ISSN 1932-6157 (print)
ISSN 1941-7330 (online)

THE ANNALS *of* APPLIED STATISTICS

An Official Journal of the Institute of Mathematical Statistics

Articles

continued

ISSN 1932-6157 (print)
ISSN 1941-7330 (online)

THE ANNALS *of* APPLIED STATISTICS

An Official Journal of the Institute of Mathematical Statistics

Articles—*Continued from front cover*

Correction

THE ANNALS OF APPLIED STATISTICS Vol. 14, No. 1, pp. 1–520 March 2020

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The Annals of Applied Statistics **[ISSN 1932-6157 (print); ISSN 1941-7330 (online)],** Volume 14, Number 1, March 2020. Published quarterly by the Institute of Mathematical Statistics, 3163 Somerset Drive, Cleveland, Ohio 44122, USA. Periodicals postage pending at Cleveland, Ohio, and at additional mailing offices.

POSTMASTER: Send address changes to *The Annals of Applied Statistics*, Institute of Mathematical Statistics, Dues and Subscriptions Office, 9650 Rockville Pike, Suite L 2310, Bethesda, Maryland 20814-3998, USA.

The Annals of Applied Statistics
2020, Vol. 14, No. 1, 1–27
https://doi.org/10.1214/19-AOAS1265

SHOPPER: A PROBABILISTIC MODEL OF CONSUMER CHOICE WITH SUBSTITUTES AND COMPLEMENTS

BY FRANCISCO J. R. RUIZ[1], SUSAN ATHEY[2] AND DAVID M. BLEI[3]

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We develop SHOPPER, a sequential probabilistic model of shopping data. SHOPPER uses interpretable components to model the forces that drive how a customer chooses products; in particular, we designed SHOPPER to capture how items interact with other items. We develop an efficient posterior inference algorithm to estimate these forces from large-scale data, and we analyze a large dataset from a major chain grocery store. We are interested in answering counterfactual queries about changes in prices. We found that SHOPPER provides accurate predictions even under price interventions, and that it helps identify complementary and substitutable pairs of products.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 28–50
https://doi.org/10.1214/19-AOAS1268

BART WITH TARGETED SMOOTHING: AN ANALYSIS OF PATIENT-SPECIFIC STILLBIRTH RISK

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This article introduces BART with Targeted Smoothing, or tsBART, a new Bayesian tree-based model for nonparametric regression. The goal of tsBART is to introduce smoothness over a single target covariate t while not necessarily requiring smoothness over other covariates x. tsBART is based on the Bayesian Additive Regression Trees (BART) model, an ensemble of regression trees. tsBART extends BART by parameterizing each tree's terminal nodes with smooth functions of t rather than independent scalars. Like BART, tsBART captures complex nonlinear relationships and interactions among the predictors. But unlike BART, tsBART guarantees that the response surface will be smooth in the target covariate. This improves interpretability and helps to regularize the estimate.

After introducing and benchmarking the tsBART model, we apply it to our motivating example—pregnancy outcomes data from the National Center for Health Statistics. Our aim is to provide patient-specific estimates of stillbirth risk across gestational age (t) and based on maternal and fetal risk factors (x). Obstetricians expect stillbirth risk to vary smoothly over gestational age but not necessarily over other covariates, and tsBART has been designed precisely to reflect this structural knowledge. The results of our analysis show the clear superiority of the tsBART model for quantifying stillbirth risk, thereby providing patients and doctors with better information for managing the risk of fetal mortality. All methods described here are implemented in the R package *tsbart*.

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Key words and phrases. Bayesian additive regression tree, ensemble method, Gaussian process, regression tree, regularization.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 51–73
https://doi.org/10.1214/19-AOAS1287

