

EFFICIENT GENOME-WIDE ASSOCIATION STUDIES AND POST-GWAS INTEGRATIVE ANALYSES FOR HUMAN CANCER AND NEURODEGENERATIVE DISEASES

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It is evident that in etiologies of human complex diseases, genetic factors play some important roles. Genome-wide association study (GWAS) is a standard technique to identify heritable genetic basis of complex diseases. In relation with GWAS, there exist some challenges in selecting input samples completely randomly, to biologically describe GWAS results, to translate them into clinical benefits and to compare germline variants achieved from GWAS with somatic mutations in creating, development and treatment of human complex diseases. Likelihood-based statistical methods are robust in estimating linkage disequilibrium when factors like non-randomness and population structures exist. Then the results of GWAS can be used for post-GWAS analyses to predict multiple biological components like genes, non-coding RNAs and transcription factor binding sites in association with complex diseases. An integrative analysis seeks to pool information from multiple GWAS results, somatic mutations and genetic drug targets of human complex disorders and the results of such analysis can provide new insight into the genetic and treatments of complex diseases. This presentation is prepared from the viewpoint that the robust statistical method can be applied to arrive at valuable results from GWAS and that primarily genetic information derived from GWAS is subject to further post-GWAS analysis to provide more biologically informative results in relation with genetics of human complex diseases that can be applied to real time clinical applications. Then the results of such analyses can be used to discuss and compare human cancers and neurodegenerative diseases from a genetic perspective. We concluded that in spite of the differences between human cancers and neurodegenerative diseases, the roles of germline and somatic mutations in creating, developments and treatments of those two kinds of human complex diseases are similar.

Biography

Zahra Mortezaei has completed her Undergraduate in Mathematics from Amirkabir University of Technology (Tehran Polytechnic), Iran and studied for Mphil degree in Mathematical physics at University of Nottingham (UK). She then completed her PhD in Bioinformatics at University of Birmingham (UK) and the University of Tehran (Iran). She is working as bioinformatician at human genetic research centre in Iran. Her recent papers in the field of Bioinformatics are:

- Mortezaei, Z., Lanjani, H., Masoudi-nejad, A., (2017) Genomics Candidate novel long noncoding RNAs, MicroRNAs and putative drugs for Parkinson's disease using a robust and efficient genome-wide association study. *Genomics*, 109(3-4):158-164.
- Mortezaei, Z., Cazier, J-B., Mehrabi, A.A., Cheng, C. and Masoudi-Nejad, A. (2018) Novel Putative Drugs and Key Initiating Genes for Neurodegenerative Diseases Determined Using Network-Based Genetic Integrative Analysis. *J Cell Biochem*, 1-13.

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