Research Output Journal of Public Health and Medicine 3(1):1-6, 2024

ROJPHM ISSN: 1115-6147

https://rojournals.org/roj-public-health-and-medicine/

Bioinformatics and Personalized Nutrition

Uwera James K.

Faculty of Biological Sciences Kampala International University Uganda

ABSTRACT

The intersection of bioinformatics and personalized nutrition offers innovative approaches to enhance individual health outcomes by integrating genomic, epigenomic, proteomic, and metabolomic data. This paper explores the role of bioinformatics in managing and analyzing the large-scale biological data required for personalized nutrition. It covers the development and application of computational tools and methods to create individualized dietary recommendations based on genetic profiles. The potential of nutrigenomics to tailor nutrition interventions, predict disease risks, and improve overall health through personalized dietary modifications is examined. Additionally, the paper discusses the challenges, future directions, and ethical considerations associated with the implementation of personalized nutrition strategies.

Keywords: Bioinformatics, Personalized Nutrition, Genomics, Nutrigenomics, Omics Technologies.

INTRODUCTION

In the late 1990s, the term 'bioinformatics' was actually well known in research areas such as molecular sequence data management, analytical and visualization tools, computational biology, and biological anthropology. The amount of data being generated by DNA and protein analysis was doubling every year, creating a heightened need for new algorithms and software that could handle and analyze this information. Bioinformatics therefore developed as a new discipline that was designed to meet these needs [1]. Bioinformatics is an interdisciplinary field of science that combines biology, computer science, information technology, and some branch of information mathematics and statistics. It is one of the latest and most exciting disciplines in life science, medicine, and industry with great potential for new product development in agri-food, pharmaceuticals, and healthcare. A major advantage of bioinformatics is that it can be applied to various age-old problems existing in biology, such as finding regulatory networks of genetic switches, designing new drugs, discovering gene sequences of desired function, and diagnosing pathogens and antibiotic-resistant pathogens in clinical environments [2]. The fundamental need for the creation of this interdisciplinary area of biological informatics is the management and interpretation of these large complex data that have been produced by investments in technologies for large-scale DNA sequencing. It is believed that DNA sequencing technology will continue to advance rapidly, producing enormous amounts of data on gene organization and expression and the functional role of its products under different developmental and environmental conditions. These results will, in turn, require the development of even more complex and robust methods of analysis. This, in turn, will drive advances in the field of bioinformatics itself [3]. No computer can formulate hypotheses and thereby intelligently help in the generation of new biological data. The task of understanding the complexity of mesoscale systems is therefore one of the most challenging current problems in statistical, computational, and mathematical physics. Many of the bioinformatics methods draw inspiration from or use techniques used in the physical sciences. This is because the problems we can address in bioinformatics are not unrelated to those in statistical mechanics. Bioinformatics approaches are characterized by an interplay of three classes of problems.

DEFINITION AND SCOPE

"Bioinformatics and Personalized Nutrition" intends to provide the reader with a broad picture of the new perspectives that the introduction of genomics, epigenomics, proteomics, and metabonomics have opened in personalized nutrition. The presentation uses a discovery to reconstruction approach, beginning with the relevant omic knowledge for personalized nutrition, followed by a presentation of the applications applied to individual health. The first part of the book is focused on the role of nutrition in the prevention and progression of chronic diseases and the possible impact of personalized nutrition on the quality of life of the individual. The second part presents the characteristics of the molecular tools that are utilized, focusing on the most relevant technologies related to the different omic sciences that can be used in personalized nutrition. This is the largest section of the book as the power of personalized nutrition lies in the description of the individual molecular microcosm and its environment. The third part, dedicated to research perspectives, illustrates both the still open debates in terms of personalized nutrition and future scientific approaches [4].

