewpoints from scientists in the industry as well as regulatory authorities

**Handbook of Statistical Genetics** David J. Balding, Martin Bishop, Chris Cannings, 2008-06-10 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

**Bayesian Biostatistics** Emmanuel Lesaffre, Andrew B. Lawson, 2012-06-18 The growth of biostatistics has been phenomenal in recent years and has been marked by considerable technical innovation in both methodology and computational practicality One area that has experienced significant growth is Bayesian methods The growing use of Bayesian methodology has taken place partly due to an increasing number of practitioners valuing the Bayesian paradigm as matching that of scientific discovery In

addition computational advances have allowed for more complex models to be fitted routinely to realistic data sets Through examples exercises and a combination of introductory and more advanced chapters this book provides an invaluable understanding of the complex world of biomedical statistics illustrated via a diverse range of applications taken from epidemiology exploratory clinical studies health promotion studies image analysis and clinical trials Key Features Provides an authoritative account of Bayesian methodology from its most basic elements to its practical implementation with an emphasis on healthcare techniques Contains introductory explanations of Bayesian principles common to all areas of application Presents clear and concise examples in biostatistics applications such as clinical trials longitudinal studies bioassay survival image analysis and bioinformatics Illustrated throughout with examples using software including WinBUGS OpenBUGS SAS and various dedicated R programs Highlights the differences between the Bayesian and classical approaches Supported by an accompanying website hosting free software and case study guides Bayesian Biostatistics introduces the reader smoothly into the Bayesian statistical methods with chapters that gradually increase in level of complexity Master students in biostatistics applied statisticians and all researchers with a good background in classical statistics who have interest in Bayesian methods will find this book useful

Genetic Data Analysis for Plant and Animal Breeding Fikret Isik,James Holland,Christian Maltecca,2017-09-09 This book fills the gap between textbooks of quantitative genetic theory and software manuals that provide details on analytical methods but little context or perspective on which methods may be most appropriate for a particular application Accordingly this book is composed of two sections The first section Chapters 1 to 8 covers topics of classical phenotypic data analysis for prediction of breeding values in animal and plant breeding programs In the second section Chapters 9 to 13 we provide the concept and overall review of available tools for using DNA markers for predictions of genetic merits in breeding populations With advances in DNA sequencing technologies genomic data especially single nucleotide polymorphism SNP markers have become available for animal and plant breeding programs in recent years Analysis of DNA markers for prediction of genetic merit is a relatively new and active research area The algorithms and software to implement these algorithms are changing rapidly This section represents state of the art knowledge on the tools and technologies available for genetic analysis of plants and animals However readers should be aware that the methods or statistical packages covered here may not be available or they might be out of date in a few years Ultimately the book is intended for professional breeders interested in utilizing these tools and approaches in their breeding programs Lastly we anticipate the usage of this volume for advanced level graduate courses in agricultural and breeding courses **Data**

**Mining in Biomedicine** Panos M. Pardalos,Vladimir L. Boginski,Alkis Vazacopoulos,2008-12-10 This volume presents an extensive collection of contributions covering aspects of the exciting and important research field of data mining techniques in biomedicine Coverage includes new approaches for the analysis of biomedical data applications of data mining techniques to real life problems in medical practice comprehensive reviews of recent trends in the field The book addresses

incorporation of data mining in fundamental areas of biomedical research genomics proteomics protein characterization and neuroscience

**Mastitis in dairy production** H. Hogeveen, 2023-08-28 Worldwide mastitis is still one of the most important diseases in the dairy sector Being a multifactorial disease caused by multiple pathogens control remains a difficult issue Mastitis not only affects the health of milk producing animals having consequences for the profitability of dairy farms it also affects the animal welfare Moreover mastitis negatively influences the milk quality having consequences for the dairy processing industry In other words mastitis affects a large part of the dairy production chain Due to ongoing scientific effort insight in mastitis in the context of increasingly complex farming systems is improving This insight leads to better methods to control mastitis either by prevention or by adequate measures e g therapy when a cow or goat or sheep gets mastitis This book reflects the current knowledge from all over the world on mastitis as it was presented during the 4th IDF International Mastitis Conference held in June 2005 in Maastricht the Netherlands The papers of the 115 oral presentations and the 13 keynote presentations are reflecting not only the current knowledge of mastitis control but are also giving ideas for future solutions for control measures

