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**ZHIJIAN CHEN**, Samuel Lunenfeld Research Institute

*Sequential Two-Phase Stratified Designs for Regional Sequencing Following Genome-Wide Association Study: A Bayesian Approach*

In focused follow-up studies, investigators may choose to sequence an entire genomic region of interest at the base pair level to identify potential causal variants. We consider Bayesian sequential two-phase designs, in which a subset of phase 1 subjects are selected from genotype categories of a genetic marker and sequenced in a target region in phase 2. At each sampling point, we apply Bayesian model averaging to account for genetic model uncertainty with an adaptive sample size allocation strategy to improve estimation efficiency of the genetic association parameter. We present numerical results for quantitative and binary traits.