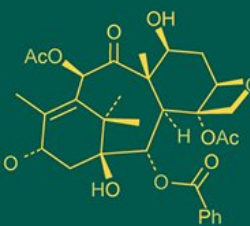
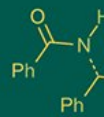


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(8): 293-304
www.biochemjournal.com
Received: 30-05-2026
Accepted: 01-07-2026

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Bioinformatics tools and multi-omics integration in food safety, allergen detection, and personalised nutrition: A systematic review

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DOI: <https://www.DOI.org/10.33545/26174693.2026.v10.i8Sd.9445>

Abstract

Bioinformatics has proved to be a crucial inter-disciplinary technique in modern food science that enables the effective processing of biological information. Some of the major fields in which bioinformatics is used include allergen identification, ensuring food safety/pathogen detection, enhancement of agricultural output, personalized nutrition, and application of multi-omics techniques. The implementation of innovative computational tools and artificial intelligence approaches, such as machine learning and prediction models like AlphaFold2, greatly widens the scope of studies related to food. They contribute to achieving a more detailed insight into the processes associated with molecular interactions, microbes, and metabolites which affect food properties. Even though there are some difficulties associated with converting theoretical findings into practical achievements, further developments hold great potential in improving both the field of study and its applications.

Keywords Bioinformatics, Food Science, Allergen Detection, Food Safety, Pathogen Identification, Personalized Nutrition,

Introduction

Bioinformatics is an interdisciplinary field that involves molecular biology and genetics, computer science, mathematics, and statistics. Data-intensive, large-scale biological problems are addressed from a computational point of view. The most frequent issues are concluding gathered data and molecular modeling of biological processes (Xu, 2018) [81]. According to the traditional belief that, bioinformatics was created to aid scientific initiatives and investigations. But its use could never be restricted in this way. In the meantime, new scientific and technological advancements have made it possible to enhance food production and public health by improving food supply safety and streamlining the food process through creative means. Numerous bioinformatic technologies have demonstrated the ability to protect public health. To ensure food and medicine safety, "regulatory bioinformatics" has been proposed as a way to create a transparent and consistent bioinformatics framework (Healy *et al.*, 2016) [34]. The US Food and Drug Administration has been using computational toxicology techniques to assist in the safety assessment of related products for several years (DeSesso, 2017) [17] (Yang *et al.*, 2009) [82]. With various success stories accredited to the application of bioinformatics approaches, it is anticipated to be beneficial in food sciences. Bioinformatics field is expanding rapidly and becoming a very essential tool for research in life sciences by integrating the traditional techniques with massive amount of data generated from the fields of comparative genomics. Numerous success examples attest to the potential benefits of applying bioinformatics techniques in the food sciences. By combining conventional methods with the vast amounts of data produced by comparative genomics, the subject of bioinformatics is growing at an alarming rate and becoming a vital tool for life sciences research. Proteomics and genomes in food science and proteomics in food research (Desiere *et al.*, 2001) [18]. Since crops play a significant role in the food sector, they must be of excellent quality, meaning they should be disease-resistant and yield a lot. We can use genomics and functional genomics to identify the genes in commercially significant crops with the aid of bioinformatics. Additionally, it can aid in the creation of transgenic crops and

the discovery of novel genes that can improve the caliber and yield of food products generated by these crops. The production of agricultural chemicals based on the ideas of signal perception transduction pathways for particular targets and the discovery of molecules that may be utilized as insecticides, herbicides, or pesticides can also benefit from this technique (Bennetzen *et al.*, 1998) ^[9]. Food plays an important role in regulating the various processes within the body like metabolic, mental, etc. However, there is always growing admiration for the role nutrition plays in halting the growth of various chronic disease. A lot of work is done to promote and improve the nutritional value and quality of food sources. It is anticipated that the growth of food bioinformatics would contribute to the provision of easy and practical means for researchers to embrace a new topic or discipline (Lemay *et al.*, 2007) ^[45]. This review primarily covers the overall role of bioinformatics in food processing and the bioinformatics tools and databases used in food research.

In this systematic review, the utilization of bioinformatic tools and the incorporation of multi-omics into food safety, allergen detection, and personalized nutrition were investigated. A systematic search of literature was conducted using several databases using key phrases like "bioinformatics," "food safety," "allergen detection," "multi-omics," and "machine learning." The inclusion criteria included studies which made use of computational techniques in food bioinformatics, explored the concept of multi-omics by looking at genomic, proteomic, metabolomics, and transcriptomics information, or employed computational techniques in food-related work, but studies with no methodology or those unrelated to bioinformatics in food science were excluded. All pertinent data from the selected studies were systematically collated and analyzed with emphasis on various tools and databases such as BLAST, UniProt, KEGG, AlphaFold2, and

QIIME2. Their application in detecting allergens, pathogens, and personalized nutrition was also looked into. In terms of quality assessment, emphasis was placed on the use of both computational and experimental methodologies, while the critical analysis emphasized the successes of the application of computational techniques, the challenges faced, and the future of AI in food bioinformatics.