INTEGRATIVE SURVIVAL ANALYSIS WITH UNCERTAIN EVENT TIMES IN APPLICATION TO A SUICIDE RISK STUDY

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The concept of integrating data from disparate sources to accelerate scientific discovery has generated tremendous excitement in many fields. The potential benefits from data integration, however, may be compromised by the uncertainty due to incomplete/imperfect record linkage. Motivated by a suicide risk study, we propose an approach for analyzing survival data with uncertain event times arising from data integration. Specifically, in our problem deaths identified from the hospital discharge records together with reported suicidal deaths determined by the Office of Medical Examiner may still not include all the death events of patients, and the missing deaths can be recovered from a complete database of death records. Since the hospital discharge data can only be linked to the death record data by matching basic patient characteristics, a patient with a censored death time from the first dataset could be linked to multiple potential event records in the second dataset. We develop an integrative Cox proportional hazards regression in which the uncertainty in the matched event times is modeled probabilistically. The estimation procedure combines the ideas of profile likelihood and the expectation conditional maximization algorithm (ECM). Simulation studies demonstrate that under realistic settings of imperfect data linkage the proposed method outperforms several competing approaches including multiple imputation. A marginal screening analysis using the proposed integrative Cox model is performed to identify risk factors associated with death following suicide-related hospitalization in Connecticut. The identified diagnostics codes are consistent with existing literature and provide several new insights on suicide risk, prediction and prevention.

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Key words and phrases. Cox model, data linkage, ECM algorithm, integrative learning, suicide prevention.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 74–93
https://doi.org/10.1214/19-AOAS1278

EFFICIENT REAL-TIME MONITORING OF AN EMERGING INFLUENZA PANDEMIC: HOW FEASIBLE?

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A prompt public health response to a new epidemic relies on the ability to monitor and predict its evolution in real time as data accumulate. The 2009 A/H1N1 outbreak in the UK revealed pandemic data as noisy, contaminated, potentially biased and originating from multiple sources. This seriously challenges the capacity for real-time monitoring. Here, we assess the feasibility of real-time inference based on such data by constructing an analytic tool combining an age-stratified SEIR transmission model with various observation models describing the data generation mechanisms. As batches of data become available, a sequential Monte Carlo (SMC) algorithm is developed to synthesise multiple imperfect data streams, iterate epidemic inferences and assess model adequacy amidst a rapidly evolving epidemic environment, substantially reducing computation time in comparison to standard MCMC, to ensure timely delivery of real-time epidemic assessments. In application to simulated data designed to mimic the 2009 A/H1N1 epidemic, SMC is shown to have additional benefits in terms of assessing predictive performance and coping with parameter nonidentifiability.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 94–115
https://doi.org/10.1214/19-AOAS1283

MODELING MICROBIAL ABUNDANCES AND DYSBIOSIS WITH BETA-BINOMIAL REGRESSION

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Using a sample from a population to estimate the proportion of the population with a certain category label is a broadly important problem. In the context of microbiome studies, this problem arises when researchers wish to use a sample from a population of microbes to estimate the population proportion of a particular taxon, known as the taxon's *relative abundance*. In this paper, we propose a beta-binomial model for this task. Like existing models, our model allows for a taxon's relative abundance to be associated with covariates of interest. However, unlike existing models, our proposal also allows for the overdispersion in the taxon's counts to be associated with covariates of interest. We exploit this model in order to propose tests not only for differential relative abundance, but also for differential variability. The latter is particularly valuable in light of speculation that *dysbiosis*, the perturbation from a normal microbiome that can occur in certain disease conditions, may manifest as a loss of stability, or increase in variability, of the counts associated with each taxon. We demonstrate the performance of our proposed model using a simulation study and an application to soil microbial data.

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Key words and phrases. Relative abundance, microbiome, correlated data, overdispersion, high throughput sequencing, beta-binomial.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 116–142
https://doi.org/10.1214/19-AOAS1290

A STATISTICAL ANALYSIS OF NOISY CROWDSOURCED WEATHER DATA

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Spatial prediction of weather elements like temperature, precipitation, and barometric pressure are generally based on satellite imagery or data collected at ground stations. None of these data provide information at a more granular or "hyperlocal" resolution. On the other hand, crowdsourced weather data, which are captured by sensors installed on mobile devices and gathered by weather-related mobile apps like `WeatherSignal` and `AccuWeather`, can serve as potential data sources for analyzing environmental processes at a hyperlocal resolution. However, due to the low quality of the sensors and the nonlaboratory environment, the quality of the observations in crowdsourced data is compromised. This paper describes methods to improve hyperlocal spatial prediction using this varying-quality, noisy crowdsourced information. We introduce a reliability metric, namely Veracity Score (VS), to assess the quality of the crowdsourced observations using a coarser, but high-quality, reference data. A VS-based methodology to analyze noisy spatial data is proposed and evaluated through extensive simulations. The merits of the proposed approach are illustrated through case studies analyzing crowdsourced daily average ambient temperature readings for one day in the contiguous United States.

