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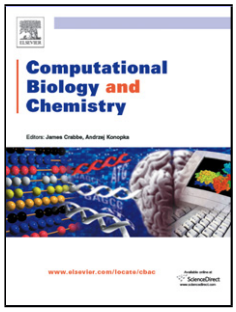

Title: Statistical and artificial neural network-based analysis to understand complexity and heterogeneity in preeclampsia

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Statistical and artificial neural network-based analysis to understand complexity and heterogeneity in preeclampsia

Abstract

Preeclampsia is a pregnancy associated disease. It is characterized by high blood pressure and symptoms that are indicative of damage to other organ systems, most often involving the liver and kidneys. If left untreated, the condition could be fatal to mother and baby. This makes it important to delineate the complexities associated with the disease at a molecular level that would help develop methods for early diagnosis. In microarray-based studies, Textoris et al. and Mirzakhani et al. have analyzed the transcriptome with a view to identify biomarkers for preeclampsia. The current study has extensively analyzed these microarray data sets to understand the complexity and heterogeneity associated with preeclampsia. A statistical multiple comparisons-based approach has been used to identify features capable of distinguishing preeclampsia from normotensive cases. These features were then used to build an artificial neural network-based machine learning model that successfully classified the samples. Further, the machine learning model was used to delineate features critical for its internal representation by extending the calliper randomization approach to the analysis of microarray data. Functional analysis of the features identified by the calliper randomization approach revealed pathways that could be crucially involved in the

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