2. Bioinformatics for food research

Research, development, or application of computational tools and approaches for expanding the use of biological, medical, behavioural, health, and nutrition data, including those to acquire, store, organize, archive, analyse, visualize, or build biological knowledge from very large and traditionally unrelated sources is the definition of bioinformatics (Desiere *et al.*, 2001) ^[18]. Bioinformatics has emerged as a crucial scientific field, causing a transformative shift in areas such as molecular medicine, comparative genomics, molecular evolution, microbial genome applications, drug discovery, and biotechnology. Nevertheless, its potential impact on food science is often underestimated, even though it holds considerable promise for advancing this domain (Holton *et al.*, 2013) ^[35]. Due to its ability to regulate metabolic, hormonal, physical, and mental processes, food is essential for preserving wellbeing. Additionally, the significance of nutrition in the development of many chronic illnesses is becoming more widely recognized. The quality and nutritional potential of different food sources are currently being promoted and enhanced through intense efforts (Holton *et al.*, 2013) ^[35]. More practically, bioinformatics is influencing food science and nutrition in areas like taste and flavor, food safety, and food quality. Bioinformatics has played a significant role in understanding the evolutionary history of taste receptors in the context of molecular evolution (Dong *et al.*, 2009; Shi & Zhang, 2006; Wooding *et al.*, 2006) ^[20, 65, 79].

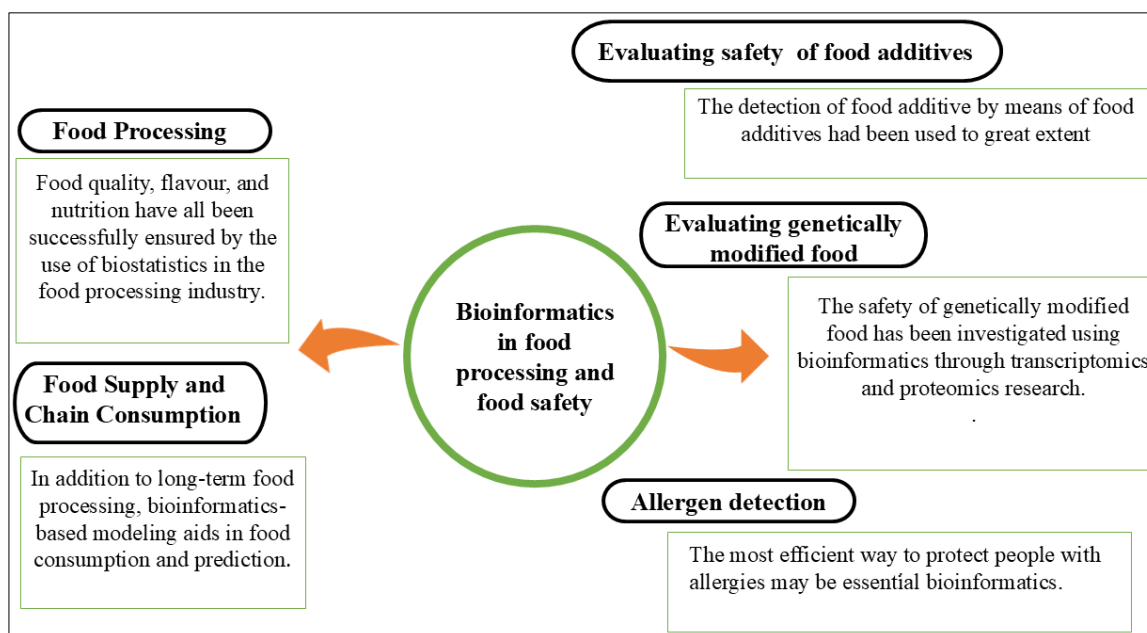


Fig 1: Application of bioinformatics in food processing and food safety. Adapted from (Xu, 2018) ^[81]

GWAS research has also been done on taste receptors, and it has been shown that glucose regulation and bitter taste receptors are related (Dotson *et al.*, 2008) ^[21]. Additionally, bioinformatic sequence similarity algorithms have been used

in relation to taste to determine homology between sweet taste receptors and brain glutamate receptors (Talevi *et al.*, 2012) ^[70]. The potential of bioinformatics in the field of food safety and quality is becoming more widely recognized

as a result of the several foodborne diseases that have been the subject of genomic sequencing initiatives (Brul *et al.*, 2006) [13]. Integrating bioinformatics with traditional methods can lead to a thorough investigation of hidden bioactive peptide sequences or sustainable sources of their protein precursors. Given the extensive data on the preclinical bioactivities of peptides derived from food, future efforts should focus on leveraging these peptides as functional ingredients to create products that offer health benefits (Udenigwe, 2014) [71]. Bioinformatics holds significant promise for various uses in the food industry, presenting nearly limitless opportunities for developing innovative methods to apply them. The vast data generated from the planned projects will elevate bioinformatics to a crucial role within the food sector. Efforts are underway to utilize bioinformatics toolkits to genetically modify transgenic plants, aiming to produce nutritious, healthy, and advantageous food products and crops, ultimately leading to a major breakthrough in the food industry (Manzoor Waidha *et al.*, 2015) [48].

