physicians, neuropsychologists, and students fully understand this syndrome and the progressions being made to help. Lastly, another benefit of this review is the correlations for treatments that may help those suffering from other chronic pain syndromes/disorders.

Posters

FORCASTING ERRORS IN STUDENT MEDIA MULTITASKING DURING HOMEWORK COMPLETION. Christopher A. Baker, Brittany E. Noah, Charles C. Calderwood, Jeffrey D. Green, Jennifer A. Joy-Gaba & Jaclyn M. Moloney, Department of Psychology, Virginia Commonwealth University, Richmond VA 23284-2018. Many students report that they multitask with media while doing homework, but we know very little about why they engage in these behaviors, when considering that they are damaging to their homework performance. We conducted a study to explore the nature and accuracy of students' predictions regarding media multitasking during homework completion. Sixty-one participants from an undergraduate psychology class predicted their mood and performance if they were and were not allowed to multitask. Participants then worked on their homework in the lab while providing mood ratings. We also obtained student permission to access homework grades. It was found that students predicted they would experience lower negative mood and performance if allowed to media multitask, but overestimated the impact of media multitasking on negative mood.

Statistics

SIMPLE GRAPHS IN POLICY PERSUASION: EXAMPLES FROM HARRISONBURG VIRGINIA AND THE U.S. SENATE. Panayotis Giannakouros[1], Lihua Chen[2], [1]Center for Computational Mathematics & Modeling, James Madison University, Harrisonburg VA, 22801, [2]Department of Mathematics & Statistics, James Madison University, Harrisonburg VA, 22801. The American Statistical Association's Ethical Guidelines for Statistical Practice call upon statisticians to "improve the public climate for, understanding of, and respect for the use of statistics throughout its range of applications." This includes supporting sound statistical practice toward serving the needs of society. In this regard, challenges can range from distrust of statistics to an over-reliance on technical procedures that can distort how problems are analyzed or can present a false sense of authority. This talk reports on a research program addressing such challenges by promoting, particularly to policy oriented economists, sensitivity to the philosophy of science and emphasis of the role of communication and data analysis to steer toward a sound and effective balance in statistical practice. We illustrate by showing how simple graphs have been provided by us in this spirit to support policy decisions in Harrisonburg Virginia and others to advocate for policy on the floor of the U. S. Senate.

THE APPLICATION OF LAST OBSERVATION CARRIED FORWARD (LOCF) IN THE PERSISTENT BINARY CASE. Jun He, Donna McClish, Department of Biostatistics, Virginia Commonwealth University, Richmond, VA 23298. In randomized clinical trials, patients often drop out before study completion, resulting in missing data. Last Observation Carried Forward (LOCF), a common method of imputation, assumes that after the point of dropout the last observed outcome is used in place of missing observation. We investigate this methods performance in analyzing persistent binary outcomes (once it occurs it will not change in the future). We ran a simulation study to see the effect of dropout rate and type of dropout (random or associated with treatment arm) on Type I error for the LOCF method of analysis. We also compared LOCF results to two versions of complete case analysis - Complete1 (excluding all observations with missing data), and Complete2 (excluding missing data when the event hasn't been observed to occur, but carrying forward observations if the event is observed to occur). LOCF was also applied to a real dataset – mammography rates in the Women Improving Screening through Education and Risk Assessment (WISER) clinical study, which had a high dropout rate. 1) If the dropout rates were equal, the three analysis methods all had appropriate Type I error; 2) If the dropout rates were unequal, the Type I error was much greater than 0.05 in both LOCF and Complete2 analysis; 3) Regardless of dropout rates, the estimated mean event rate was underestimated in the LOCF analysis and overestimated in the Complete2 analysis, while Complete1 analysis had the closest estimated mean event rate to the Full dataset. In the WISER study, we found that LOCF method underestimated final event rate.

MODELING CENSORED DISCRETE SURVIVAL TIME IN HIGH-DIMENSIONAL SETTINGS. Kyle Ferber, Kellie J. Archer, Department of Biostatistics, VA Commonwealth University, Richmond, VA 23298. The defining characteristic of high-dimensional data is that the number of subjects, n, is much smaller than the number of features, p. The design matrix will be singular in these situations, so standard regression techniques such as ordinary least squares are not appropriate. Regularization, also referred to as penalization, introduces bias into the parameter estimates in exchange for a reduction in variance, resulting in more stable estimates. This has been shown to be an effective method for modeling high-dimensional data. The generalized monotone incremental forward stagewise (GMIFS) algorithm is capable of fitting a penalized ordinal response model to high-dimensional data. Furthermore, a forward continuation ratio model with a complementary log-log link is appropriate for modeling discrete survival data in high-dimensions. We altered the log-likelihood of this model to account for the presence of censored observations and used the GMIFS algorithm to fit a model to predict short-, intermediate-, and long-term survival in patients diagnosed with acute myeloid leukemia (AML). The dataset contained $p = 270$ covariates including clinical data as well as proteomic data from $n = 191$ patients diagnosed with AML. We tested the performance of our method by examining the prediction accuracy of the fitted model in terms of resubstitution error and cross validation. The results demonstrated that our model is effective for modeling discrete survival time.

