A COPULA-BASED APPROACH TO DIFFERENTIAL GENE EXPRESSION ANALYSIS

Linda Chaba[1], John Odhiambo[1], Bernard Omolo[2]

[1]Strathmore University; [2]University of South Carolina--Upstate

ABSTRACT

Melanoma is a major public health concern in the developed world. Melanoma research has been enhanced by the introduction of microarray technology, whose main aim is to identify genes that are associated with outcomes of interest in melanoma biology and disease progression. Many statistical methods have been proposed for gene selection but so far none of them is regarded as the standard method. In addition, none of the proposed methods have applied copulas to identify genes that are associated with quantitative traits. In this study, we developed a copula-based approach to identify genes that are associated with quantitative traits in the systems biology of melanoma. To assess the statistical properties of model, we evaluated the power, the false-rejection rate and the true-rejection rate using simulated gene expression data. The model was then applied to a melanoma dataset for validation. Comparison of the copula approach with the Bayesian and other parametric approaches was performed, based on the false discovery rate (FDR), the value of R-square and prognostic properties. It turned out that the copula model was more robust and better than the others in the selection of genes that were biologically and clinically significant.

Key words: copula; gene expression; melanoma; microarray; quantitative trait