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Key words and phrases. Veracity score, geostatistics, robust kriging, hyperlocal spatial prediction.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 143–159
https://doi.org/10.1214/19-AOAS1297

SURFACE TEMPERATURE MONITORING IN LIVER PROCUREMENT VIA FUNCTIONAL VARIANCE CHANGE-POINT ANALYSIS

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Liver procurement experiments with surface-temperature monitoring motivated Gao et al. (*J. Amer. Statist. Assoc.* **114** (2019) 773–781) to develop a variance change-point detection method under a smoothly-changing mean trend. However, the spotwise change points yielded from their method do not offer immediate information to surgeons since an organ is often transplanted as a whole or in part. We develop a new practical method that can analyze a defined portion of the organ surface at a time. It also provides a novel addition to the developing field of functional data monitoring. Furthermore, numerical challenge emerges for simultaneously modeling the variance functions of 2D locations and the mean function of location and time. The respective sample sizes in the scales of 10,000 and 1,000,000 for modeling these functions make standard spline estimation too costly to be useful. We introduce a multistage subsampling strategy with steps educated by quickly-computable preliminary statistical measures. Extensive simulations show that the new method can efficiently reduce the computational cost and provide reasonable parameter estimates. Application of the new method to our liver surface temperature monitoring data shows its effectiveness in providing accurate status change information for a selected portion of the organ in the experiment.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 160–177
https://doi.org/10.1214/19-AOAS1304

ASSESSING WAGE STATUS TRANSITION AND STAGNATION USING QUANTILE TRANSITION REGRESSION

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Workers in Taiwan overall have been suffering from long-lasting wage stagnation since the mid-1990s. In particular, there seems to be little mobility for the wages of Taiwanese workers to transit across wage quantile groups. It is of interest to see if certain groups of workers, such as female, lower educated and younger generation workers, suffer from the problem more seriously than the others. This work tries to apply a systematic statistical approach to study this issue, based on the longitudinal data from the Panel Study of Family Dynamics (PSFD) survey conducted in Taiwan since 1999. We propose the quantile transition regression model, generalizing recent methodology for quantile association, to assess the wage status transition with respect to the marginal wage quantiles over time as well as the effects of certain demographic and job factors on the wage status transition. Estimation of the model can be based on the composite likelihoods utilizing the binary, or ordinal-data information regarding the quantile transition, with the associated asymptotic theory established. A goodness-of-fit procedure for the proposed model is developed. The performances of the estimation and the goodness-of-fit procedures for the quantile transition model are illustrated through simulations. The application of the proposed methodology to the PSFD survey data suggests that female, private-sector workers with higher age and education below postgraduate level suffer from more severe wage status stagnation than the others.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 178–201
https://doi.org/10.1214/19-AOAS1302

TFISHER: A POWERFUL TRUNCATION AND WEIGHTING PROCEDURE FOR COMBINING *p*-VALUES

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The *p*-value combination approach is an important statistical strategy for testing global hypotheses with broad applications in signal detection, meta-analysis, data integration, etc. In this paper we extend the classic Fisher's combination method to a unified family of statistics, called TFisher, which allows a general truncation-and-weighting scheme of input *p*-values. TFisher can significantly improve statistical power over the Fisher and related truncation-only methods for detecting both rare and dense "signals." To address wide applications, analytical calculations for TFisher's size and power are deduced under any two continuous distributions in the null and the alternative hypotheses. The corresponding omnibus test (oTFisher) and its size calculation are also provided for data-adaptive analysis. We study the asymptotic optimal parameters of truncation and weighting based on Bahadur efficiency (BE). A new asymptotic measure, called the asymptotic power efficiency (APE), is also proposed for better reflecting the statistics' performance in real data analysis. Interestingly, under the Gaussian mixture model in the signal detection problem, both BE and APE indicate that the soft-thresholding scheme is the best, the truncation and weighting parameters should be equal. By simulations of various signal patterns, we systematically compare the power of statistics within TFisher family as well as some rare-signal-optimal tests. We illustrate the use of TFisher in an exome-sequencing analysis for detecting novel genes of amyotrophic lateral sclerosis. Relevant computation has been implemented into an R package *TFisher* published on the Comprehensive R Archive Network to cater for applications.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 202–220
https://doi.org/10.1214/19-AOAS1301

