Bayesian Semiparametric Methods For Joint Modeling

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A New Class of Bayesian Semi-Parametric Joint Longitudinal-Survival Models for Biomarker Discovery
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Semiparametric Bayesian Joint Modeling with Applications in Toxicological Risk Assessment

GWENDOLYN JESUS

Semi-parametric Bayesian Functional Mapping with Irregular Sparse Longitudinal Data Oxford University Press
This volume is a critical exposition of the data and analyses from a full decade of rigorous research into how age-related changes at the individual level, along with other factors, contribute to morbidity, disability and mortality risks at the broader population level. After summarizing the state of our knowledge in the field, individual chapters offer enlightening discussion on a range of key topics such as age trajectory analysis in select and general populations, incidence/age patterns of major chronic illnesses, and indices of cumulative deficits and their use in characterizing and understanding the detailed properties of individual aging. The book features comprehensive statistical analyses of unique longitudinal data sets including the unique resource of the Framingham Heart Study, with its more than 60 years of follow-up. Culminating in penetrating conclusions about the insights gained from the work involved, this book adds much to our understanding of the links between aging and human health.

Nonparametric Bayesian Inference in Biostatistics Princeton University Press
High-throughput sequencing technologies are widely used to study microbial ecology across species and habitats in order to understand the impacts of microbial communities on host health, metabolism, and the environment. Due to the dynamic nature of microbial communities, longitudinal microbiome analyses play an essential role in these types of investigations. Key questions in microbiome studies aim at identifying specific microbial taxa, enterotypes, genes, or metabolites associated with specific outcomes, as well as potential factors that influence microbial communities. However, the characteristics of microbiome data, such as sparsity and skewedness, combined with the nature of data collection, reflected often as uneven sampling or missing data, make commonly employed statistical approaches to handle repeated measures in longitudinal studies inadequate. Therefore, many researchers have begun to investigate methods that could improve incorporating these features when studying clinical, host, metabolic, or environmental associations with longitudinal microbiome data. In addition to the inferential aspect, it is also

becoming apparent that visualization of high dimensional data in a way which is both intelligible and comprehensive is another difficult challenge that microbiome researchers face. Visualization is crucial in both the analysis and understanding of metagenomic data. Researchers must create clear graphic representations that give biological insight without being overly complicated. Thus, this Research Topic seeks to both review and provide novels approaches that are being developed to integrate microbiome data and complex metadata into meaningful mathematical, statistical and computational models. We believe this topic is fundamental to understanding the importance of microbial communities and provides a useful reference for other investigators approaching the field.

Bayesian Statistical Modelling CRC Press

This book is a tribute to Professor Pedro Gil, who created the Department of Statistics, OR and TM at the University of Oviedo, and a former President of the Spanish Society of Statistics and OR (SEIO). In more than eighty original contributions, it illustrates the extent to which Mathematics can help manage uncertainty, a factor that is inherent to real life. Today it goes without saying that, in order to model experiments and systems and to analyze related outcomes and data, it is necessary to consider formal ideas and develop scientific approaches and techniques for dealing with uncertainty. Mathematics is crucial in this endeavor, as this book demonstrates. As Professor Pedro Gil highlighted twenty years ago, there are several well-known mathematical branches for this purpose, including Mathematics of chance (Probability and Statistics), Mathematics of communication (Information Theory), and Mathematics of imprecision (Fuzzy Sets Theory and others). These branches often intertwine, since different sources of uncertainty can coexist, and they are not exhaustive. While most of the papers presented here address the three aforementioned fields, some hail from other Mathematical disciplines such as Operations Research; others, in turn, put the spotlight on real-world studies and applications. The intended audience of this book is mainly statisticians, mathematicians and computer scientists, but practitioners in these areas will certainly also find the book a very interesting read.