3. Key areas of bioinformatics in food research

3.1 Bioinformatics in allergen detection

Allergens have a relatively wide sequence and structural similarity due to their many different origins, which results in identical IgE reactions. It is not surprising that the most important resource for research on food allergies is bioinformatics. Several databases are mainly focused on food allergies, including AllerMatch (Fiers, Kleter, Nijland, Peijnenburg, Nap, & van Ham, 2004) [24, 25], Informal FARRP Allergen database and SDAP (Mari *et al.*, 2006) [49] show the use of bioinformatics in the area. Bioinformatics can play an important role in developing improved technology for the detection and characterization of food allergens. However, the full realization of this potential will depend on the development of allergen-specific databases as well as improved methods for data mining within these databases (Gendel, 2004) [31].

With the addition of structural bioinformatics, homology of common bioinformatics is systematically carried out to raise the potential allergenicity and cross-reactivity of proteins (Jenkins *et al.*, 2005) [39]. The utility of such methodologies has incited the WHO to incorporate sequences similarity search as a feature of the rules for evaluating allergenicity for food that's genetically modified (Joint & Organization, 2001) [40]. Recently, a various of bioinformatics techniques have been applied to the development of allergen diagnostics in order to predict peanut sensitivity using machine learning (Lin *et al.*, 2012) [46].

A great deal of information about food allergens is contained within large archival databases such as GenBank (Gendel, 2004) [31] and the European Molecular Biology Laboratory (EMBL) database (Stoesser *et al.*, 2003) [67]. The Protein Information Resource (PIR) database (Wu *et al.*, 2003) [80] and PubMed (Wheeler *et al.*, 2003) [77]. On the one hand, this information is difficult to locate. For example, many allergen protein sequences are not identified as such in GenBank (Gendel, 1998) [30]. On the other hand, searching GenBank using the keyword "allergen" results in a large number of immune system proteins involved in the allergic response (Gendel, 1998) [30]. Thus, there is no straightforward way to conduct an allergen-specific (much less food allergen-specific) data analysis using GenBank or the other large sequence databases. Similar problems exist with PubMed. For example, a search using the keyword "Ara h2" (a peanut allergen) returned 76 hits, of which more than 65 were unrelated to allergy (most of these involved unrelated genes or chemicals with "ara" as an acronym or abbreviation). In addition, the archival databases are inconsistent in the treatment of some data, such as whether the sequences for alternate alleles are identified as independent sequences. Therefore, bioinformatic analysis of food allergens requires the use of specialized databases. Several examples of allergen-related databases are described below (Gendel, 2004) [31]. There are different online allergen databases, as listed in Table 1

Table 1: Allergen database

Allergen database	URL	References
SDAP	https://fermi.utmb.edu/	(Ivanciuc <i>et al.</i> , 2003) [37]
Allergome	https://www.allergome.org/	(Mari <i>et al.</i> , 2006) [49]
BIFS	https://sarep.ucdavis.edu/research/ExtensionEd-Networks/BIFS	(Schein <i>et al.</i> , 2007) [63]
FARRP	https://farrp.unl.edu/farrp-resources/farrp-databases/	(Gendel & Jenkins, 2006) [32]
Protall	https://tox.charite.de/protox3/	(Schein <i>et al.</i> , 2007) [63]
WHO/IUIS	https://allergen.org/	(Schein <i>et al.</i> , 2007) [63]
AllFam	https://www.meduniwien.ac.at/allfam/	(Radauer <i>et al.</i> , 2008)

3.2 Bioinformatics in food safety and pathogen detection

Bioinformatics plays a crucial role in food safety, particularly in the detection of microorganisms and pathogens that can cause spoilage, contamination, and disease. Food can act as a culture medium for pathogens, potentially leading to illness or death, making scientific supervision essential (Akalin, 2006) [2]. Microbiological tests are required to prevent food poisoning outbreaks (Yang *et al.*, 2009) [82]. Bioinformatics is crucial in enhancing food safety systems by enabling the rapid and dependable detection of foodborne pathogens through the analysis of high-throughput biological data. Bioinformatics enables precise identification and molecular profiling of harmful bacteria present in food by combining genomic and

proteomic databases with molecular methods like PCR, next-generation sequencing, and whole-genome sequencing. During foodborne outbreaks, these technologies enable epidemiological monitoring, help identify contamination sources, and assess virulence factors and antibiotic resistance. Bioinformatics-based techniques improve early warning systems and reduce the danger of widespread foodborne diseases by providing higher sensitivity, faster findings, and enhanced accuracy when compared to conventional microbiological procedures. (Soroushianfar *et al.*, 2025) [66]. Ensuring that food intended for human consumption is free of hazardous pollutants and pathogenic agents that might compromise public health is known as food safety. (Buckley & Reid, 2010; Fung *et al.*, 2018;

Jeevanandam *et al.*, 2022) [14, 26, 38]. Lack of compliance with food safety regulations significantly enhances the chances of developing food-borne diseases that may either be mild cases of food poisoning or serious diseases that might even result in fatalities. This leads to many problems for society as well as food producers and distributors in terms of losses. According to WHO, about 600 million people get affected every year due to food-related illness (Mohammad *et al.*, 2018; Raspor, 2008) [61]. The safety of food is at risk due to various biological agents like bacteria, viruses, parasites, algae toxins, and fungus toxins, among others, some of which may cause chronic health conditions such as immunotoxicity, nephrotoxicity, teratogenicity, and endocrine disruption (Feng *et al.*, 2016; Gallo *et al.*, 2020; Kendall *et al.*, 2003) [22, 27, 44]. Moreover, Human exposure to hazardous heavy metals like lead, cadmium, mercury, and arsenic has increased due to industrialization. These metals are persistent in the food chain and have a variety of harmful effects. (Balali-Mood *et al.*, 2021; Carvalho, 2017) [6, 15]. The following vulnerable groups include newborns, pregnant women, the elderly, and people with compromised immune systems, thus highlighting the need for stringent food safety procedures to avoid any outbreaks (Kendall *et al.*, 2003) [44].