SEMIPARAMETRIC SINGLE-INDEX MODELING FOR SPATIALLY CORRELATED DATA. Hamdy. F. F. Mahmoud, Inyoung, Kim, Department of Statistics, Virginia Polytechnic Institute & State University, Blacksburg, VA 24061. In this paper, we propose two semiparametric single index models for spatially correlated data. One additively separates the nonparametric function and spatially correlated random effects, while the other does not separate the nonparametric function and spatially correlated random effects. We estimate these two models using two algorithms based on Markov Chain Expectation Maximization algorithm. Our approaches are compared using simulations, suggesting that the semiparametric single index nonadditive model provides more accurate estimates of spatial correlation. The advantage of our approach is demonstrated using the mortality data of seven cities, South Korea from January, 2000 to December, 2007.

BAYESIAN INFERENCE OF MULTILEVEL MODEL WITH SPATIALLY VARYING COEFFICIENTS. H. Moradi Rekabdarkolaee, Department of Statistical Sciences & Operations Research, Virginia Commonwealth University, Richmond, VA, 23284-3083. In spatial data analysis, sometimes we face to cases which the data are nested in different geological category, thus has intra class correlation. In addition, the response variable and covariates in first level are depend to second level variables, so we face to a multilevel problem. This setting is a generalization of linear models which along with modeling of response variable, the coefficients will be modeling too. In this study, we introduce an extended multilevel spatial model in which the coefficients are also spatially varying. Hence, it could provide more flexibility in modeling. The analysis is performed under a Bayesian paradigm and the MCMC method is developed to carry out posterior analysis. The proposed methodology is illustrated through an application to a data set of canopy vegetation percentage of Plour region at north of Iran.

GENERALIZING MCFADDEN'S CONDITIONAL LOGIT MODEL WITH GAUSSIAN COPULA. Arjun Poddar, N. Rao Chaganty, Department of Mathematics & Statistics, Old Dominion University, Norfolk VA 23529. Conditional logit model is a widely popular method to analyze discrete choice data. Originally publicized by McFadden (1974), this model assumes that the random components of the underlying utility functions follow independent Gumbel distributions. However, in practice the independence assumption may be violated and a more reasonable model should account for the dependence. In this research we use the Gaussian copula with compound symmetric correlation matrix to construct a general multivariate model for the joint distribution of the utilities. The induced dependence on the utilities and the choice probabilities are studied using analytic expressions and simulations. For regression with consumer and product specific covariates, we derive expressions for the likelihood function, score functions and the Fisher information. We use numerical methods and computer code to obtain the maximum likelihood estimates and standard errors.

Comparison of our model with other competing methods and practical applicability is illustrated using real world consumer preference data.

SIMULATING DEPENDENT BINARY DATA WITH RANDOM EFFECTS. Aobo Wang, Roy T. Sabo, Department of Biostatistics, Virginia Commonwealth University, Richmond, Virginia 23298-0032. Dependent binary data can be simply simulated using the multinomial sampling method. We extend this method to simulate dependent binary data with clustered random effect structures. Several distributions are considered for constructing random effects among cluster-specific parameters and effect sizes, including the normal, uniform and beta distributions. We present results from simulation studies to show proof of concept for the multinomial sampling method in creating data sets of repeated-measure binary outcomes with clustered random effect structures in various scenarios. The simulation studies show that multinomial sampling method can be successfully adapted to simulate dependent binary data with desired random effect structures.

COMPOSITIONAL DATA ANALYSIS. Theodore Chang, Department of Statistics, University of Virginia, Charlottesville, VA 22904-4135. Suppose we have a sample of rocks and $x_1,..., x_p$ is the weight of p minerals within the rock. Usually we assume that $x_1 + ... + x_p$ represents the total weight of a sample element, so x_p might be 'other'. Then $x_1,..., x_p$ are called the 'open' variables. Let $y_i = x_i / (x_1 + ... + x_p)$ denote the proportions, or 'closed' variables, such that $y_1 + ... + y_p = 1$. This is an example of compositional data. Another example might be data on time allocation: e.g. x_1 is the time spent eating, x_2 the time spent watching TV, etc.. John Aitchison (JRSS B 1982) proposed an approach to analyzing this type of data. We examine the geometry of moving from open to closed variables and, in that light, the mathematical attractiveness of the Aitchison approach.

Structural Biology, Biochemistry, and Biophysics

BIOPHYSICAL CHARACTERIZATION OF NATURALLY OCCURING TITIN M10 MUTATIONS. Michael W. Rudloff, Alec N. Woosley & Nathan T. Wright. Department of Chemistry & Biochemistry, James Madison University, Harrisonburg, Virginia 22807. The giant proteins titin and obscurin are important for sarcomeric organization, stretch response, and sarcomerogenesis in myofibrils. The extreme C-terminus of titin (the M10 domain) binds to the N-terminus of obscurin (the Ig1 domain) in the M-band. The high-resolution structure of human M10 has been solved, along with M10 bound to one of its two known molecular targets, the Ig1 domain of obscurin-like. Multiple M10 mutations are linked to limb-girdle muscular dystrophy type 2J (LGMD2J) and tibial muscular dystrophy (TMD). The effect of the M10 mutations on protein structure and function has not been thoroughly characterized. We have engineered all four of the naturally occurring human M10 missense mutants and