MODIFYING THE CHI-SQUARE AND THE CMH TEST FOR POPULATION GENETIC INFERENCE: ADAPTING TO OVERDISPERSION

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Evolve and resequence studies provide a popular approach to simulate evolution in the lab and explore its genetic basis. In this context, Pearson's chi-square test, Fisher's exact test as well as the Cochran–Mantel–Haenszel test are commonly used to infer genomic positions affected by selection from temporal changes in allele frequency. However, the null model associated with these tests does not match the null hypothesis of actual interest. Indeed, due to genetic drift and possibly other additional noise components such as pool sequencing, the null variance in the data can be substantially larger than accounted for by these common test statistics. This leads to p-values that are systematically too small and, therefore, a huge number of false positive results. Even, if the ranking rather than the actual p-values is of interest, a naive application of the mentioned tests will give misleading results, as the amount of overdispersion varies from locus to locus. We therefore propose adjusted statistics that take the overdispersion into account while keeping the formulas simple. This is particularly useful in genome-wide applications, where millions of SNPs can be handled with little computational effort. We then apply the adapted test statistics to real data from *Drosophila* and investigate how information from intermediate generations can be included when available. We also discuss further applications such as genome-wide association studies based on pool sequencing data and tests for local adaptation.

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Key words and phrases. Chi-square test, CMH test, overdispersion, experimental evolution, evolve and resequence, genetic drift, pool sequencing.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 221–240
https://doi.org/10.1214/19-AOAS1296

A HIERARCHICAL BAYESIAN MODEL FOR PREDICTING ECOLOGICAL INTERACTIONS USING SCALED EVOLUTIONARY RELATIONSHIPS

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Identifying undocumented or potential future interactions among species is a challenge facing modern ecologists. Recent link prediction methods rely on trait data; however, large species interaction databases are typically sparse and covariates are limited to only a fraction of species. On the other hand, evolutionary relationships, encoded as phylogenetic trees, can act as proxies for underlying traits and historical patterns of parasite sharing among hosts. We show that, using a network-based conditional model, phylogenetic information provides strong predictive power in a recently published global database of host-parasite interactions. By scaling the phylogeny using an evolutionary model, our method allows for biological interpretation often missing from latent variable models. To further improve on the phylogeny-only model, we combine a hierarchical Bayesian latent score framework for bipartite graphs that accounts for the number of interactions per species with host dependence informed by phylogeny. Combining the two information sources yields significant improvement in predictive accuracy over each of the submodels alone. As many interaction networks are constructed from presence-only data, we extend the model by integrating a correction mechanism for missing interactions which proves valuable in reducing uncertainty in unobserved interactions.

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Key words and phrases. Ecological networks, composite likelihood, iterated conditional modes, presence-only networks, link prediction.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 241–256
https://doi.org/10.1214/19-AOAS1253

BAYESIAN FACTOR MODELS FOR PROBABILISTIC CAUSE OF DEATH ASSESSMENT WITH VERBAL AUTOPSIES

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The distribution of deaths by cause provides crucial information for public health planning, response and evaluation. About 60% of deaths globally are not registered or given a cause, limiting our ability to understand disease epidemiology. Verbal autopsy (VA) surveys are increasingly used in such settings to collect information on the signs, symptoms and medical history of people who have recently died. This article develops a novel Bayesian method for estimation of population distributions of deaths by cause using verbal autopsy data. The proposed approach is based on a multivariate probit model where associations among items in questionnaires are flexibly induced by latent factors. Using the Population Health Metrics Research Consortium labeled data that include both VA and medically certified causes of death, we assess performance of the proposed method. Further, we estimate important questionnaire items that are highly associated with causes of death. This framework provides insights that will simplify future data

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Key words and phrases. Bayesian latent model, cause of death, conditional dependence, multivariate data, verbal autopsies, survey data.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 257–275
https://doi.org/10.1214/19-AOAS1307

ESTIMATING THE HEALTH EFFECTS OF ENVIRONMENTAL MIXTURES USING BAYESIAN SEMIPARAMETRIC REGRESSION AND SPARSITY INDUCING PRIORS