**Statistics for Veterinary and Animal Science** Aviva Petrie, Paul Watson, 2013-02-28 Banish your fears of statistical analysis using this clearly written and highly successful textbook Statistics for Veterinary and Animal Science Third Edition is an introductory text which assumes no previous knowledge of statistics It starts with very basic methodology and builds on it to encompass some of the more advanced techniques that are currently used This book will enable you to handle numerical data and critically appraise the veterinary and animal science literature Written in a non mathematical way the emphasis is on understanding the underlying concepts and correctly interpreting computer output and not on working through mathematical formulae Key features Flow charts are provided to enable you to choose the correct statistical analyses in different situations Numerous real worked examples are included to help you master the procedures Two statistical packages SPSS and Stata are used to analyse data to familiarise you with typical computer output The data sets from the examples in the book are available as electronic files to download from the book s companion website in ASCII Excel SPSS Stata and R Workspace formats allowing you to practice using your own software and fully get to grips with the techniques A clear indication is provided of the more advanced or obscure topics so that if desired you can skip them without loss of continuity New to this edition New chapter on reporting guidelines relevant to veterinary medicine as a ready reference for those wanting to follow best practice in planning and writing up research New chapter on critical appraisal of randomized controlled trials and observational studies in the published literature a template is provided which is used to critically appraise two papers New chapter introducing specialist topics ethical issues of animal investigations spatial statistics veterinary surveillance and statistics in molecular and quantitative genetics Expanded glossaries of notation and terms Additional exercises and further explanations added throughout to make the book more comprehensive Carrying out statistical procedures and interpreting the results is an integral part of veterinary and animal science This is the only book on



statistics that is specifically written for veterinary science and animal science students researchers and practitioners

**Statistical Methods in Molecular Evolution** Rasmus Nielsen, 2005-04-21 In the field of molecular evolution inferences about past evolutionary events are made using molecular data from currently living species With the availability of genomic data from multiple related species molecular evolution has become one of the most active and fastest growing fields of study in genomics and bioinformatics Most studies in molecular evolution rely heavily on statistical procedures based on stochastic process modelling and advanced computational methods including high dimensional numerical optimization and Markov Chain Monte Carlo This book provides an overview of the statistical theory and methods used in studies of molecular evolution It includes an introductory section suitable for readers that are new to the field a section discussing practical methods for data analysis and more specialized sections discussing specific models and addressing statistical issues relating to estimation and model choice The chapters are written by the leaders of field and they will take the reader from basic introductory material to the state of the art statistical methods This book is suitable for statisticians seeking to learn more about applications in molecular evolution and molecular evolutionary biologists with an interest in learning more about the theory behind the statistical methods applied in the field The chapters of the book assume no advanced mathematical skills beyond basic calculus although familiarity with basic probability theory will help the reader Most relevant statistical concepts are introduced in the book in the context of their application in molecular evolution and the book should be accessible for most biology graduate students with an interest in quantitative methods and theory Rasmus Nielsen received his Ph D from the University of California at Berkeley in 1998 and after a postdoc at Harvard University he assumed a faculty position in Statistical Genomics at Cornell University He is currently an Ole R. Merz Fellow at the University of Copenhagen and holds a Sloan Research Fellowship He is an associate editor of the Journal of Molecular Evolution and has published more than fifty original papers in peer reviewed journals on the topic of this book From the reviews Overall this is a very useful book in an area of increasing importance Journal of the Royal Statistical Society I find Statistical Methods in Molecular Evolution very interesting and useful It delves into problems that were considered very difficult just several years ago the book is likely to stimulate the interest of statisticians that are unaware of this exciting field of applications It is my hope that it will also help the wet lab molecular evolutionist to better understand mathematical and statistical methods Marek Kimmel for the Journal of the American Statistical Association September 2006 Who should read this book We suggest that anyone who deals with molecular data who does not and anyone who asks evolutionary questions who should not ought to consult the relevant chapters in this book Dan Graur and Dror Berel for Biometrics September 2006 Coalescence theory facilitates the merger of population genetics theory with phylogenetic approaches but still there are mostly two camps phylogeneticists and population geneticists Only a few people are moving freely between them Rasmus Nielsen is certainly one of these researchers and his work so far has merged many population genetic and phylogenetic aspects of biological research under

the umbrella of molecular evolution Although Nielsen did not contribute a chapter to his book his work permeates all its chapters This book gives an overview of his interests and current achievements in molecular evolution In short this book should be on your bookshelf Peter Beerli for Evolution 60 2 2006

**Analyzing Ecological Data** Alain Zuur,Elena N. Ieno,Graham M. Smith,2007-08-29 Which test should I apply During the many years of working with ecologists biologists and other environmental scientists this is probably the question that the authors of this book hear the most often The answer is always the same and along the lines of What are your underlying questions What do you want to show The answers to these questions provide the starting point for a detailed discussion on the ecological background and purpose of the study This then gives the basis for deciding on the most appropriate analytical approach Therefore a better start ing point for an ecologist is to avoid the phrase test and think in terms of analy sis A test refers to something simple and unified that gives a clear answer in the form of a p value something rarely appropriate for ecological data In practice one has to apply a data exploration check assumptions validate the models per haps apply a series of methods and most importantly interpret the results in terms of the underlying ecology and the ecological questions being investigated Ecology is a quantitative science trying to answer difficult questions about the complex world we live in Most ecologists are aware of these complexities but few are fully equipped with the statistical sophistication and understanding to deal with them

*Genomics of Cereal Crops* Shabir Hussain Wani,Anuj Kumar,2022-06-13 This volume details different genomic methods and resources to explore cereal genomics Chapters guide readers through crop genomes Next Generation Sequencing NGS technologies protocol for CRISPR editing transgenic wheat NGS approach virus induced gene silencing VIGS genomic tools computational prediction of ncRNAs miRNAs ceRNAs in cereal crops genotyping by sequencing GBS Bayesian method single cell sequencing genome wide association study GWAS QTL interval mapping whole genome bisulfite sequencing genome imprinting and methods for study the receptor metabolite interaction Authoritative and cutting edge Genomics of Cereal Crops aims to be a useful and practical guide to new researchers and experts looking to expand their knowledge