Detection of foodborne pathogens is crucial in ensuring that food is safe for consumption to prevent disease outbreaks and protect the general public from harm. Conventional microbiological tests used to detect pathogens in food products have been shown to be tedious, time-consuming, and not very sensitive, thus limiting their effectiveness in controlling contamination. The application of bioinformatics in food safety can be considered revolutionary due to its role in carrying out highly advanced computerized analysis of biological information generated using nucleic acid-based detection, next-generation sequencing, metagenomics, and whole-genome sequencing. Pathogens can be detected quickly without the need for culture, characterized at the strain level, and virulence and antibiotic resistance genes identified. Artificial intelligence plays an important role in monitoring pathogen infections in food using prediction models and early outbreak alert systems among others (Syaiful Khoiri & Victor Davy Moussango, 2024) [68]. Overall, the analysis comes to the conclusion that further developments in artificial intelligence and bioinformatics will be essential to bolstering international food safety regulations and averting outbreaks of foodborne illness.

3.3 Omics integration in the food system

Food is essential for maintaining and improving human health in addition to sating hunger. Consequently, swiftly identifying potentially harmful contaminants in food, as well as understanding their negative impacts on food components, nutrients, and consumer health, is of utmost importance. This need has sparked increased scientific interest in foodomics, a burgeoning interdisciplinary field that explores the functional and nutritional attributes of food through the use of integrated advanced omics technologies (Valdés *et al.*, 2021) [73]. Omics-based methods, such as genomics, transcriptomics, proteomics, and metabolomics, produce extensive datasets that allow for a systematic and logical assessment of food safety issues. Genomics, in particular, examines genes, their expression patterns, and biological roles, offering detailed genetic insights into biological contaminants found in food and food products.

The advent of modern high-throughput genomic tools, especially next-generation sequencing and whole-genome sequencing, has greatly decreased the time and expense associated with microbial genome analysis. Whole-genome sequencing has emerged as a powerful tool for the surveillance, monitoring, rapid identification, and outbreak investigation of foodborne pathogens based on their genetic profiles, thereby aiding in the development of preventive strategies for future outbreaks (WHO, 2020). Moreover, in the development of novel plant-based medicinal molecules, it is important to study the biosynthetic pathway in order to understand their mechanism of actions. Through genomic studies, it is possible to determine the functional genes responsible for the biosynthesis of secondary metabolites and gain more information on their biological origin, regulation, and development. The development of sequencing techniques has provided us with deeper knowledge about the chemistry of different plants. By utilizing the latest genomic techniques such as high-throughput sequencing, restriction site-associated DNA sequencing, and genotyping by sequencing in the study of medicinal plants, we have been able to get more insights into the biosynthesis pathways through which secondary metabolites are produced (Boutanaev *et al.*, 2015; Hao & Xiao, 2015; Mehta & Hasija, 2018) [12, 33, 51].

The application of multi-omics techniques has emerged as an effective way to study food systems by linking the composition of microbes to their functionality, attributes, and safety outcomes. Methods involving one specific omics like genomics or metabolomics give limited information since the functionalities of biology in the food environment arise from complex interactions between genes, transcripts, proteins, and metabolites. This is why the combination of all metagenomics, metatranscriptomics, proteomics, and metabolomics can be used to provide a detailed description of microbial actions in food production (Ferrocinio *et al.*, 2022) [23]. In the context of modern food systems biology, the role played by omics is central as it helps in making predictions, managing fermentations, and conducting risks assessments. The combination of these omics with conventional microbiology and robust experimentation provides practical knowledge that improves the quality and safety of food as well as its sustainability.

3.4 Bioinformatics in personalised nutrition

Personalized nutrition aims at improving overall wellbeing and preventing diseases by Personalizing nutritional advice in accordance with personal genetic, biochemical, and environmental traits of an individual. Due to the rapid advancements in high-throughput sequencing technologies and increasing availability of omics information, it has become possible to better understand complex relations between nutrition, genetics, and well-being. Bioinformatics approaches that utilize information from multiple omics levels are essential for processing large and complex data generated in personalized nutrition research. This article explores the significance of bioinformatics in personalized nutrition, emphasizing its key applications in genomics, metabolomics, and microbiome research (Approaches & Nutrition, 2022) [4]. The genomic approach, when implemented properly, should be able to predict biological inclinations but not necessarily specific consequences. Such inclinations can be positively affected by the universal principles of healthy eating that are more universal than it

