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Innate responses were not born equal

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Abstract

The mass of publicly available genomic datasets, incorporate within them valid data that can be very beneficial for clinical decisions. The challenge is to decipher the true signals from the noise. We developed a specially designed method for scanning datasets of responders and non-responders to different treatments and finding the most statistically powerful predictive genomic signatures. The signature found for predicting response to Interferon in HCV patients ,was found to be consistent in similar triggering of the innate response as in Dengue virus, Influenza, Poliovirus, Western Nile and PBMC of healthy people. Realizing that the signature genes are sent to battle with the virus challenge ,mathematical equations can be assigned to describe the battle dynamics, and biological simulations can be carried out to evaluate each individual response, based on these measured gene expressions. This has the benefit of selecting an optimal dose strategy per each patient. Hence these genes serve not only as biomarkers for predicting responders or non responders ,but can enable manipulating the treatment based on the individual 's signature to change the fate of the non responders.

Biography

Yoav Smith has a B.S.E.E from the Electrical Department of the Technion in Haifa Israel, an M.S.E.E. from the University of Pittsburg, USA and a Ph.D from the Hebrew University Medical School ,Jerusalem Israel. In the last 10 years he directs the activity of the Genomic Data Unit in the Hadassah Medical School ,which deals with all aspects of gene expression studies done by many research groups both academic and clinic. His work is published in more than 20 papers in reputed journals along with 4 registered patents and 5 new pending applications for patents. He also is a founder of a startup company in the field of personal medicine. Yoav teaches courses in visualization and analysis of data to Masters and Ph.D level students.