Biostatistics

405  H. Hung, C.-Y. Liu, H. Horng-Shing Lu
Sufficient dimension reduction with additional information

422  S. V. Masiuk, S. V. Shklyar, A. G. Kukush, R. J. Carroll, I. N. Kovgan, I. A. Likhtarov
Estimation of radiation risk in presence of classical additive and Berkson multiplicative errors in exposure doses

437  Y. Zhong, R. J. Cook
Augmented composite likelihood for copula modeling in family studies under biased sampling

453  E. E. Gabriel, D. Follmann
Augmented trial designs for evaluation of principal surrogates

468  C. Luo, J. Liu, D. K. Dey, K. Chen
Canonical variate regression

484  K. Hasenstab, C. Sugar, D. Telesca, S. Jeste, D. Şentürk
Robust functional clustering of ERP data with application to a study of implicit learning in autism

499  Y. Huang
Evaluating and comparing biomarkers with respect to the area under the receiver operating characteristics curve in two-phase case-control studies

523  S. B. Kim, S. M. Bartell, D. L. Gillen
Inference for the existence of hormetic dose–response relationships in toxicology studies

537  K. H. Hellton, M. Thoresen
Integrative clustering of high-dimensional data with joint and individual clusters

549  Y. Zang, S. Liu, Y. Yuan
Optimal marker-strategy clinical trial design to detect predictive markers for targeted therapy

Efficient quantile marginal regression for longitudinal data with dropouts

576  J. P. Kim, T. Sit, Z. Ying
Accelerated failure time model under general biased sampling scheme

589  D. Xu, M. J. Daniels, A. G. Winterstein
Sequential BART for imputation of missing covariates

603  T. Sugimoto, T. Sozu, T. Hamasaki, S. R. Evans
Corrigendum: A logrank test-based method for sizing clinical trials with two co-primary time-to-event endpoints