

Biostatistics

- 1 R. Salway, J. Wakefield**
A hybrid model for reducing ecological bias
- 18 R. Tibshirani, P. Wang**
Spatial smoothing and hot spot detection for CGH data using the fused lasso
- 30 M. Y. Park, T. Hastie**
Penalized logistic regression for detecting gene interactions
- 51 H. Shim, S. Keleş**
Integrating quantitative information from ChIP-chip experiments into motif finding
- 66 J.-L. Dortet-Bernadet, N. Wicker**
Model-based clustering on the unit sphere with an illustration using gene expression profiles
- 81 Y.-H. Chen, N. Chatterjee, R. J. Carroll**
Retrospective analysis of haplotype-based case-control studies under a flexible model for gene-environment association
- 100 Y. Luan, H. Li**
Group additive regression models for genomic data analysis
- 114 R. Feng, H. Zhang**
A score test for linkage analysis of ordinal traits based on IBD sharing
- 128 D. Amaratunga, J. Cabrera, V. Kovtun**
Microarray learning with ABC
- 137 R. M. Pfeiffer, R. J. Carroll, W. Wheeler, D. Whitby, S. Mbulaiteye**
Combining assays for estimating prevalence of human herpesvirus 8 infection using multivariate mixture models
- 152 R. H. Keogh**
Inverse sampling of controls in a matched case-control study
- 159 T. J. Cole, M. Cortina-Borja, J. Sandhu, F. P. Kelly, H. Pan**
Nonlinear growth generates age changes in the moments of the frequency distribution: the example of height in puberty
- 172 R. D. Riley, J. R. Thompson, K. R. Abrams**
An alternative model for bivariate random-effects meta-analysis when the within-study correlations are unknown
- 187 H. Schwender, K. Ickstadt**
Identification of SNP interactions using logic regression
- 199** *Biostatistics* - Referees of Manuscripts Submitted Mid-2006 to Mid-2007