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Mixed linear model approaches of association mapping for complex traits based on omics variants

Complex traits are controlled by 4 omics variants of SNPs, transcripts, proteins, and metabolites. We proposed mixed linear model approaches for association mapping SNPs (QTSs), transcripts (QTTs), proteins (QTPs) and metabolites (QTMs) to complex traits. Precise prediction for genetic architecture of complex traits has been impeded by the limited understanding on genetic effects of complex traits, especially on locus-by-locus interaction (GxG) and locus-by-environment interaction (GxE). The analysis of large omics datasets, especially two-loci interaction analyses, involves intensive computation. A GPU-based mapping software (QTXNetwork) has been developed for detecting multiple loci on large-scale omics data, and for estimating variance components of genetic effects. By analyzing datasets of SNPs and transcripts for mouse and drosophila datasets, we demonstrated that unbiased estimation could be obtained for genetic effects of causal loci. Transcript association can efficiently detect causal transcript loci on complex traits (QTTs), and on other transcripts (tQTTs), proteins (tQTPs) and metabolites (tQTMs). Association mapping for startle in *Drosophila* revealed high heritability for 85 QTTs (0.996) and 48 QTSs (0.935). The QTTs were also controlled by other 86 tQTTs (0.804~0.998) and 25 tQTSs (0.115~0.423). Both real data analyses and Monte Carlo simulations demonstrated that genetic effects and environment interaction effects could be estimated with no bias and high statistical power by using the proposed approaches.

Biography

Jun Zhu has completed his PhD co-major in Statistics and Genetics from NC State University and Post-doctoral studies from NC State University Department of Statistics. He is now the Director of Institute of Bioinformatics, and has been serving as Dean of College and Vice-President in Zhejiang University. He has published more than 260 papers with more than 9000 citations in reputed journals.

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