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The use of artificial intelligence for the prediction of optimal drug therapies in the treatment of ovarian cancer

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A primary goal of precision cancer medicine is the accurate prediction of optimal drug therapies based upon the personalized molecular profiles of patient tumors. We recently introduced open source access to a support vector machine (SVM)-based algorithm for the predictive response of cancers to seven widely prescribed chemotherapeutic drugs. We previously reported the employment of this algorithm to predict the collective sensitivities of 273 ovarian cancer patients to these seven drugs with an observed group accuracy of 82% (Linear regression p value = 0.0031, $R^2 = 0.8201$). In this talk, I report on the use of the algorithm to predict the individual responsiveness of 23 randomly selected ovarian cancer patients to seven chemotherapeutic drugs. The overall accuracy of the model to predict the drug response of these 23 patients was 87%. The potential clinical utility of the algorithm for the identification of promising chemotherapies for the treatment of patients resistant to first-line therapies will be discussed.

Biography

John F McDonald is Professor, School of Biological Sciences and Associate Dean Director of Georgia Institute of Technology. His research interest Using Genomics to design personalize cancer therapies, The role of non-encoding RNAs in cancer cancer stem cell therapy, The application of Nanotechnology to cancer diagnostics and therapy. His research areas mainly include cancer biology, drug design, development and delivery systems biology.

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