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Humans are routinely exposed to mixtures of chemical and other environmental factors, making the quantification of health effects associated with environmental mixtures a critical goal for establishing environmental policy sufficiently protective of human health. The quantification of the effects of exposure to an environmental mixture poses several statistical challenges. It is often the case that exposure to multiple pollutants interact with each other to affect an outcome. Further, the exposure-response relationship between an outcome and some exposures, such as some metals, can exhibit complex, nonlinear forms, since some exposures can be beneficial and detrimental at different ranges of exposure. To estimate the health effects of complex mixtures, we propose a flexible Bayesian approach that allows exposures to interact with each other and have nonlinear relationships with the outcome. We induce sparsity using multivariate spike and slab priors to determine which exposures are associated with the outcome and which exposures interact with each other. The proposed approach is interpretable, as we can use the posterior probabilities of inclusion into the model to identify pollutants that interact with each other. We utilize our approach to study the impact of exposure to metals on child neurodevelopment in Bangladesh and find a nonlinear, interactive relationship between arsenic and manganese.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 276–298
https://doi.org/10.1214/19-AOAS1310

FEATURE SELECTION FOR GENERALIZED VARYING COEFFICIENT MIXED-EFFECT MODELS WITH APPLICATION TO OBESITY GWAS

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Motivated by an empirical analysis of data from a genome-wide association study on obesity, measured by the body mass index (BMI), we propose a two-step gene-detection procedure for generalized varying coefficient mixed-effects models with ultrahigh dimensional covariates. The proposed procedure selects significant single nucleotide polymorphisms (SNPs) impacting the mean BMI trend, some of which have already been biologically proven to be "fat genes." The method also discovers SNPs that significantly influence the age-dependent variability of BMI. The proposed procedure takes into account individual variations of genetic effects and can also be directly applied to longitudinal data with continuous, binary or count responses. We employ Monte Carlo simulation studies to assess the performance of the proposed method and further carry out causal inference for the selected SNPs.

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Key words and phrases. Genome-wide association study, mixed effects, ultrahigh dimensional longitudinal data, varying coefficient models.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 299–338
https://doi.org/10.1214/19-AOAS1303

OPTIMAL ASSET ALLOCATION WITH MULTIVARIATE BAYESIAN DYNAMIC LINEAR MODELS

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We introduce a fast, closed-form, simulation-free method to model and forecast multiple asset returns and employ it to investigate the optimal ensemble of features to include when jointly predicting monthly stock and bond excess returns. Our approach builds on the Bayesian dynamic linear models of West and Harrison (*Bayesian Forecasting and Dynamic Models* (1997) Springer), and it can objectively determine, through a fully automated procedure, both the optimal set of regressors to include in the predictive system and the degree to which the model coefficients, volatilities and covariances should vary over time. When applied to a portfolio of five stock and bond returns, we find that our method leads to large forecast gains, both in statistical and economic terms. In particular, we find that relative to a standard no-predictability benchmark, the optimal combination of predictors, stochastic volatility and time-varying covariances increases the annualized certainty equivalent returns of a leverage-constrained power utility investor by more than 500 basis points.

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Key words and phrases. 62C10, 62P20, 91B28, 91B84.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 339–356
https://doi.org/10.1214/19-AOAS1309

MODELING WILDFIRE IGNITION ORIGINS IN SOUTHERN CALIFORNIA USING LINEAR NETWORK POINT PROCESSES

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This paper focuses on spatial and temporal modeling of point processes on linear networks. Point processes on linear networks can simply be defined as point events occurring on or near line segment network structures embedded in a certain space. A separable modeling framework is introduced that posits separate *formation* and *dissolution* models of point processes on linear networks over time. While the model was inspired by spider web building activity in brick mortar lines, the focus is on modeling wildfire ignition origins near road networks over a span of 14 years. As most wildfires in California have human-related origins, modeling the origin locations with respect to the road network provides insight into how human, vehicular and structural densities affect ignition occurrence. Model results show that roads that traverse different types of regions such as residential, interface and wildland regions have higher ignition intensities compared to roads that only exist in each of the mentioned region types.

