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Estimation of missing values for gene interaction data coming from high throughput technologies

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Advancements in high-throughput genetic screening technologies have enabled us to systematically study how gene interactions between pairs of genes can affect phenotypes of certain traits. However, these advancements also pose other challenges to researchers in the management and analysis of the vast amount of data being produced. One of the problems related with this is the significant amount of missing interaction scores that cannot be scanned by the screening technologies or were filtered out from the datasets for technical reasons. This will significantly affect and bias downstream analysis. Therefore, there is an immediate need to impute those missing data more precisely. This study evaluates existing missing value imputation techniques on large-scale quantitative data matrices from synthetic genetic array (SGA) and epistatic mini array profiling (E-MAP) screening technologies. Different existing methods that are usually applied for imputation purposes were evaluated against various conditions and performance accuracies. This best performing imputation approach, based on weighted correlation between nearest-neighbors', is now modified and can be used in any gene interaction data. Hereby, this study removed the limitation of a method already developed for this purpose and gives a more flexible, optimized and best performing method. This method can now be effectively used in the pre-processing of gene interaction scores by researchers towards a genome-wide analysis such as identification of global functional networks, gene clustering, etc. for a more accurate and less biased results and biological interpretations.

Biography

Gashaw Mekuria is currently a PhD candidate in Biostatistics at University of Tampere School of Health Sciences, Finland. He holds an MSc in Bioinformatics from University of Turku, Finland and a BSc in Statistics from Addis Ababa University, Ethiopia.

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