may seem. Through epigenetic processes such as DNA methylation and histone acetylation, the body maintains homeostasis irrespective of the diet. As part of this approach, the task of nutrigenomics is to determine the best combination of population-specific genotypes and diets. Nevertheless, consumer interest is motivated more by an appeal to the biological uniqueness through genomics rather than by actual interests in receiving genome-based nutrition advice. Strong genotype-diet interactions will most probably be found among genetically similar and geographically isolated populations, which would allow researchers to achieve more in terms of discovering relevant information. Ultimately, the biological diversity cannot be easily explained and remains diverse because it is part of natural complexity that exceeds genomics' comprehension capabilities (da Silva Anastacio, 2024) ^[16]. Figure 2 illustrates a bioinformatics-based multi-omics approach for individualized nutrition, illustrating the process of converting intricate biological data into practical dietary plans. The layers to the left in the diagram are the biological input layers, which include genomics (SNPs), epigenomics (DNA methylation), transcriptomics, proteomics, metabolomics, gut microbiome, and factors relating to lifestyle such as diet and exercise. In the core of all these processes, bioinformatics serves as the integrative mechanism. At this stage, different datasets are transformed using data integration workflows, which are then analyzed through machine learning, pathway analysis, and network

modeling. This will help to extract biological sense from omics data and discover connections between genes and diets that affect health conditions (Nourazarain & Vaziri, 2025) ^[59].

The research has been undertaken with respect to Personalized nutrition. Bioinformatics-based personalized nutrition is characterized by a combination of multi-omics data with systems biology approaches to predict and improve diet-metabolism relationships at the individual level. The advancements, including the Nutrition Toolbox, make it possible to convert real foods to in silico diets for specific metabolites through using carefully constructed food composition databases and incorporate them into metabolic models. With the help of models of human metabolism and microbiome-informed models that can be integrated into constraint-based reconstruction and analysis (COBRA), it is feasible to conduct mechanistic analysis of human microbiome co-metabolism and metabolism change due to diet. The incorporation of in silico diets together with optimization procedures allows one to identify minimum dietary changes needed to satisfy certain metabolic objectives, which contributes to the implementation of precision nutrition strategies. Despite some limitations, such as the assumption about steady-state metabolism and partial bioavailability of nutrients, bioinformatics-based dietary modeling is a significant stage towards the development of predictive, personalized, and systems nutrition science (Nap *et al.*, 2026) ^[55].

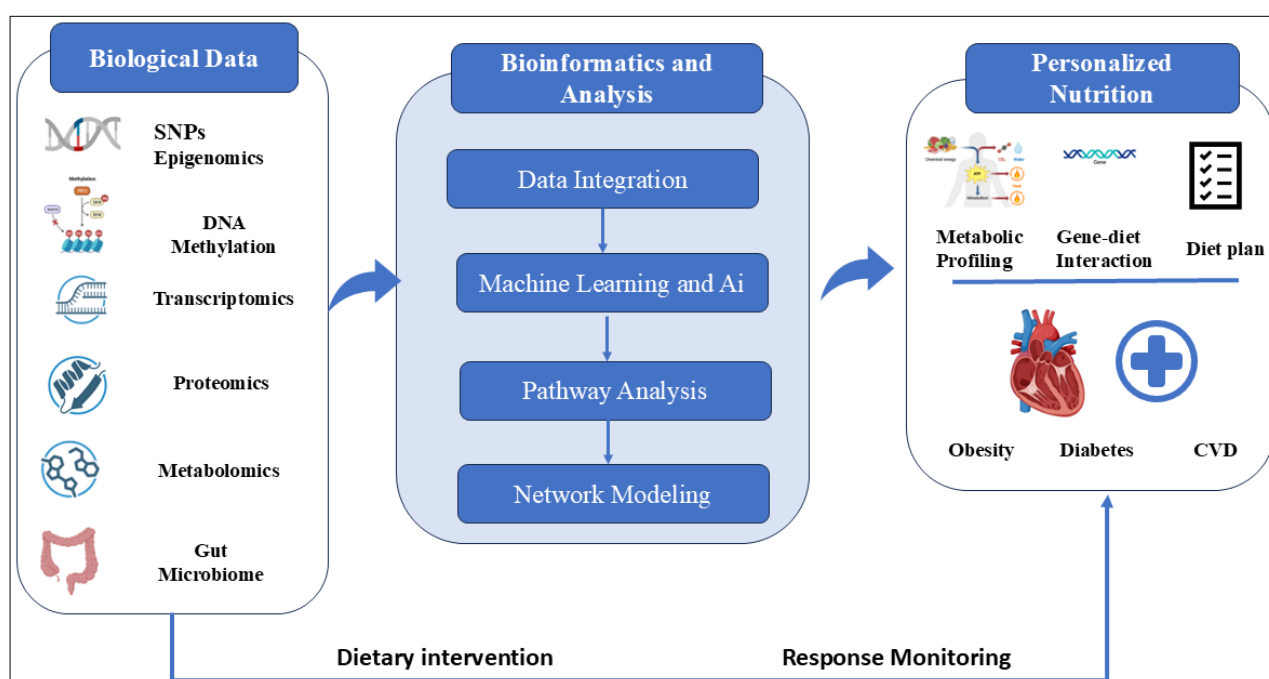


Fig 2: bioinformatics-based multi-omics approach for individualized nutrition, illustrating the process of converting intricate biological data into practical dietary plans

Table 2: Bioinformatics and Computational Approaches in Personalised Nutrition Research