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Key words and phrases. Point processes, linear network, spatiotemporal modeling, pseudolikelihood, Berman–Turner method, spider webs, wildfires, ignition origins, road networks.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 357–380
https://doi.org/10.1214/19-AOAS1299

REGRESSION FOR COPULA-LINKED COMPOUND DISTRIBUTIONS WITH APPLICATIONS IN MODELING AGGREGATE INSURANCE CLAIMS

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In actuarial research a task of particular interest and importance is to predict the loss cost for individual risks so that informative decisions are made in various insurance operations such as underwriting, ratemaking and capital management. The loss cost is typically viewed to follow a compound distribution where the summation of the severity variables is stopped by the frequency variable. A challenging issue in modeling such outcomes is to accommodate the potential dependence between the number of claims and the size of each individual claim. In this article we introduce a novel regression framework for compound distributions that uses a copula to accommodate the association between the frequency and the severity variables and, thus, allows for arbitrary dependence between the two components. We further show that the new model is very flexible and is easily modified to account for incomplete data due to censoring or truncation. The flexibility of the proposed model is illustrated using both simulated and real data sets. In the analysis of granular claims data from property insurance, we find substantive negative relationship between the number and the size of insurance claims. In addition, we demonstrate that ignoring the frequency-severity association could lead to biased decision-making in insurance operations.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 381–408
https://doi.org/10.1214/19-AOAS1306

ESTIMATING AND FORECASTING THE SMOKING-ATTRIBUTABLE MORTALITY FRACTION FOR BOTH GENDERS JOINTLY IN OVER 60 COUNTRIES

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Smoking is one of the leading preventable threats to human health and a major risk factor for lung cancer, upper aerodigestive cancer and chronic obstructive pulmonary disease. Estimating and forecasting the smoking attributable fraction (SAF) of mortality can yield insights into smoking epidemics and also provide a basis for more accurate mortality and life expectancy projection. Peto et al. (*Lancet* **339** (1992) 1268–1278) proposed a method to estimate the SAF using the lung cancer mortality rate as an indicator of exposure to smoking in the population of interest. Here, we use the same method to estimate the all-age SAF (ASAF) for both genders for over 60 countries. We document a strong and cross-nationally consistent pattern of the evolution of the SAF over time. We use this as the basis for a new Bayesian hierarchical model to project future male and female ASAF from over 60 countries simultaneously. This gives forecasts as well as predictive distributions that can be used to find uncertainty intervals for any quantity of interest. We assess the model using out-of-sample predictive validation and find that it provides good forecasts and well-calibrated forecast intervals, comparing favorably with other methods.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 409–432
https://doi.org/10.1214/19-AOAS1311

MEASURING HUMAN ACTIVITY SPACES FROM GPS DATA WITH DENSITY RANKING AND SUMMARY CURVES

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Activity spaces are fundamental to the assessment of individuals' dynamic exposure to social and environmental risk factors associated with multiple spatial contexts that are visited during activities of daily living. In this paper we survey existing approaches for measuring the geometry, size and structure of activity spaces, based on GPS data, and explain their limitations. We propose addressing these shortcomings through a nonparametric approach called density ranking and also through three summary curves: the mass-volume curve, the Betti number curve and the persistence curve. We introduce a novel mixture model for human activity spaces and study its asymptotic properties. We prove that the kernel density estimator, which at the present time, is one of the most widespread methods for measuring activity spaces, is not a stable estimator of their structure. We illustrate the practical value of our methods with a simulation study and with a recently collected GPS dataset that comprises the locations visited by 10 individuals over a six months period.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 433–451
https://doi.org/10.1214/19-AOAS1312

A COMPARISON OF PRINCIPAL COMPONENT METHODS BETWEEN MULTIPLE PHENOTYPE REGRESSION AND MULTIPLE SNP REGRESSION IN GENETIC ASSOCIATION STUDIES

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Principal component analysis (PCA) is a popular method for dimension reduction in unsupervised multivariate analysis. However, existing ad hoc uses of PCA in both multivariate regression (multiple outcomes) and multiple regression (multiple predictors) lack theoretical justification. The differences in the statistical properties of PCAs in these two regression settings are not well understood. In this paper we provide theoretical results on the power of PCA in genetic association testings in both multiple phenotype and SNP-set settings. The multiple phenotype setting refers to the case when one is interested in studying the association between a single SNP and multiple phenotypes as outcomes. The SNP-set setting refers to the case when one is interested in studying the association between multiple SNPs in a SNP set and a single phenotype as the outcome. We demonstrate analytically that the properties of the PC-based analysis in these two regression settings are substantially different. We show that the lower order PCs, that is, PCs with large eigenvalues, are generally preferred and lead to a higher power in the SNP-set setting, while the higher-order PCs, that is, PCs with small eigenvalues, are generally preferred in the multiple phenotype setting. We also investigate the power of three other popular statistical methods, the Wald test, the variance component test and the minimum p-value test, in both multiple phenotype and SNP-set settings. We use theoretical power, simulation studies, and two real data analyses to validate our findings.