TOOLS AND TECHNIQUES

Several kinds of technologies fall under the term "bioinformatics". The basic division is between in silico tools and experimental tools. Experimental bioinformatics includes data acquisition, among which is genome sequencing, proteomics, and gene expression. This equipment generates vast amounts of data; for example, a single human microarray (a protein array that tests for genetic or environmental differences at a single-nucleotide resolution) can assay 10,000 genes. Approximately 10 to 15 GB of data is produced per microarray every hour. The resulting dataset may include more than 25,000 data records ordered in a one-million-row table. All of this data is essential, though, to realize the continued rebuilding of both private and public databases. Suitable tools are used to identify, separate, sort, and proportionally represent this data. As large bodies of research revealing more and more complex correlations are revealed, patterns, models, footprints, and network diagrams further explain how that data fits together with specific linked variables. Among notable work is that of the Human Metabolome Database (HMDB). More frequently, data is fitted into a model. One of the diminishing returns in bioinformatics is that when new patterns are found and fit into their place in the model, the model must change to update itself. This method, however, will continually add substantial value to food pattern groups and the custom diet plans. Groups are created with foods that form complex models. Trends within that group are data, including means, variances, and descriptions of increasingly chunkier, higher-level patterns and habits. The acquired datasets are then mined in order to spuriously find significant relationships. Data is worth more measurement opportunities as long as footprints, bio-patterns, and the models they inhabit align with needs. The human body is a full-range research project that is worth the measurement. That data is a glimpse of how the individual will metabolically process that food. Proteomics and genomics are cost-effective profiling technologies of primary foods. In particular, proteomic testing methods and optimal protein use standards are moving towards systems in use by research authorities. To understand a metabolomic system, however, the answers are food plus human. Personalized testing to acquire ideogram information and metabolic rate by using the Clinical Metabolomic Protocol of bloodwork while enabling success with the Clinical Genomics Protocol can be beneficial [5].

GENOMICS AND NUTRIGENOMICS

In the strongest terms, the most we may predict by means of genomics is disposition, and this can be modified uphill by the universal desiderata of healthful existence which modern societies pursue for their own reasons, including nutrition, which is thus hardly more personalized than it ever was. Epigenetics allows normal metabolisms to prevail against many nutritional constraints by differential methylations or acetylations, and nutrigenomics is a pursuit for the best genotypic match between population-specific variants in the genome and the diet. The vast consumer interest is not as much in querying the genome for guidelines to appropriate nutrition as it is in using genomics to provide some global definition of biological individualism that will confirm what most people really want to know, which is that their dietary inclinations can be apparently justified. This can be done for the odd homogeneous and isolated community, which our funds are more wisely spent in studying. Nature, the ever more familiar adversary, will always maintain incomprehensible variety [6]. Nutrigenomics occupies an unsatisfactory space between our perception of desirably specific nutritional advice, the complexity of the biological problem, and the projection of personal biodelusions that genomics is taken to afford. The alleged promise is that it will soon provide them for just about everyone. Such a mismatch between expectation and return is certainly not sustainable, but equally certain is the retention of a colossal capacity in genomics to illuminate genetic predispositions and their interactions with a vast array of lifestyle, healthful behavior,

and risk tendencies that conventional populationized medical science either ignores or implicitly or explicitly repudiates. The human genome is about 3,000 Mbp, and its full determination would be challenging were it not for the one-two-three codesigner strategy of private funders, which has guilt-induced state-sponsored large-scale genomics programs, all of which have now entered advanced phases.

