

Industry Practice Expo Invited Talk

Mining the Digital Universe of Data to Develop Personalized Cancer Therapies

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ABSTRACT

The development of a personalized approach to medical care is now well recognized as an urgent priority. This approach is particularly important in oncology, where it is well understood that each cancer diagnosis is unique at the molecular level, arising from a particular and specific collection of genetic alterations. Furthermore, taking a personalized approach to oncology may expedite the treatment process, pre-empting therapeutic decisions based on fewer data in favor of treatments targeted to an individual's tumor. This directed course may be key to survival for many patients who are terminal or have failed standard therapies.

I will discuss a personalized cancer therapy program we have initiated that involves DNA and RNA sequencing of a patient's tumor and germline DNA and the projection of high-dimensional features extracted from these data onto predictive network models constructed by integrating large-scale, high dimensional data that exists for the patient's cancer type. From the causal network inference procedures to the ensemble-based classification methods, big data analytics is front and center for interpreting large-scale patient data in the context of the digital universe of information that exists for the patient's condition.

Categories and Subject Descriptors

I.2.1 [Artificial Intelligence]: Medicine and science.

General Terms

Design, Experimentation, Performance

Keywords

DNA Sequencing; Personalized Cancer Therapies; RNA Sequencing

Bio

Dr. Eric Schadt is Chairman and Professor of the Department of Genetics and Genomic Sciences at the Icahn School of Medicine at Mount Sinai and the Director of the Institute for Genomics and Multiscale Biology at Mount Sinai. Previously, Dr. Schadt had been the Chief Scientific Officer at Pacific Biosciences, overseeing the scientific strategy for the company, including creating the vision for next-generation sequencing applications of the company's technology. Dr. Schadt is also a founding member of Sage Bionetworks, an open access genomics initiative designed to build and support databases and an accessible platform for creating innovative, dynamic models of disease. Dr. Schadt's current efforts at Mount Sinai involve the generation and integration of large-scale, high-dimension molecular, cellular, and clinical data to build more predictive models of disease, a research direction motivated by the genomics and systems biology research he led at Merck to elucidate common human diseases and drug response using novel computational approaches applied to genetic and molecular profiling data. Dr. Schadt received his B.S. in applied mathematics/computer science from California Polytechnic State University, his M.A. in pure mathematics from UCD, and his Ph.D. in bio-mathematics from UCLA (requiring Ph.D. candidacy in molecular biology and mathematics).

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