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Key words and phrases. Dimension reduction, principal component analysis, eigen-values, hypothesis testing, multiple phenotypes, minimum p-value test, SNP-set, variance-component test.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 452–472
https://doi.org/10.1214/19-AOAS1316

ESTIMATING CAUSAL EFFECTS IN STUDIES OF HUMAN BRAIN FUNCTION: NEW MODELS, METHODS AND ESTIMANDS

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Neuroscientists often use functional magnetic resonance imaging (fMRI) to infer effects of treatments on neural activity in brain regions. In a typical fMRI experiment, each subject is observed at several hundred time points. At each point, the blood oxygenation level dependent (BOLD) response is measured at 100,000 or more locations (voxels). Typically, these responses are modeled treating each voxel separately, and no rationale for interpreting associations as effects is given. Building on Sobel and Lindquist (*J. Amer. Statist. Assoc.* **109** (2014) 967–976), who used potential outcomes to define unit and average effects at each voxel and time point, we define and estimate both "point" and "cumulated" effects for brain regions. Second, we construct a multisubject, multivoxel, multirun whole brain causal model with explicit parameters for regions. We justify estimation using BOLD responses averaged over voxels within regions, making feasible estimation for all regions simultaneously, thereby also facilitating inferences about association between effects in different regions. We apply the model to a study of pain, finding effects in standard pain regions. We also observe more cerebellar activity than observed in previous studies using prevailing methods.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 473–493
https://doi.org/10.1214/19-AOAS1315

A HIERARCHICAL DEPENDENT DIRICHLET PROCESS PRIOR FOR MODELLING BIRD MIGRATION PATTERNS IN THE UK

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Environmental changes in recent years have been linked to phenological shifts which in turn are linked to the survival of species. The work in this paper is motivated by capture-recapture data on blackcaps collected by the British Trust for Ornithology as part of the Constant Effort Sites monitoring scheme. Blackcaps overwinter abroad and migrate to the UK annually for breeding purposes. We propose a novel Bayesian nonparametric approach for expressing the bivariate density of individual arrival and departure times at different sites across a number of years as a mixture model. The new model combines the ideas of the hierarchical and the dependent Dirichlet process, allowing the estimation of site-specific weights and year-specific mixture locations, which are modelled as functions of environmental covariates using a multivariate extension of the Gaussian process. The proposed modelling framework is extremely general and can be used in any context where multivariate density estimation is performed jointly across different groups and in the presence of a continuous covariate.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 494–517
https://doi.org/10.1214/19-AOAS1295

BAYESIAN MIXED EFFECTS MODELS FOR ZERO-INFLATED COMPOSITIONS IN MICROBIOME DATA ANALYSIS

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Detecting associations between microbial compositions and sample characteristics is one of the most important tasks in microbiome studies. Most of the existing methods apply univariate models to single microbial species separately, with adjustments for multiple hypothesis testing. We propose a Bayesian analysis for a generalized mixed effects linear model tailored to this application. The marginal prior on each microbial composition is a Dirichlet process, and dependence across compositions is induced through a linear combination of individual covariates, such as disease biomarkers or the subject's age, and latent factors. The latent factors capture residual variability and their dimensionality is learned from the data in a fully Bayesian procedure. The proposed model is tested in data analyses and simulation studies with zero-inflated compositions. In these settings and within each sample, a large proportion of counts per microbial species are equal to zero. In our Bayesian model a priori the probability of compositions with absent microbial species is strictly positive. We propose an efficient algorithm to sample from the posterior and visualizations of model parameters which reveal associations between covariates and microbial compositions. We evaluate the proposed method in simulation studies, and then analyze a microbiome dataset for infants with type 1 diabetes which contains a large proportion of zeros in the sample-specific microbial compositions.

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Key words and phrases. Truncated dependent Dirichlet processes, latent factor model, type 1 diabetes.