GENOMICS BASICS

Advancements in genomics have enhanced our understanding of different genetic variations in the population. Individuals have around 20,000–24,000 genes. For example, genes code proteins that play a significant role in disease development and progression. Several genes may interact with environmental and lifestyle factors to cause diseases including heart disease, insulin resistance, obesity, osteoporosis, some types of cancer, and others. Genes also interact with dietary factors too. Consequently, research in genetics and nutritional sciences has been conducted for many years focusing on interindividual differences with the aim of developing personalized dietary recommendations [7]. Genetic variations resulting from single-nucleotide polymorphisms (SNPs) may cause amino acid changes (non-synonymous SNP), modification in the protein coding/protein function, or changes in splicing of introns in pre-messenger RNA (mRNA). Variations in gene content, the genome structure i.e., insertions, deletions, gene duplications, and inversions, also have phenotypic significance. Furthermore, the impact of several sequences of bases that are not genes such as promoters, enhancers, gene deserts, and others within the noncoding portion of the genome in the expression and function of genes has led to a deeper understanding of human genetics. Given these genetic components, studies in genetics and personal nutrition have the potential to give relevant and precise personal recommendations to reduce the onset and progression of detrimental nutrition-related health outcomes.

NUTRIGENOMICS OVERVIEW

A relatively new research area is emerging called nutrigenomics that uses molecular approaches to study how nutritional components interact with the genome. Nutritional genomics is defined as the study of the effects of foods or food constituents on health and well-being, which are at least partly mediated by the genetic variation of an individual. Nutrigenomics takes into account individual differences and the different influences of specific dietary components on the genome. Nutritional genomics research plays a significant role in the development of personalized nutrigenomes and diets tailored to individual genetic profiles [8]. Nutritional genomics aims to identify the influence that an individual's genotype has on how effective and safe nutrients, bioactive substances, and diet supplements are. In turn, this may lead to the tailoring of nutritional elements to the individual, allowing a preventive approach to healthcare. Dietary modifications can then be made based on the individual's genotype and can be incorporated into personalized nutrition. Nutrigenomics can play an important role in addressing obesity and poor diets associated with the worldwide epidemic of obesity. The prevention and treatment of obesity is a critical part of addressing poor diet and overnutrition, which are the leading causes of increased weight and obesity.

DATA ANALYSIS IN PERSONALIZED NUTRITION

In personalized nutrition, data analysis aims at identifying interactions between nutrients and genotypes (or other biomarkers assessed at the molecular level), health/phenotype, and environmental exposures, and at predicting an individual's risk of contracting diseases from such interactions. Genome-wide association studies (GWAS), targeted genomics (focusing on genes, co-factors, and enzymes related to metabolic pathways of dietary relevance), DNA sequencing, DNA microarrays, and proteomics/metabolomics are instrumental tools in identifying functional relationships among diet, genes, and metabolic pathways. Equation-based approaches and decision tree analyses are frequently used to describe and develop models identifying the relationships among dietary components and their interactions with genotypes explaining diseases related to metabolic pathways. Databases and related spatial and optimization data structures assembled with detailed, integrated, and manually curated information from publicly available sources permit exploration and analyses of omics data in personalized nutrition [9]. Integration of nutrients (as categorical or continuous variables) allows for the application of dimension reduction techniques to analyze relationships between genome-wide data and outcomes, in a way that simplifies the latter in a disease probability score. Solutions from such analyses are generally used to develop practical models to help guide the design of personalized recommendations for an individual's specific dietary needs and can be integrated into consumer-oriented decision support tools. When nutrient intake is described using distributions, treatments based on finite mixture residual mean models allow for consideration of related non-linear, possibly pleiotropic relationships and the relevant non-identifiability issues. With the availability of omics data, epistasis may lead to a potential multitude of

non-identified genetically determined pathophysiological regulatory processes and to a possible high level of misspecification of associated built-in mechanistic models. Furthermore, the high number of dietary and genome-wide potential biomarkers that might be included as covariates in the latter models compare poorly with the large number of fed individuals, considering either the random and specificities within human studies or from the model-building process. Under the resulting non-verifiable conditions, biased, non-consistent, and low-powered model solutions might result.

