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Data mining of urine H1-NMR data for metabolomics analysis of T2D disease

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This work deals with metabolome screening of blood plasma by nuclear magnetic resonance H1-NMR. The main focus is the bio-marker discovery of T2D disease by means of NMR and pattern recognition methods. Specifically, attention is paid to data acquisition, data pretreatment, data preprocessing and multivariate analysis of metabolomics data. We propose BinPCA or what we called: "metabogram" as a data mining approach for pre-processing data using binning method, for visualizing it using PCA and for reducing the noise and brining the group effect of metabolites using regularized sparse vector machine algorithm to discover the biological variations of metabolites measurable by NMR and other analytical methods. These biological variations in healthy individuals form a base line for detecting significant fluctuations in disease inflicted people. Inter-individual fluctuations in metabolites concentrations in the healthy people versus disease inflicted people are compared with analytical variations and found to be much smaller. In addition, variation in T2D metabolites abundance in gender's and group age is demonstrated.

Biography

Halima Bensmail has completed her Ph.D. from the University of Paris VI and INRIA (France) and postdoctoral studies from University of Washington, Seattle and Fred Hutchinson Cancer Research Center. She held positions of assistant and associate Professor of Biostatistics at the University of Tennessee and E. Virginia Medical School. She is currently a senior scientist and the director of computational sciences and Engineering center at Qatar Computing Research Institute (QCRI), Qatar Foundation. She reviews grants for the American National Institute of Health (NIH), National Science Foundation (NSF), Qatar National Research Funds (QNRF) and Department of Energy (DOE), taught Ph.D. course on computational Bayesian Statistics for System Biology and has published more than 30 papers in reputed journals such as PLOS One, JASA, Bioinformatics, Evolutionary Bioinformatics and served as an associate editor for reputed journal and co-chair for international conferences.

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