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EDITORIAL

Diabetes and data in many forms

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Traditionally, capture, analysis, and usage of data were difficult. Information technology has altered the equation between capture and usability: generation of data exploded; constraints exist in analysis and appropriate use.

The rich source of clinical and biochemical data in diabetes was usually recorded on paper. It was efficient to document, but laborious to retrieve and analyze. Availability of information technology revolutionized all these. The use of electronic medical records (EMR) makes it possible to capture biographical, clinical, and biochemical data at one point and on follow-up [1, 2].

In its early years, biological science was descriptive: observing and classifying different parts of the biological system. The Human Genome Project provided a path for the ultimate in a reductionist approach: defining the units of information in terms of the nucleotide sequences which code for biological effects [3]. It is now widely accepted that information science and molecular biology have shared concepts.

To bring information technology into clinical context is beset with difficulties. Primarily, it depends on the purpose for which the data would be used (clinical care, clinical focus on a narrow area, clinical audit—although these are not mutually exclusive). Ultimately, there is a tradeoff between the depth of information that is gathered and the time that is available for each subject. This is a crucial aspect in converting paper-based record system to electronic medical records, as the advantages of the latter are many. Good software is given, but the bottleneck in converting to EMR is "process design, understanding and supporting workflows, and the economic and social aspects of organizational change."

Once the system is in place, advantages are obvious: structured entry of information, near-instantaneous recall, and built in rules for diagnosis and advice [1, 2].

The data can be utilized in ways other than for the purpose it was originally obtained. For instance, it could be subjected to predictive modeling using neural network methods. In the current issue, Duggal et al. used machine learning methods to predict readmission of patients who were discharged from a hospital [4]. From 9381 records, random forest was the optimal classifier using area under precision-recall curve to identify risk factors. Neural network methods have the ability to "learn" as larger sets of data are provided. It differs from statistical methods, which operate on the available circumscribed data. Machine-learning tools were used in other applications such as detecting adverse drug events from electronic medical records [5].

Access to mobile telephony led to development of mHealth apps. In this issue of the journal, Jha et al. [6] compared the effectiveness of electronic health and mobile health platform with conventional care in diabetes. A pilot study from a tertiary care hospital showed a reduction in HbA1c. Diabetes knowledge and quality of life were better in the group managed by electronic health and mobile health record.

The World Health Organization published a document on mHealth strategy [7]. eHealth is defined as the "use of information and communication technology for health" with an objective to improve service delivery and outcomes utilizing computers, internet, and mobile phones. Advantages eHealth include promotion of healthy lifestyle and improved decisions by ensuring access to care even in remote places. Of relevance to diabetes, eHealth and mHealth can be employed in remote

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monitoring, health education, and continual training in self-care. Studies from India have shown mHealth is feasible and improves health outcomes in subjects with diabetes. Text messaging improved health behavior related to diabetes [8]. Similarly, a pilot study of mHealth intervention was compared to usual care in three metropolitan cities across India over a 6-month period [9]. The Gather system, built on behavioral change theories to support self-management and to improve communication with physicians, resulted in improved A1c levels, similar to an earlier study reported by Shetty et al. [10]. A systematic review on web-based remote monitoring systems in the self-management of type 2 diabetes concluded that there is complexity involved in the technology as well as in its implementation [11]. These must be addressed.

Rapid advances in technology are bringing in innovative methods of low-cost, efficient care for subjects with diabetes [12]. These have been described as affording "a more fluid, real-time, and patient-centric" treatment by way of access to education material, integration of biochemical data in improving self-care [13]. More than 1000 mobile apps exist, related to chronic diseases including diabetes. The apps related to diabetes allow logging and tracking patient data, as well as exporting the data to EMRs. A number of publications show that these apps are feasible and effective in improving clinical outcomes [14]. Work in progress consists of being able to add notes to data, tracking lab results, and employing identifiers such as bar codes [15]. These apps are expected to be certified for quality control by regulatory agencies.

There have been interesting attempts where data is analyzed to learn how built environment is related to health and well-being. Built environment refers to environments that are modified by humans, which influences their behavior leading to changes in lifestyle [16]. Urban sprawl typically found in developed western countries contributes to increasing sedentary lifestyle and obesity and diabetes.

