Variance component model to account for sample structure in genome-wide association studies

Hyun Min Kang[1,2,8], Jae Hoon Sul[3,8], Susan K Service[4], Noah A Zaitlen[5], Sit-yee Kong[4], Nelson B Freimer[4], Chiara Sabatti[6] & Eleazar Eskin[3,7]

Rapid variance components–based method for whole-genome association analysis

Gulnara R Svishcheva[1], Tatiana I Axenovich[1], Nadezhda M Belonogova[1], Cornelia M van Duijn[2] & Yurii S Aulchenko[1]

Genome-wide efficient mixed-model analysis for association studies

Xiang Zhou[1] & Matthew Stephens[1,2]

Mixed linear model approach adapted for genome-wide association studies

Zhiwu Zhang[1], Elhan Ersoz[1], Chao-Qiang Lai[2], Rory J Todhunter[3], Hemant K Tiwari[4], Michael A Gore[5], Peter J Bradbury[6], Jianming Yu[7], Donna K Arnett[8], Jose M Ordovas[2,9] & Edward S Buckler[1,6]