Applied Bayesian Semiparametric Methods with Special Application to the Accelerated Failure Time Model and to Hierarchical Models for Screening Semiparametric Bayesian Joint Modeling with Applications in Toxicological Risk AssessmentAbstract: Many dose-response studies collect data on correlated outcomes. For example, in developmental toxicity studies, uterine weight and presence of malformed pups are measured on the same dam. Joint modeling can result in more efficient inferences than independent models for each outcome. Most methods for joint modeling assume standard parametric response distributions. However, in toxicity studies, it is possible that response distributions vary in location and shape with dose, which may not be easily captured by standard models. To address this issue, we propose a semiparametric Bayesian joint model for a binary and continuous response. In our model, a kernel stick-breaking process (KSBP) prior is assigned to the distribution of a random effect shared across outcomes, which allows flexible changes in distribution shape with dose shared across outcomes. The model also includes outcome-specific fixed effects to allow different location effects.Bayesian Non- and Semi-parametric Methods and Applications

Using semi-parametric models with Gaussian kernels, a variable selection process is proposed. Through simulations, the proposed method, which can select either continuous or discrete variables which may have complex interactions, is evaluated. The method is employed in a real data application to identify important CpG sites and single nucleotide polymorphisms (SNPs) in a set of genes such that DNA methylation of those sites and SNPs may have joint effects on allergic sensitization.

Biodemography of Aging CRC Press

In longitudinal studies it is often of interest to investigate how a marker that is repeatedly measured in time is associated with a time to an event of interest, e.g., prostate cancer studies where longitudinal PSA level measurements are collected in conjunction with the time-to-recurrence. Joint Models for Longitudinal and Time-to-Event Data: With Applications in R provides a full treatment of random effects joint models for longitudinal and time-to-event outcomes that can be utilized to analyze such data. The content is primarily explanatory, focusing on applications of joint modeling, but sufficient mathematical details are provided to facilitate understanding of the key features of these models. All illustrations put forward can be implemented in the R programming language via the freely available package JM written by the author. All the R code used in the book is available at: http://jmr.r-forge.r-project.org/

Semiparametric Bayesian Inference in Autoregressive Panel Data Models Frontiers Media SA

This edited collection discusses the emerging topics in statistical modeling for biomedical research. Leading experts in the frontiers of biostatistics and biomedical research discuss the statistical procedures, useful methods, and their novel applications in biostatistics research. Interdisciplinary in scope, the volume as a whole reflects the latest advances in statistical modeling in biomedical research, identifies impactful new directions, and seeks to drive the field forward. It also fosters the interaction of scholars in the arena, offering great opportunities to stimulate further collaborations. This book will appeal to industry data scientists and statisticians, researchers, and graduate students in biostatistics and biomedical science. It covers topics in: Next generation sequence data analysis Deep learning, precision medicine, and their applications Large scale data analysis and its applications Biomedical research and modeling Survival analysis with complex data structure and its applications.

Handbook of Missing Data Methodology CRC Press

Presents an introduction to Bayesian statistics, presents an emphasis on Bayesian methods (prior and posterior), Bayes estimation, prediction, MCMC,Bayesian regression, and Bayesian analysis of statistical modelsof dependence, and features a focus on copulas for risk management Introduction to Bayesian Estimation and Copula Models of Dependence emphasizes the applications of Bayesian analysis to copula modeling and equips readers with the tools needed to implement the procedures of Bayesian estimation in copula models of dependence. This book is structured in two parts: the first four chapters serve as a general introduction to Bayesian statistics with a clear emphasis on parametric estimation and the following four chapters stress statistical models of dependence with a focus of copulas. A review of the main concepts is discussed along with the basics of Bayesian statistics including prior information and experimental data, prior and posterior distributions, with an emphasis on Bayesian parametric estimation. The basic mathematical background of both Markov chains and Monte Carlo integration and simulation is also provided. The authors discuss statistical models of dependence with a focus on copulas and present a brief survey of pre-copula dependence models. The main definitions and notations of copula models are summarized followed by discussions of real-world cases that address particular risk management problems. In addition, this book includes: • Practical examples of copulas in use including within the Basel Accord II documents that regulate the world banking system as well as examples of Bayesian methods within current