Psychosocial measures were assessed in relation to built environment using Guttman's smallest space analysis [17]. Relations among the psychosocial measures were accounted for by "one facet with three axial sets of variables:" (a) positive well-being and energy; (b) satisfaction, impact, and social worry and diabetes worry; and (c) anxiety and depression. Prevention methods can be devised keeping the relation of built environment and psychosocial stressors. It is of interest that the data was obtained over the course of years primarily for evaluation of various psychosocial aspects of diabetes [18, 19].

The data can be analyzed using neural network methods to predict the psychological outcome based on key clinical and biographical factors [20]. Similarly, clinical data can be analyzed to identify trends in the prevalence and other characters of diseases [21, 22].

But it is really after the publication of the human genome, in all its iterations, that biological data and information science were recognized to be intertwined. While in the past, data is difficult to obtain and analyze, newer molecular biological approaches turned the cart around—where a lot more data were available. Challenges exist to develop statistical, mathematical, and computational methods to understand and utilize [23].

There has been continuing documentation of gene expression studies in different situations: among offspring who had one parent with type 2 diabetes [24], PPARG (Pro12Ala) polymorphisms [25], and variants of a TCF7L2 gene in the north east part of Uttar Pradesh [26]. An earlier editorial in the journal summarized aspects of such studies [27].

The avowed practical implementation of the HGP was personalization of drugs; although benefits have been hard to come by, attempts are being made to match genetic profile with the individual. A review of personalized drug use in diabetes is published in this issue [28]. Although genetic variants and metabolomics studies using omics technologies have the potential to be used as biomarkers [29], translatable results are scarce. Despite a number of common variants being associated with type 2 diabetes, they explain only a very small fraction of the disease heritability. A recent effort to improve the predictive value by studying infrequent and rare variants showed they did not have a significant role in predisposing to the disease [30]. Resultantly, the major limitation in applying diabetes genomics to clinical care is the lack of genomic findings which can be used in clinical practice [31]. The way forward seems to consist of improved understanding of genetic variant interactions with environmental factors [32]. Given the low penetrance of most alleles in type 2 diabetes and poor predictive value, methods must be devised to communicate the risks accruing from genetic factors so that beneficial health outcomes can be achieved [33]. Alongside, there is an increasing need for trained researchers at the "intersection of computer science, statistics, mathematics, and their discipline of interest" to deal with data-rich but (as yet) discovery-poor situation [34, 35].

Of the many ways in which genomic data can be analyzed, the ability to impute evolutionary pathways, as demonstrated by the phylogenetic and promoter analysis of IAP gene with diabetes in the current issue of the journal, is exciting [36]. The phylogenetic and the gene promoter analysis suggested that "regulatory elements for beta cell death caused by pancreatic amyloidosis" could lead to T2DM. This is similar to the hypothesis based on bioinformatics analysis that the enzyme butyrylcholinesterase could be related to the pathogenesis of Alzheimer's disease and type 2 diabetes mellitus [37]. The hypothesis was followed up by an animal study in which streptozotocin-induced diabetes in albino Wistar rats showed a decline in cognitive function and an increased serum butyrylcholinesterase [38]. A series of other studies have suggested that it could be one of the mediators between type 2 diabetes mellitus and Alzheimer's disease [39]. Of greater interest is

the potential of evaluating individuals having variant butyryl-cholinesterase proteins and their susceptibility or protection from metabolic syndrome and its associated abnormalities [40, 41].

Advances in these fields not only require conceptual and technical collaboration to devise treatable options [35] but could also involve ethical issues such as the ownership of data and providing access of genetic data to the participants, i.e., in other words, to answer the question "who owns the data [42]?"

Besides analysis of biological data, availability of other forms of data provides innovative methods to assess poverty and to understand how social interactions are related to health outcomes [43, 44].

So we are at a juncture where there is a deluge of data. Methods must be devised to collect, annotate, and understand it, rather than be overwhelmed. One can expect to deal not just with science but with society, ethics, and law. Interesting times await.

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