Department of Biomedical Informatics

Arizona State University

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Biomedical Informatics Weekly Seminar Series

From Linkage Disequilibrium Mapping to NGS of Complex Traits: Modeling, Solution and Examples

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April 13th, 2017 (2:45 p.m. – 4:00 p.m)
Room Sj 1-149 , Samuel C. Johnson Research Bldg.
Mayo Clinic Scottsdale

Speaker's Bio: Jiangtao Luo is an Assistant Professor in the Department of Biostatistics at University of Nebraska Medical Center. Dr. Luo is an expert in statistical computing, research design, linear models, generalized linear models, longitudinal data analysis, survival analysis, clinical trials and Bayesian methods. He has conducted research designs and statistical consulting services for biomedical research for more than 10 years. In addition to methodology research in statistics, Dr. Luo's research focus is on the application of statistics in computational biology, public health, genetics, and genomics (next generation sequence, RNA expression, protein expression, QTL etc.).

Dr. Luo completed his PhD in Statistics at University of Florida and his post-doctoral training at Penn State Medical Center. Dr. Luo has collaborated with physicians, nurses, dentists, cardiologists, surgeons, oncologists, geneticists etc., and he has published 40 peer-reviewed papers and served as biostatistician on numerous research projects. Currently he is the study biostatistician for 3 RO1 projects with a total funding of more than $10M. Dr. Luo has served as the biostatistician reviewer for three national review panels, the Data Safety and Monitoring Committee of Buffett Cancer Center for two years and the Clinical Trial and Transitional Center for five years.

Talk Abstract: In genetic mapping of complex traits using molecular markers, we often face the challenge of solving a mixture model with multiple components specified by a frequency structure different from ordinary mixture models. We describe an elegant algorithm to solve this special form of mixture model, showing great power for gene detection. We prove that our estimators are a hybrid of conditional Newton's method and EM algorithm and obey a Rao-Blackwellization process. These estimators are not only asymptotically consistent, but also have small standard errors. We further prove a capture theorem and quadratic convergence of the algorithm. Computer simulation is used to test the algorithm, with results supporting our theoretical findings. The new algorithm is used to analyze genetic data from an obesity genetic project, validating its practical usefulness and utilization.

NGS and related recent research advances are also discussed.