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Artificial neural network algorithms for biomarker discovery and pathway modeling

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Cancer is a complex disease with a myriad of forms and prognoses occurring within each type. For example, in breast cancer using genomic profiling in excess of 80 sub types have been identified. The ability to characterize the disease for each patient may offer the potential to assess the molecular sub-type of the disease and thus accurately determine the patients' prognostic outcome. Methodologies such as mass spectrometry-based proteomics, RNASeq and gene expression arrays offer the potential for characterization of disease derived samples using a huge number of proteins or genes. This depth of information while providing a comprehensive overview of a disease state also proves problematic in its complexity. One has to search through potentially hundreds of thousands of pieces of information for consistent features that address a clinical question in the population. The human mind is very good at finding patterns in a system but is not able to conduct the task repetitively for large numbers of parameters. Conversely computers are very good at searching for features in such a data space, but previously defined statistical methods are not able to cope with the high complexity. Here, we present the application of Artificial Neural Networks (ANNs, a form of artificial intelligence having the characteristics of both human pattern recognition and computer automated searching) to finding genomic solutions to questions in cancer. Here, we present the use of a range of statistical and artificial intelligence-based machine learning techniques to develop prognostic models for breast cancer. Here, we present results of use of ANN algorithms for biomarker discovery, whereby we have undertaken a parallel analysis of multiple molecular databases for breast cancer and have identified markers that drive proliferation and thus predict response to anthracycline.

Biography

Graham Ball is Professor of Bioinformatics at Nottingham Trent University and CSO of CompanDX UK and CompanDX China Ltd. He is Associate Director at the John Van Geest Cancer Research Centre and Biostatistics Lead on three clinical projects. He has been involved in the development and validation of bioinformatics algorithms using Artificial Neural Networks for the last 18 years. He has 115 journal papers and five patents in this area. After a PhD, (UN funded) and a Post-Doc modelling environmental interactions with ANNs at NTU, in 2000, he has shifted the focus of his analysis to proteomic and genomic data searching for proteins and genes associated with cancer. His current research interests are directed at the classification and characterization of biological systems including diagnostic and classification modelling of microbial pathogens, cancer clinical pathology, allergic responses and viral diseases through the use of ANNs and other machine learning techniques. He is involved in the molecular characterization of breast cancer with Prof. Ian Ellis' team at Nottingham University Hospitals Trust.

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