Tool	Research Focus	Data Types Used	Computational/Bioinformatics Approach	summery	References
Nutrition Toolbox	In silico diet generation and optimisation	Food composition, metabolomics, microbiome	COBRA framework, whole-body metabolic models (WBMs), flux balance analysis	Converts real foods into metabolite-resolved diets; enables personalized diet optimization	(Nap <i>et al.</i> , 2026) ^[55]
Virtual Metabolic Human (VMH)	Human microbiome co-metabolism	Genomics, metabolomics, microbiome	Genome-scale metabolic modeling	Integrates host physiology and microbiome metabolism	(Noronha <i>et al.</i> , 2019) ^[58]
Nutrition Algorithm	Targeted diet optimization	Metabolite-level dietary data	Linear optimization with metabolic models	Identifies minimal dietary changes for desired metabolic outcomes	(Weston & Thiele, 2023) ^[76]
Nutrigenomics Studies	Gene diet interactions	Genomics, transcriptomics	SNP analysis, pathway enrichment	Identifies genetic variants influencing dietary responses	(Ordovas & Corella, 2004) ^[60]
Nutrieptigenomics Research	Epigenetic adaptation to diet	Epigenomics, transcriptomics	Differential methylation and acetylation analysis	Explains diet-induced metabolic plasticity beyond genetics	(Mathers, 2008) ^[50]

Bioinformatics has emerged as a fundamental element in personalized nutrition by facilitating the integration of multi-omics data, dietary details, and systems biology models to elucidate and forecast individual differences in nutritional responses. Through the use of various computational approaches, including genome-scale and whole-body metabolic models, actual food becomes an input at the level of metabolism. This allows for a better understanding of diet-host-microbiome interactions at the mechanism level and contributes to optimizing diets. Despite the advances that these methods bring into nutritional science by shifting from general guidelines applicable to all individuals to more precise and personalized ones, there are many obstacles such as data heterogeneity, overly simplified models, and lack of clinical validation. There are also ethical concerns relating to privacy and access that emphasize the need for responsible bioinformatics approaches. However, developments in the field of multi-omics, machine learning, and longitudinal measurements will hopefully contribute to improved and relevant personalized nutrition in the future (Molitor, 2021) ^[53].

3.5 Artificial intelligence and machine learning in bioinformatics

Bioinformatics and machine learning technologies have gained recognition as effective means of reducing foodborne infections and enhancing food safety procedures in recent years (Soroushianfar *et al.*, 2025) ^[66]. Bioinformatics makes it possible to identify and track diseases and disease-causing agents more precisely by analyzing biological data. These methods can anticipate disease outbreaks and determine the source of contamination using genomic data. A potent tool for food safety, machine learning is proficient at analyzing large amounts of data and finding hidden patterns (Ding *et al.*, 2023; Ge *et al.*, 2017; Nayak *et al.*, 2020) ^[29, 56]. It can recognize adverse patterns in the food production and distribution chain because to this special abilities, which enables it to make prompt and accurate judgments during emergencies. In the context of global food safety, these cutting-edge tactics drive by bioinformatics and machine

learning are extremely significant since they are essential in stopping outbreaks of foodborne illness.

In the process of developing new food products, food quality analysis is crucial (Aung & Chang, 2014) ^[5]. Food safety, nutritional value, and market value are all impacted by quality. However, because food items are biochemically complex, it is now crucial to apply sophisticated analytical technologies related to proteomics, genomics, and big data to fully identify the molecular characteristics of food ingredients and track possible variations in quality (Aung & Chang, 2014; Jeevanandam *et al.*, 2022; Valdés *et al.*, 2021b) ^[5, 38, 73]. AI is the umbrella term for a variety of technologies intended to imitate human intelligence, allowing computers to simulate cognitive processes including learning, thinking, planning, and decision-making. Fundamentally, artificial intelligence (AI) combines machine learning (ML), deep learning, computer vision, and natural language processing, among other methods, to speed up progress in a variety of domains and sectors (Ding *et al.*, 2023) ^[19]. The food and pharmaceutical industries are among the many sectors that are increasingly considering bioinformatics and artificial intelligence (AI), two dynamic and cutting-edge data science areas (Iqbal & Kumar, 2023; Malik *et al.*, 2024; Vora *et al.*, 2023) ^[36, 47, 75]. As an interdisciplinary science, bioinformatics combines biological sciences, mathematics, and information technology, which aims to process and analyze biological data using advanced computing tools (Bayat, 2002; Vashisht & Thakral, 2024; Vora *et al.*, 2023) ^[8, 74, 75]. This science makes it possible to study biological structures and processes in greater detail and uses big data to help researchers and industry professionals find hidden patterns and linkages in biological systems. Without explicit programming, machine learning enhances a system's capacity to learn from data and perform better (Jordan & Mitchell, 2015) ^[41]. These technologies have greatly improved quality control and management in food safety (Ghashi & Njobeh, 2024; Nerkar *et al.*, 2023) ^[28, 57]. The conventional procedures for monitoring and assessing food quality have been superseded by more sophisticated and precise techniques. For example, an article describes how to use machine learning and the Internet of Things (IoT) to

monitor perishable commodities. High-resolution cameras are used in the suggested system to take pictures, which are then sent via Internet of Things devices to a cloud server. The K-means clustering technique is used to segment the photos prior to uploading. After principal component analysis (PCA) is used to extract important features, the images are classified using machine learning models that have been trained. This method improves the monitoring of perishable food items by utilizing IoT, image processing, and machine learning (Nerkar *et al.*, 2023) ^[57].

