

Statistics Seminar

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Zoom

BiNetPeR: A Bipartite Network-Based Penalized Regression Method For eQTL Mapping

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Abstract: Identification and characterization of the expression quantitative trait loci (eQTLs), the genetic variations that regulate the expression of genes can greatly help us better understand the cellular mechanisms underlying human complex diseases. With the accumulation and the availability of a large volume of gene expression data and single nucleotide polymorphism (SNP) genotype data, it is important and challenging to develop more powerful statistical methods and more efficient computational tools for the eQTL mapping. In this paper, we propose a new method called BiNetPeR (Bipartite Network-based Penalized Regression) to identify the eQTLs. Most of the existing methods that use the SNP-SNP network generally construct the SNP-SNP network only from the SNP information and/or the SNP genotypes without the consideration the gene expression data or the relationship between the SNPs and the gene expression. BiNetPeR utilizes the SNP-SNP network projected from the SNP-gene bipartite network which is constructed based on the significant marginal associations between the SNPs and the gene expression levels. BiNetPeR also uses the Laplacian matrix of SNP-SNP network to control the amount of regularization for smoothness in the penalized regression. We perform the extensive simulation studies to evaluate and compare the performance of our proposed method with two commonly methods, FastLORS and mtLasso2G. Simulation studies show that our method outperforms FastLORS and mtLasso2G in terms of average Area Under the Curve (AUC) in most situations.

Bio: Dr. Kui Zhang holds the Dave House Endowed Professorship in Statistics, Data Mining and Data Analytics at Michigan Tech. He obtained his PhD in probability and statistics from Beijing University in 1999 and joined the Department of Mathematical Sciences at Michigan Technological University as a full professor in August of 2015.

Dr. Zhang did his postdoctoral training in statistical genetics at Yale University from 1999 to 2001 and at University of Southern California from 2001 to 2003. He was a faculty member in the Department of Biostatistics at the University of Alabama at Birmingham from 2003 to 2015. Dr. Zhang has published more than 100 papers in peer reviewed journals and had a number of grants funded by NIH.

Dr. Zhang's methodological research interests focus on the development of novel statistical methods and efficient computational and bioinformatics tools to address scientific problems in biomedical fields, especially in statistical genetics and statistical genomics. He has also been actively involved in many applied studies during his research career.