BIOINFORMATICS IN DIETARY ASSESSMENT

Throughout the last years, there has been a growing interest in the application of bioinformatics approaches to personalized nutrition. Amongst the different aspects that should be taken into account in personalized nutrition, dietary assessment is one of the fundamental steps that will provide individuals and populations with appropriate and adequate nutritional recommendations. The use of bioinformatics in dietary assessment allows optimizing and, in certain cases, standardizing the tools commonly used by subjects, thus facilitating the collection of the required data for the proper study of the nutritional and health status of the populations. For a broader analysis of data, the scientific community has seen the utility of different high-throughput sequencing approaches that allow deeply exploring the human body, including gut, mouth, and skin, amongst others. Such methodologies have been used to advance into the development of personalized nutrition recommendations, through the development of precision nutrition [2]. Nevertheless, bioinformatics tools have been used to perform and think ahead the instruments that can be used in the assessment of food consumption. The proper application of bioinformatics will bring a step further and provide researchers and students of nutritional aspects different and useful tools for dietary assessment through the development of novel, accessible, and practical tools that are easy to use and are adapted to the actual needs of the study, including the population under study. Moreover, bioinformatics tools will aid the incorporation of the new policies and recommendations that are currently being explored and developed for universal application.

MACHINE LEARNING IN NUTRITIONAL GENOMICS

Now that we have reviewed the idea of personalized nutrition, let us briefly consider the main bioinformatic strategies that can make them a reality. We will shift our focus from big omics data to the second layer data that can be created from the omics data. This layer of data already captures important features relevant for exploring what the big omics data can tell us about phenotypes. The big omics data, which captures the essence of an individual, is otherwise difficult to work with for daily practical nutrition and health guidance. It can be personalized to make the information relevant to that person [10]. Surely food impacts the output of the biochemical pathways, shown in the big omics data, as inherently part of the description of the biochemical machines. Some input foods into the biochemical machinery may be marginal or intermediate nutrients as they only contribute to intermediate products. But some nutrition input foods can scavenge from the by-products or the output relevant nutrition elements. In addition, the biochemical outputs themselves may be the scavenger nutrients. When we look closer at the big omics data, both food inputs and biochemical outputs provide nutrition information needed for health management. In the following abstracted discussion, we will look at both aspects of the nutritional genomics: the direct and the harvested physiologically indirectly through the phenotype. The first is encoded into the input biochemical pathways and the latter reflects the biochemical output status and the obtained benefits.

CHALLENGES AND FUTURE DIRECTIONS

Although the application of bioinformatics approaches to personalized nutrition has so far been promising, several challenges should be faced in the future. On the one hand, it is not always easy to assess the intake of nutrients by using simple strategies since it does not consider the relative absorption of different forms. On the other hand, the association between the variation in the single-nucleotide polymorphisms of some genes (mainly ER, VDR, and PCSK1) and nutrient intake could help us to predict the response to diet in several diseases and thereby help us to apply more cost-effective and individualized nutrition interventions. In the future, omics-driven research that aims to develop computer-based tools will help to customize individual diets and predict the long-term efficacy of diet-related interventions. Systems biology models of metabolism will also help us to better understand the metabolic pathways that adjust to match the individual dietary constraint of specific foods or nutrients, eventually leading to an optimization of metabolic health. This change in focus, from quantifying established and often global dietary recommendations to an in-depth understanding in the context of the individual, has also important implications for the food industry, retailers, and personalized medical practice. Furthermore, motivating and managing behavior change in this food context is important since the frequency and

manner in which information is provided could be a key to improving the quality of health (bespoke advice rather than generic messaging).