FDA recommendations • Step-by-step procedures of multivariate data analysis and copula modeling, allowing readers to gain insight for their own applied research and studies • Separate reference lists within each chapter and end-of-the-chapter exercises within Chapters 2 through 8 • A companion website containing appendices: data files and demo files in Microsoft® Office Excel®, basic code in R, and selected exercise solutions Introduction to Bayesian Estimation and Copula Models of Dependence is a reference and resource for statisticians who need to learn formal Bayesian analysis as well as professionals within analytical and risk management departments of banks and insurance companies who are involved in quantitative analysis and forecasting. This book can also be used as a textbook for upper-undergraduate and graduate-level courses in Bayesian statistics and analysis. ARKADY SHEMYAKIN, PhD, is Professor in the Department of Mathematics and Director of the Statistics Program at the University of St. Thomas. A member of the American Statistical Association and the International Society for Bayesian Analysis, Dr. Shemyakin's research interests include informationtheory, Bayesian methods of parametric estimation, and copula models in actuarial mathematics, finance, and engineering. ALEXANDER KNIAZEV, PhD, is Associate Professor and Head of the Department of Mathematics at Astrakhan State University in Russia. Dr. Kniazev's research interests include representation theory of Lie algebras and finite groups, mathematical statistics, econometrics, and financial mathematics.

Frontiers of Statistical Decision Making and Bayesian Analysis Springer

Abstract: Many dose-response studies collect data on correlated outcomes. For example, in developmental toxicity studies, uterine weight and presence of malformed pups are measured on the same dam. Joint modeling can result in more efficient inferences than independent models for each outcome. Most methods for joint modeling assume standard parametric response distributions. However, in toxicity studies, it is possible that response distributions vary in location and shape with dose, which may not be easily captured by standard models. To address this issue, we propose a semiparametric Bayesian joint model for a binary and continuous response. In our model, a kernel stick-breaking process (KSBP) prior is assigned to the distribution of a random effect shared across outcomes, which allows flexible changes in distribution shape with dose shared across outcomes. The model also includes outcome-specific fixed effects to allow different location effects.

A Semi-Parametric Bayesian Approach to the Instrumental Variable Problem Springer Nature

In studying the progression of a disease and to better predict time to death (survival data), investigators often collect repeated measures over time (longitudinal data) and are interested in testing the association between risk factors, including collected repeated measures, and time to death. One such example is testing the association between the biomarker serum albumin that is measured repeatedly on end-stage renal disease (ESRD) patients. A modeling framework that is capable of modeling longitudinal and survival outcomes simultaneously is called a joint longitudinal-survival model.Joint longitudinal-survival models have received a great deal of attention over the past years where many different joint models have been proposed. Joint models commonly make parametric assumptions on either the functional form of the repeated measures or on the distribution of survival times. In this dissertation we are interested in joint models that are robust to common parametric and semi-parameteric survival and longitudinal assumptions. We propose a flexible Bayesian joint longitudinal-survival framework that avoids common parametric and semi-parameteric assumptions. More specifically, our modeling framework incorporates a flexible longitudinal component by utilizing Gaussian process (GP) technique. This technique avoids any explicit functional assumption on the trajectory of the repeated measures. Our modeling framework also uses Dirichlet process (DP) prior to avoid explicit distributional assumptions on survival times.We further extend our framework to modeling multiple longitudinal processes simultaneously. We propose a multivariate joint longitudinal-survival technique to jointly model the association between multiple longitudinal processes with survival outcomes. Our proposed technique is capable of taking correlation between longitudinal processes into account. This is particularly useful when observed measures from different longitudinal processes are taken at different frequencies. That means, some longitudinal processes are observed less frequently compared to other longitudinal processes. By jointly modeling these processes, one can take the correlation between the processes into account, and hence, better estimate the trajectory of the processes including those less frequent ones.Our proposed joint modeling frameworks use Dirichlet process techniques. Therefore, understanding parameter estimation in these models is vital. Using synthetic longitudinal and survival data, we compare parameter estimation under DPM models as opposed to commonly used parametric techniques. We are particularly interested in evaluation of the performance of the model in parameter estimation when a population consists of sub-populations with latent features that are different across subgroups. We propose a Dirichlet process mixture survival model that is capable of detecting latent subpopulations characterized by differing baseline risks for mortality. Our proposed technique is particularly useful when interest lies in estimation of the conditional effect of covariates as opposed to estimates that are marginalized across all subpopulations.Throughout, our work is motivated by data on patients with end stage renal disease (ESRD), a condition where the kidneys are no longer capable of cleaning blood sufficiently enough to sustain life. In this context a modeling framework capable of finding mortality-related biomarkers, which are measured longitudinally over time, can significantly help physicians and practitioners to lower mortality among these patients.