**Handbook of Statistical Systems Biology** Michael Stumpf,David J. Balding,Mark Girolami,2011-09-09 Systems Biology is now entering a mature phase in which the key issues are characterising uncertainty and stochastic effects in mathematical models of biological systems The area is moving towards a full statistical analysis and probabilistic reasoning over the inferences that can be made from mathematical models This handbook presents a comprehensive guide to the discipline for practitioners and educators in providing a full and detailed treatment of these important and emerging subjects Leading experts in systems biology and statistics have come together to provide insight in to the major ideas in the field and in particular methods of specifying and fitting models and estimating the unknown parameters This book Provides a comprehensive account of inference techniques in systems biology Introduces classical and Bayesian statistical methods for complex systems Explores networks and graphical modeling as well as a wide range of statistical models for dynamical systems Discusses various applications for

statistical systems biology such as gene regulation and signal transduction Features statistical data analysis on numerous technologies including metabolic and transcriptomic technologies Presents an in depth presentation of reverse engineering approaches Provides colour illustrations to explain key concepts This handbook will be a key resource for researchers practising systems biology and those requiring a comprehensive overview of this important field

*Jatropha, Challenges for a New Energy Crop* Sujatha Mulpuri, Nicolas Carels, Bir Bahadur, 2019-03-29 *Jatropha curcas* or physic nut is a small tree that in tropical climates produces fruits with seeds containing 38% oil The physic nut has the potential to be highly productive and is amenable to subculture in vitro and to genetic modification It also displays remarkable diversity and is relatively easy to cross hybridize within the genus Thanks to these promising features *J. curcas* is emerging as a promising oil crop and is gaining commercial interest among the biofuel research communities However as a crop physic nut has been an economic flop since 2012 because the species was not fully domesticated and the average productivity was less than 2 t ha which is below the threshold of profitability 7 t ha could be reached and it is contributing to new markets in some countries As such it is important for research to focus on the physiology and selective breeding of *Jatropha* This book provides a positive global update on *Jatropha* a crop that has suffered despite its promising agronomic and economic potential The editors have used their collective expertise in agronomy botany selective breeding biotechnology genomics and bioinformatics to seek out high quality contributions that address the bottleneck features in order to improve the economic trajectory of physic nut breeding

Likelihood Bayesian And Mcmc Methods In Genetics: Bestsellers in 2023 The year 2023 has witnessed a noteworthy surge in literary brilliance, with numerous engrossing novels enthralling the hearts of readers worldwide. Lets delve into the realm of top-selling books, exploring the captivating narratives that have charmed audiences this year. The Must-Read : Colleen Hoover "It Ends with Us" This heartfelt tale of love, loss, and resilience has captivated readers with its raw and emotional exploration of domestic abuse. Hoover skillfully weaves a story of hope and healing, reminding us that even in the darkest of times, the human spirit can prevail. Uncover the Best : Taylor Jenkins Reids "The Seven Husbands of Evelyn Hugo" This spellbinding historical fiction novel unravels the life of Evelyn Hugo, a Hollywood icon who defies expectations and societal norms to pursue her dreams. Reids absorbing storytelling and compelling characters transport readers to a bygone era, immersing them in a world of glamour, ambition, and self-discovery. Likelihood Bayesian And Mcmc Methods In Genetics : Delia Owens "Where the Crawdads Sing" This captivating coming-of-age story follows Kya Clark, a young woman who grows up alone in the marshes of North Carolina. Owens spins a tale of resilience, survival, and the transformative power of nature, captivating readers with its evocative prose and mesmerizing setting. These popular novels represent just a fraction of the literary treasures that have emerged in 2023. Whether you seek tales of romance, adventure, or personal growth, the world of literature offers an abundance of captivating stories waiting to be discovered. The novel begins with Richard Papen, a bright but troubled young man, arriving at Hampden College. Richard is immediately drawn to the group of students who call themselves the Classics Club. The club is led by Henry Winter, a brilliant and charismatic young man. Henry is obsessed with Greek mythology and philosophy, and he quickly draws Richard into his world. The other members of the Classics Club are equally as fascinating. Bunny Corcoran is a wealthy and spoiled young man who is always looking for a good time. Charles Tavis is a quiet and reserved young man who is deeply in love with Henry. Camilla Macaulay is a beautiful and intelligent young woman who is drawn to the power and danger of the Classics Club. The students are all deeply in love with Morrow, and they are willing to do anything to please him. Morrow is a complex and mysterious figure, and he seems to be manipulating the students for his own purposes. As the students become more involved with Morrow, they begin to commit increasingly dangerous acts. The Secret History is a brilliant and suspenseful novel that will keep you speculating until the very end. The novel is a warning tale about the dangers of obsession and the power of evil.

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