An Introduction to Second-generation p-values and Their Use in Statistical Practice

Instructors: Jeffrey D. Blume, School of Data Science, University of Virginia, and Megan H. Murray, Biostatistics, Vanderbilt University

When: Saturday, October 22, 2022, 10 AM – 1 PM

Location: via Zoom (link will be posted on Eventbrite.com)

Cost: $15 general/$0 students and retirees

Registration: will be available on Eventbrite.com

Abstract: Second-generation p-values were recently proposed to address the well-known imperfections of classical p-values. Their implementation can largely be thought of as codifying ‘good standard practice’ for interpreting and reporting classical p-values. Second-generation p-values maintain the favorable properties of classical p-values while emphasizing scientific relevance to expand their utility, functionality, and applicability. In particular, they can report evidence in favor of the alternative, in favor of the null hypothesis, or neither (inconclusive); they automatically incorporate an adjustment for multiple comparisons and multiple looks; they have lower false discovery rates than classical p-values; and they are easier to interpret. Second-generation p-values have been shown to work well in regularized models. They also lead to significantly improved model selection procedures in linear and generalized linear models. Also, second-generation p-values are non-denominational in the sense that they are readily applied in frequentist, likelihood and Bayesian settings.
Outline and Objectives: This course will briefly revisit the history of p-values as originally envisioned in significance and hypothesis testing, and the resulting controversy over their scientific interpretation. The importance of distinguishing between three key inferential quantities (the measure of the strength of evidence, design error rates, and false discovery rates for observed data) will be illustrated. The second-generation p-value will be introduced and contrasted with standard methods. The workshop will explain how to design studies in which the second-generation p-value is used as the primary mode of inference. We will cover computation of second-generation p-values (in R), guidelines for presenting results, and when appropriate, how to present accompanying false discovery rates. Multiple examples will be presented using data from clinical trials, observations studies and high-dimensional analysis of large-scale data. Advanced applications in model selection, adaptive monitoring of clinical trials, and regularized models will be shown if time allows. Mathematical details will be kept to a minimum, e.g., statistical properties will be presented but without mathematical proof.

About the instructors:

- **Jeffrey D. Blume, Ph.D.** is the Quantitative Foundation Associate Dean for Academic and Faculty Affairs and Professor of Data Science at the School of Data Science at the University of Virginia. He recently moved from Vanderbilt University where he served as Vice-Chair for Education in the Department of Biostatistics and Director of Graduate Education in the Data Science Institute. Professor Blume is a fellow of the American Statistical Association and has extensive experience in the operation, analysis, and methodological aspects of Clinical Trials and in the analysis of a wide array of biomedical research. He has won numerous awards for his teaching and mentoring, and for his work on racial disparities in lung cancer screening. His statistical research focuses on the foundations of statistical inference, mediation modeling, diagnostic clinical trials and prediction modeling. Professor Blume has published extensively on the foundations of statistical inference, particularly on likelihood methods for measuring statistical evidence, and he authored the origin publications on second-generation p-values.

- **Megan H. Murray** is a Ph.D. candidate in Biostatistics at Vanderbilt University working with Professor Blume. Her methods research focuses on evaluating and extending the statistical properties of second-generation p-values and on characterizing false discovery rate methodology. She recently co-authored a paper describing her development of a R package (“FDRestimation”) for computing, estimating, and visualizing false discovery rates (currently on CRAN). Her biomedical research has focused in the areas of lung cancer, particularly in assessing racial disparities in lung cancer diagnosis, and of graduate student survey data, specifically evaluating if a positive mentor experience leads to more published papers or shorter time to graduation. Megan has won several teaching awards in both Biostatistics and Data Science at Vanderbilt.