Bayesian Thinking, Modeling and Computation Springer

An intermediate-level treatment of Bayesian hierarchical models and their applications, this book demonstrates the advantages of a Bayesian approach to data sets involving inferences for collections of related units or variables, and in methods where parameters can be treated as random collections. Through illustrative data analysis and attention to statistical computing, this book facilitates practical implementation of Bayesian hierarchical methods. The new edition is a revision of the book Applied Bayesian Hierarchical Methods. It maintains a focus on applied modelling and data analysis, but now using entirely R-based Bayesian computing options. It has been updated with a new chapter on regression for causal effects, and one on computing options and strategies. This latter chapter is particularly important, due to recent advances in Bayesian computing and estimation, including the development of rjags and rstan. It also features updates throughout with new examples. The examples exploit and illustrate the broader advantages of the R computing environment, while allowing readers to explore alternative likelihood assumptions, regression structures, and assumptions on prior densities. Features: Provides a comprehensive and accessible overview of applied Bayesian hierarchical modelling Includes many real data examples to illustrate different modelling topics R code (based on rjags,

jagsUI, R2OpenBUGS, and rstan) is integrated into the book, emphasizing implementation Software options and coding principles are introduced in new chapter on computing Programs and data sets available on the book's website

Bayesian Nonparametrics Springer

Spatial point pattern data are routinely encountered. A flexible regression model for the underlying intensity is essential to characterizing and understanding the pattern. Spatial point processes are a widely used to model for such data. Additional measurements are often available along with spatial points, which are called marks. Such data can be modeled using marked spatial point processes. The first part of this dissertation focuses on the heterogeneity of point processes. We propose a Bayesian semiparametric model where the observed points follow a spatial Poisson process with an intensity function which adjusts a nonparametric baseline intensity with multiplicative covariate effects. The baseline intensity is approached with a powered Chinese restaurant process (PCRP) prior. The parametric regression part allows for variable selection through the spike-slab prior on the regression coefficients. An efficient Markov chain Monte Carlo (MCMC) algorithm is developed. The performance of the methods is validated in an extensive simulation study and the Beilschmiedia pendula trees data. Spatial smoothness is often observed in some environmental spatial point pattern data, and the PCRP may have lower efficiency for such data since it allows more flexibility without any spatial constraint. Distance dependent Chinese restaurant process (ddCRP) can be easily realized by introducing a decay function to Chinese restaurant process. The second part of this dissertation introduces the ddCRP model with Bayesian inference methods, whose performance is illustrated using simulation study. In the third part, we investigate the marked spatial point process, which is motivated by the basketball shot data. We develop a Bayesian joint model of the mark and the intensity, where the intensity is incorporated in the mark's model as a covariate. An MCMC algorithm is developed to draw posterior samples from this model. Two Bayesian model comparison criteria, the modified Deviance Information Criterion and the modified Logarithm of the Pseudo-Marginal Likelihood, are developed to assess the fitness of different models focusing on the mark. Simulation study and application to NBA basketball shot data are conducted to show the performance of proposed methods.

Novel Approaches in Microbiome Analyses and Data Visualization CRC Press

Quantile regression constitutes an ensemble of statistical techniques intended to estimate and draw inferences about conditional quantile functions. Median regression, as introduced in the 18th century by Boscovich and Laplace, is a special case. In contrast to conventional mean regression that minimizes sums of squared residuals, median regression minimizes sums of absolute residuals; quantile regression simply replaces symmetric absolute loss by asymmetric linear loss. Since its introduction in the 1970's by Koenker and Bassett, quantile regression has been gradually extended to a wide variety of data analytic settings including time series, survival analysis, and longitudinal data. By focusing attention on local slices of the conditional distribution of response variables it is capable of providing a more complete, more nuanced view of heterogeneous covariate effects. Applications of quantile regression can now be found throughout the sciences, including astrophysics, chemistry, ecology, economics, finance, genomics, medicine, and meteorology. Software for quantile regression is now widely available in all the major statistical computing environments. The objective of this volume is to provide a comprehensive review of recent developments of quantile regression methodology illustrating its applicability in a wide range of scientific settings. The intended audience of the volume is researchers and graduate students across a diverse set of disciplines.

