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Guifang Fu* (gfu@math.binghamton.edu), Department of Mathematical Sciences, Binghamton University, Vestal, NY, and **Randall Reese** and **Xiaotian Dai**. *Interaction Feature Screening for Ultrahigh Dimensional Data*.

Big data with ultrahigh dimensions has become increasingly important in diverse scientific fields. For example, genome-wide association studies identify important loci by screening over half a million single-nucleotide polymorphisms (SNPs). Clinical study findings imply that complex diseases are very likely regulated by interactions among multiple genes (i.e., epistasis) rather than by one genetic variant within a single gene. However, selecting important interaction effects from an ultrahigh dimension of features is extremely challenging in terms of computational feasibility and statistical accuracy. In this presentation, I introduce a novel interaction screening procedure based on the joint cumulant correlation (JCM-SIS). The implementation of JCM-SIS does not require model specification or data type restriction for responses or predictors. We have performed four simulations under various conditions to comprehensively demonstrate that JCM-SIS is empirically accurate, robust, and computationally viable for features in ultrahigh dimensional space. We apply JCM-SIS to screen two-way interactions for 731,442 SNPs, a computational feat unprecedented in current literature. We also prove that JCM-SIS is theoretically sound and possesses strong sure screening consistency. . (Received August 15, 2019)