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The Annals of Applied Statistics
2020, Vol. 14, No. 1, 518–520
https://doi.org/10.1214/19-AOAS1320
Main article: https://doi.org/10.1214/16-AOAS1001

CORRECTION: SENSITIVITY ANALYSIS FOR AN UNOBSERVED MODERATOR IN RCT-TO-TARGET-POPULATION GENERALIZATION OF TREATMENT EFFECTS

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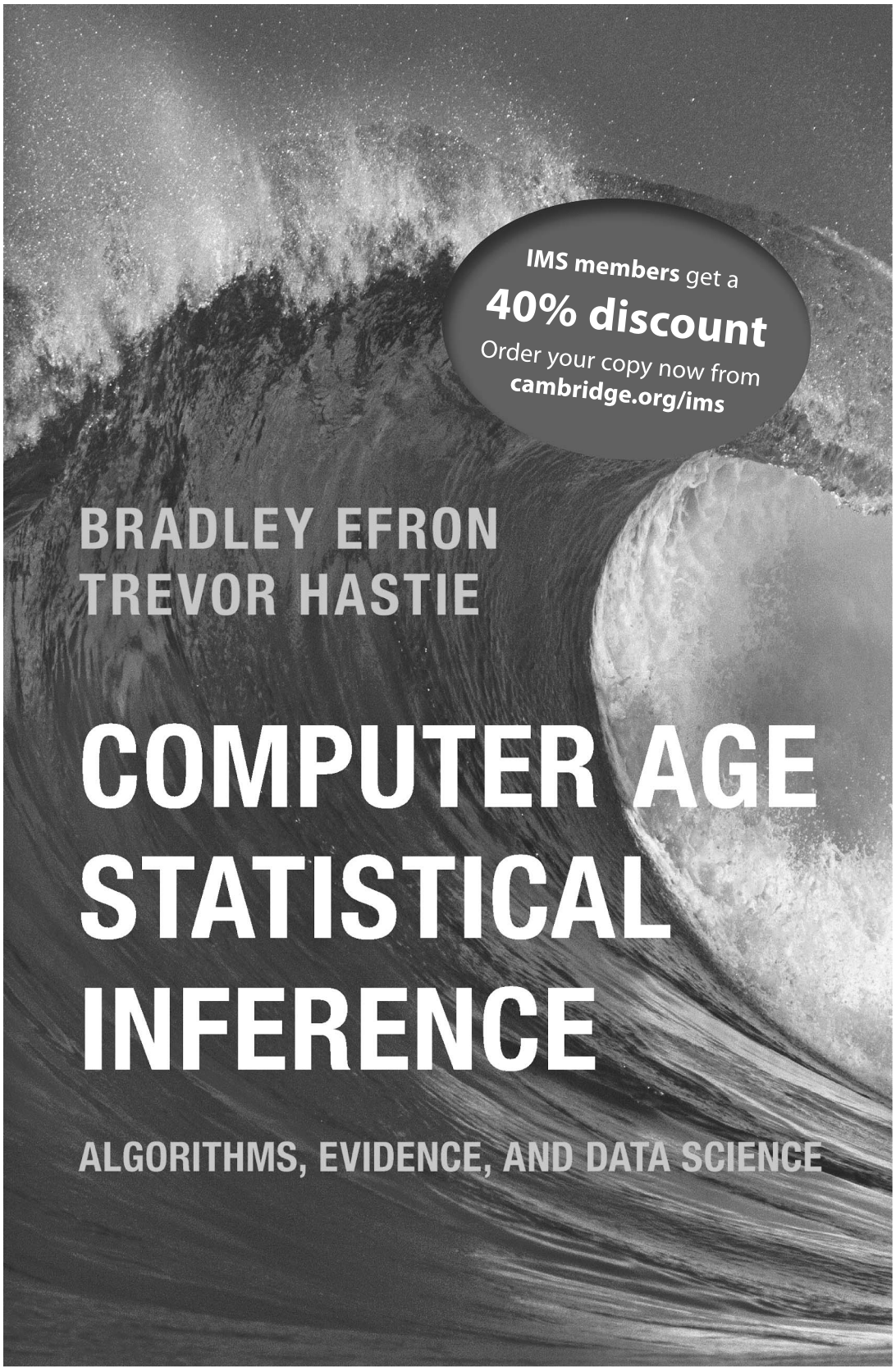
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