Applied Statistics in Biomedicine and Clinical Trials Design CRC Press

Winner of the 2016 De Groot Prize from the International Society for Bayesian Analysis Now in its third edition, this classic book is widely considered the leading text on Bayesian methods, lauded for its accessible, practical approach to analyzing data and solving research problems. Bayesian Data Analysis, Third Edition continues to take an applied approach to analysis using up-to-date Bayesian methods. The authors—all leaders in the statistics community—introduce basic concepts from a data-analytic perspective before presenting advanced methods. Throughout the text, numerous worked examples drawn from real applications and research emphasize the use of Bayesian inference in practice. New to the Third Edition Four new chapters on nonparametric modeling Coverage of weakly informative priors and boundary-avoiding priors Updated discussion of cross-validation and predictive information criteria Improved convergence monitoring and effective sample size calculations for iterative simulation Presentations of Hamiltonian Monte Carlo, variational Bayes, and expectation propagation New and revised software code The book can be used in three different ways. For undergraduate students, it introduces Bayesian inference starting from first principles. For graduate students, the text presents effective current approaches to Bayesian modeling and computation in statistics and related fields. For researchers, it provides an assortment of Bayesian methods in applied statistics. Additional materials, including data sets used in the examples, solutions to selected exercises, and software instructions, are available on the book's web page.

Emerging Topics in Modeling Interval-Censored Survival Data CRC Press

Over the past decades a great deal of effort has been expended in the collection and compilation of high quality data on cancer incidence and mortality in the United States. These data have largely been used in the creation and disbursement of descriptive statistics concerning the state of cancer in the U.S. The information available through these statistics present limited information concerning spatial or temporal trends in the course of cancer in the U.S. Recently, there have been more efforts made to investigate these trends. Smoothing is the practice of modeling data in order to eliminate random variation from the observed data and provide estimates of the underlying process. Models are developed here that incorporate a number of techniques for smoothing spatial and spatio-temporal data. These include an additive model and two joint spatio-temporal models. Data analyzed includes mortality due to female breast cancer in Missouri from 1969-2000 and survey responses to the Missouri Turkey Hunting Survey, conducted by the Missouri Department of Conservation.

Bayesian Semi-parametric Methods for Non-ignorable Dropout Cambridge University Press

Handbook of Survival Analysis presents modern techniques and research problems in lifetime data analysis. This area of statistics deals with time-to-event data that is complicated by censoring and the dynamic nature of events occurring in time. With chapters written by leading researchers in the field, the handbook focuses on advances in survival analysis techniques, covering classical and Bayesian approaches. It gives a complete overview of the current status of survival analysis and should inspire further research in the field. Accessible to a wide range of readers, the book provides: An introduction to various areas in survival analysis for graduate students and novices A reference

to modern investigations into survival analysis for more established researchers A text or supplement for a second or advanced course in survival analysis A useful guide to statistical methods for analyzing survival data experiments for practicing statisticians

Bayesian Statistical Methods Springer

Bayesian Statistical Methods provides data scientists with the foundational and computational tools needed to carry out a Bayesian analysis. This book focuses on Bayesian methods applied routinely in practice including multiple linear regression, mixed effects models and generalized linear models (GLM). The authors include many examples with complete R code and comparisons with analogous frequentist procedures. In addition to the basic concepts of Bayesian inferential methods, the book covers many general topics: Advice on selecting prior distributions Computational methods including Markov chain Monte Carlo (MCMC) Model-comparison and goodness-of-fit measures, including sensitivity to priors Frequentist properties of Bayesian methods Case studies covering advanced topics illustrate the flexibility of the Bayesian approach: Semiparametric regression Handling of missing data using predictive distributions Priors for high-dimensional regression models Computational techniques for large datasets Spatial data analysis The advanced topics are presented with sufficient conceptual depth that the reader will be able to carry out such analysis and argue the relative merits of Bayesian and classical methods. A repository of R code, motivating data sets, and complete data analyses are available on the book’s website. Brian J. Reich, Associate Professor of Statistics at North Carolina State University, is currently the editor-in-chief of the Journal of Agricultural, Biological, and Environmental Statistics and was awarded the LeRoy & Elva Martin Teaching Award. Sujit K. Ghosh, Professor of Statistics at North Carolina State University, has over 22 years of research and teaching experience in conducting Bayesian analyses, received the Cavell Brownie mentoring award, and served as the Deputy Director at the Statistical and Applied Mathematical Sciences Institute.