ETHICAL CONSIDERATIONS

The privacy and security of healthcare and well-being operations are critical. Due to the applied data, issues about informed consent, opt-out, and data anonymization must be considered. Indeed, the use of biological information in personalized nutrition is likely to be an area of especially complex regulation, given that it contains both personal data and genetic data that has implications for the health of the individual but may not be considered health data. First, researchers show that, even as human well-being may benefit, anxieties over privacy and discrimination may dominate people's attitudes toward personalized nutrition, dampening both public enthusiasm and participation in personalized nutrition research and development. Second, even those who believe they are making thoughtful choices informed by accurate information may be wrong. Unless the public information environment changes for the better, the potential of personalized nutrition to benefit individuals and the public's health may remain unmet. Third, if we do eventually achieve an environment where evidence supports clear public health benefits from personalized nutrition interventions and patient rights are effectively protected, another potential line of attack to generate disease as a product of lifestyle choices may entail repercussions for insured persons or those who receive healthcare coverage from social security funds and with respect to fractional premiums in health insurance. The product of lifestyle choices that are typically excluded from health insurance coverage is overnutrition, which can lead to many chronic diseases, including type II diabetes, cardiovascular diseases, various cancers, and musculoskeletal diseases. In the public opinion, this product should be distinguished from genetic diseases or other chronic diseases related to less frequent lifestyle damaging factors. Since personal responsibility in deciding about the diet is relevant to the onset of overnutrition, there is a perception that protection of insured persons should be considered, and specific control measures should be implemented to prevent overnutrition. Sucrose, fructose, and glucose are the primary nutritional elements of sweetened beverages, which, consumed in moderate amounts, can be metabolized without harm. On the other hand, chronic overconsumption of sweetened beverages increases the risk of developing metabolic syndrome, type 2 diabetes, cardiovascular disease, and gout.

TECHNOLOGICAL ADVANCEMENTS

Recent technological advancements have significantly impacted the field of genomics. Currently, researchers are able to sequence the entire DNA of an individual, commonly referred to as whole-genome sequencing (WGS). In comparison, whole exome sequencing (WES) refers to the identification of genetic variations located only in the protein-coding regions of the DNA, which typically account for 1-2% of the genome. There are also a number of genotyping kits that determine genotypes at a large number of genome-wide SNP markers for one, or thousands of, individuals. Genetic variations identified through these processes include single-nucleotide polymorphisms (SNPs), insertions and deletions (Indels), copy number variations (CNVs), and structural variants (SVs). However, population studies have largely shown a lack of major, common genetic effects on common complex diseases and traits. Therefore, a large number of studies are currently conducted to identify the association between rare variants (defined as having minor allele frequency, MAF of the variant <0.05), and a large number of common, complex diseases and traits, including obesity, type 2 diabetes, cancer, and others, such as allergies or blood levels of certain compounds that are important for nutrition, thereby advancing the most appropriate diet according to individual's genetic make-up.

REFERENCES

1. Baxevanis AD, Bader GD, Wishart DS. Bioinformatics. 2020. [HTML]
2. Sak J, Suchodolska M. Artificial intelligence in nutrients science research: a review. Nutrients. 2021. mdpi.com
3. Dai X, Shen L. Advances and trends in omics technology development. Frontiers in Medicine. 2022. frontiersin.org
4. Ramos-Lopez O, Martinez JA, Milagro FI. Holistic integration of omics tools for precision nutrition in health and disease. Nutrients. 2022. mdpi.com
5. Bahmani M, O'Lone CE, Juhász A, Nye-Wood M, Dunn H, Edwards IB, Colgrave ML. Application of mass spectrometry-based proteomics to barley research. Journal of Agricultural and Food Chemistry. 2021 Jul 28;69(31):8591-609. acs.org
6. da Silva Anastacio V. Nutrigenetics & Nutrigenomics and Its clinical application. 2024. stmarys.ac.uk
7. Khan AH. The Impact of Sequencing Human Genome on the Evolution of Life on Earth. katalystpublishers.com. katalystpublishers.com

8. Marcum JA. Nutrigenetics/nutrigenomics, personalized nutrition, and precision healthcare. Current nutrition reports. 2020. [HTML]
9. Molitor C. A bioinformatics and genotyping approach exploring personalised nutrition.. 2021. cranfield.ac.uk
10. Ordovas JM, Berciano S. Personalized nutrition and healthy aging. Nutrition Reviews. 2020. oup.com

CITATION: Uwera James K. (2024). Bioinformatics and Personalized Nutrition. Research Output Journal of Public Health and Medicine 3(1):1-6