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Alternative direction minimization methods for phenotype prediction and variable selection

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Abstract

Next generation sequencing (NGS) technologies will generate unprecedentedly massive (thousands or even ten thousands of individuals) and highly-dimensional (ten or even dozens of millions) genomic and epigenomic variation data. Due to advances in measurement technologies and communications, a large panel of physiological data including all medical treatments and outcomes accumulated over the patient's lifetime is monitored and collected. Analysis of these extremely big and diverse types of data sets provide invaluable information for disease prediction, prevention, diagnosis and treatment, but also pose great computational challenges. To address these challenges, we formulate phenotype prediction and variable selection into a sparse sufficient high dimensional reduction problem and develop a novel alternative direction optimization algorithm to solve high dimensional data reduction problem. The developed algorithms were applied to the NHLBI's Exome Sequencing data and whole genome sequencing data with 13 lip metabolism phenotypes. The results are very encouraging. Our works address the paradigm shift in genomic and health care data analysis from standard multivariate data analysis to functional data analysis, from low dimensional data analysis to high dimensional data analysis, from independent sampling to dependent sampling, from single type data analysis to integrate multiple types of data analysis, and from individual PC to parallel computing.

Biography

Momiao Xiong has completed his Ph.D from University of Georgia and postdoctoral studies from University of Southern California. He is Professor in Division of Biostatistics and Human Genetics Center, University of Texas School of Public Health. He has published more than 100 papers in reputed journals and serving as an editorial board member of 12 Journals.