On Bayesian Methods for Spatial Point Processes Elsevier

Dropout is a common problem in longitudinal studies; when the probability of dropout depends on unobserved outcomes, even after conditioning on available data, data may be missing not at random, and dropout is not ignorable. Selection, frailty, and mixture model frameworks have been proposed to adjust for dropout; however, most methods rely on parametric assumptions about the distribution of dropout times and the relationship between the outcome and dropout time. We propose two Bayesian semi-parametric frameworks to account for dropout, including a natural cubic B-spline varying coefficient model and a Dirichlet process mixture model. These methods can model longitudinal Gaussian outcomes as well as non-normal outcomes in the exponential family, while relaxing common parametric assumptions and making inference more robust. These methods are extended to the joint modeling of two correlated longitudinal outcomes in the presence of dropout. We apply these methods to investigate longitudinal changes in CD4+ T cell count, viral load, and viral load suppression in two HIV cohort studies.

A Bayesian Semi-Parametric Approach to Variable Selection Frontiers Media SA

This book reviews and develops Bayesian non-parametric and semi-parametric methods for applications in microeconometrics and quantitative marketing. Most econometric models used in microeconomics and marketing applications involve arbitrary distributional assumptions. As more data becomes available, a natural desire to provide methods that relax these assumptions arises. Peter Rossi advocates a Bayesian approach in which specific distributional assumptions are replaced with more flexible distributions based on mixtures of normals. The Bayesian approach can use either a large but fixed number of normal components in the mixture or an infinite number bounded only by the sample size. By using flexible distributional approximations instead of fixed parametric models, the Bayesian approach can reap the advantages of an efficient method that models all of the structure in the data while retaining desirable smoothing properties. Non-Bayesian non-parametric methods often require additional ad hoc rules to avoid "overfitting," in which resulting density approximates are nonsmooth. With proper priors, the Bayesian approach largely avoids overfitting, while retaining flexibility. This book provides methods for assessing informative priors that require only simple data normalizations. The book also applies the mixture of the normals approximation method to a number of important models in microeconometrics and marketing, including the non-parametric and semi-parametric regression models, instrumental variables problems, and models of heterogeneity. In addition, the author has written a free online software package in R, "bayesm," which implements all of the non-parametric models discussed in the book.

Generalized Linear Models Springer Nature

This volume is a unique combination of papers that cover critical topics in biostatistics from academic, government, and industry perspectives. The 6 sections cover Bayesian methods in biomedical research; Diagnostic medicine and classification; Innovative Clinical Trials Design; Modelling and Data Analysis; Personalized Medicine; and Statistical Genomics. The real world applications are in clinical trials, diagnostic medicine and genetics. The peer-reviewed contributions were solicited and selected from some 400 presentations at the annual meeting of the International Chinese Statistical Association (ICSA), held with the International Society for Biopharmaceutical Statistics (ISBS). The conference was held in Bethesda in June 2013, and the material has been subsequently edited and expanded to cover the most recent developments.

The Mathematics of the Uncertain Springer

This book primarily aims to discuss emerging topics in statistical methods and to booster research, education, and training to advance statistical modeling on interval-censored survival data. Commonly collected from public health and biomedical research, among other sources, interval-censored survival data can easily be mistaken for typical right-censored survival data, which can result in erroneous statistical inference due to the complexity of this type of data. The book invites a group of internationally leading researchers to systematically discuss and explore the historical development of the associated methods and their computational implementations, as well as emerging topics related to interval-censored data. It covers a variety of topics, including univariate interval-censored data, multivariate interval-censored data, clustered interval-censored data, competing risk interval-censored data, data with interval-censored covariates, interval-censored data from electric medical records, and misclassified interval-censored data. Researchers, students, and practitioners can directly make use of the state-of-the-art methods covered in the book to tackle their problems in research, education, training and consultation.

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