The integration of machine learning (ML) with bioinformatics has significantly transformed analytical methods in food microbiology and safety science. As omics technologies produce more intricate, high-dimensional datasets, ML frameworks have become essential for deriving biologically relevant insights. Supervised algorithms, such as support vector machines (SVM), random forest (RF), and artificial neural networks (ANN), have shown substantial effectiveness in classification tasks like antimicrobial resistance (AMR) profiling, pathogen source attribution, and biomarker identification. For instance, unsupervised techniques, including PCA and hierarchical clustering, have proven helpful in identifying patterns and reducing dimensions in multi-omics layers. However, there are still significant hurdles to be addressed. First, overfitting remains a risk due to the so-called "curse of dimensionality," with many features compared to few samples. Secondly, the different formats of the data collected on proteomics and transcriptomics levels further exacerbate the problem of integration. Thirdly, deep learning models, including VAE and RNN, display great potential in terms of their capability to model non-linear cross-modal biological interactions; however, these models' highly complicated architecture inevitably prevents them from being interpretable - a vital feature since false negative predictions could affect public health adversely. Explainable AI techniques, such as SHAP and LIME, partially address this challenge, although their applications in food safety research have yet to become systematic. Besides, the lack of standardized approaches in using various platforms (mixOmics, MOFA, and GenoML among others) leads to methodological issues in comparing results obtained in other studies. Finally, the process of automation facilitated by tools like AutoXAI4Omics can lead to the creation of black-box methodologies, whereby researchers would apply the output while being unaware of their underlying model assumptions (Bansal *et al.*, 2025) ^[7].

4 Tools and databases used in bioinformatics

4.1 Sequence analysis and alignment tools

BLAST (Basic Local Alignment Search Tool) is at the core of most bioinformatics pipelines where sequence comparisons play an important role. According to (Altschul *et al.*, 1990) ^[3] and subsequent improvements, BLAST enables rapid comparison of sequences against extensive databases in a matter of a few seconds. In food science, BLAST search is indispensable for matching sequences found in environmental food samples with known allergens, toxin-generating genes, and pathogenic organisms. Moreover, (Sayers *et al.*, 2021) ^[62] reported a significant improvement in the detection capabilities of BLAST for short and highly conserved regions in food-related protein sequences in 2022. Besides BLAST, multiple alignment programs, such as MUSCLE and CLUSTALW, are useful

for comparing homologous sequences between organisms. This allows for tracing the evolution of taste receptors, metabolic enzymes, and pathogenic factors of microorganisms in food environments.

4.2 Protein databases and functional annotation

Once a gene sequence is identified, understanding what it does requires rich, well-curated databases. UniProt, and specifically its manually annotated Swiss-Prot component, serves as the premier resource for this purpose. With over 570,000 manually reviewed entries as of 2021, UniProt provides functional annotations, domain information, post-translational modifications, and literature links for proteins across all organisms (The UniProt Consortium, 2021). For food bioinformatics, this means researchers can rapidly characterize novel enzymes from fermentation microbiota, identify potential cross-reactive allergen proteins, or annotate the proteome of food spoilage organisms. NCBI GenBank, arguably the most comprehensive nucleotide database in the world, partners seamlessly with protein databases to provide a two-way bridge between gene and protein-level information (Sayers *et al.*, 2021) ^[62].

The KEGG (Kyoto Encyclopedia of Genes and Genomes) database takes functional annotation further by placing genes and proteins within the context of metabolic and signalling pathways. Updated in 2023 to include expanded entries on food-relevant metabolisms such as polyphenol biosynthesis and short-chain fatty acid production, KEGG has become an invaluable tool for nutritional bioinformatics (Kanehisa *et al.*, 2023) ^[43]. Researchers studying the fermentation of dairy products, wine, or sourdough now routinely map their metagenomic findings onto KEGG pathways to understand how microbial communities shape flavour, texture, and nutritional quality.

4.3 Structural bioinformatics: from sequence to shape

Perhaps the most dramatic development in recent bioinformatics history has been the emergence of AlphaFold2, developed by DeepMind and published by (Jumper *et al.*, 2021) ^[42]. This artificial intelligence-based tool predicts the three-dimensional structure of proteins from their amino acid sequences with near-experimental accuracy. From a food science perspective, this advance offers a range of possibilities immediately relevant to the field: knowing the exact structure of allergens makes cross-reactivity prediction possible, having the structure of food enzymes facilitates the rational engineering process, and understanding the structure of bioactive peptides accelerates their use as functional components in food products. All proteins from the UniProt database can be found on the AlphaFold Protein Structure Database website with predicted three-dimensional structures provided.

The microbial communities within the food matrixes, regardless of whether these matrices include a wheel of mature cheese, kimchi in a jar, or microbial communities on the surfaces of food-processing facilities, exert substantial impact on food safety and quality. Analyzing such communities requires specific metagenomics approaches. QIIME2 (Quantitative Insights Into Microbial Ecology 2) is one of the top metagenomics software packages currently available; it is also recognized as the best open-source platform for microbiome analysis with ASV-based approach (Bolyen *et al.*, 2019) ^[11]. In recent times, QIIME2 was applied to study the bacterial and fungal communities

present in fermented drinks, probiotics, and minimally processed vegetables; thus, it will be of great value when developing strategies for improving the quality of such products. As regards functional metagenomics studies, some software tools that allow gene prediction and annotation include MetaGeneMark and Prokka (Besemer *et al.*, 2001; Seemann, 2014) ^[10, 64]. Once used on samples of foodstuffs, such software allows for the detection of antimicrobial resistance genes, toxin encoding operons, and bioactive compound gene clusters. The Galaxy server has additionally increased accessibility by offering an online interface that enables complicated next-generation sequencing analysis pipelines to be executed without the need for command line knowledge (Afgan *et al.*, 2018) ^[11].

4.4 Protein interaction networks and pathway mapping

While the study of individual proteins is important, the study of their interactions in a biological system is called network bioinformatics. The STRING database, which collects data on the interactions between proteins based on experimental evidence, computational predictions, and literature, plays a crucial role in this area. In its latest version from 2021, the database covers more than 14,000 organisms (Szkłarczyk *et al.*, 2021) ^[69]. STRING networks have played an important role in food research in mapping

metabolic interactions among fermentation consortia, host-pathogen interactions for food-related infections, and identifying essential regulatory nodes in biosynthetic pathways of secondary metabolites in foods. As the relevance of food allergies to public health is well recognized, specific allergen databases play a significant role in food bioinformatics. AllerMatch and the more recently developed AllerHunter have applied sequence similarity and motif approaches to predict allergic potentials of novel proteins especially when these proteins arise from genetic modification or food processing (Fiers, Kleter, Nijland, Peijnenburg, Nap, & Van Ham, 2004) ^[24, 25]. It is evident that machine learning-based computational frameworks have significantly increased the ability to find hidden epitopes in allergens when compared to BLAST based methods (Muh *et al.*, 2009) ^[54]. These databases run hand-in-hand with WHO and CODEX guidelines, thus playing a crucial role in the evaluation of novel proteins and genetically modified organisms. Table 3 summarizes the most widely used bioinformatics tools and databases in food research, highlighting their categories, primary functions, and specific applications within food science and processing technology. This overview reflects the current state of the field as shaped by research published primarily between 2019 and 2024.

Table 3: Key Bioinformatics Tools and Databases Applied in Food Science Research (2019-2024)

Tool / Database	Category	Primary Function	Application in Food Bioinformatics	Reference
BLAST	Sequence Analysis	Nucleotide & protein sequence alignment	Allergen homology detection, pathogen gene identification	(Altschul <i>et al.</i> , 1990) ^[3]
UniProt/Swiss-Prot	Protein Database	Annotated protein sequences & functions	Functional annotation of food-relevant proteins & enzymes	(“UniProt: The Universal Protein Knowledgebase in 2025,” 2025) ^[72]
NCBI GenBank	Nucleotide Database	Repository of annotated nucleotide sequences	Foodborne pathogen genome storage & retrieval	(Sayers <i>et al.</i> , 2021) ^[62]
STRING	Protein Interaction	Protein-protein interaction networks	Mapping metabolic pathways in fermentation & food spoilage	(Szkłarczyk <i>et al.</i> , 2021) ^[69]
KEGG	Pathway Database	Metabolic and signalling pathway maps	Nutritional metabolism, bioactive compound pathways	(Kanehisa <i>et al.</i> , 2023) ^[43]
Galaxy Platform	Workflow/Pipeline	Bioinformatics pipeline execution	NGS data analysis for pathogen detection & food metagenomics	(Afgan <i>et al.</i> , 2018) ^[11]
QIIME2	Metagenomics	Microbiome sequence analysis	Fermented food microbiome profiling	(Bolyen <i>et al.</i> , 2019) ^[11]
AllerHunter / AllerMatch	Allergen Database	Allergen cross-reactivity prediction	GM food safety evaluation, allergen risk screening	(Fiers, Kleter, Nijland, Peijnenburg, Nap, & Van Ham, 2004) ^[24, 25]
AlphaFold2	Structural Bioinformatics	AI-based protein 3D structure prediction	Enzyme engineering, bioactive peptide structure elucidation	(Jumper <i>et al.</i> , 2021) ^[42]
MetaGeneMark / Prokka	Genome Annotation	Gene prediction & functional annotation	Characterization of microbial genomes in food environments	(Besemer <i>et al.</i> , 2001; Seemann, 2014; “UniProt: The Universal Protein Knowledgebase in 2025,” 2025) ^[10, 64, 72]

Taken altogether, these techniques form a continuum of analytic ability - from basic sequence to function identification, from single molecules to entire ecological systems. The thing that gives one hope is the rapid rate at which these newer techniques, which increasingly employ machine learning and artificial intelligence, are being

incorporated into existing technologies. The influence of AlphaFold2 in structure determination within structural biology has shown that bioinformatics through the use of AI is capable of things thought impossible by computational methods before. One can hope for no less in the future in

areas such as sequence classification and nutritional modeling.

5 Advantages and limitations of bioinformatics

Bioinformatics has revolutionized food science into an efficient and highly accurate analytical field through the use of computers in analyzing biological information in ways never before possible using experimental procedures alone. One of its main strengths is its ability to conduct parallel screening of various types of foods, food proteins, proteolytic enzymes, and microbes that can take a significantly reduced period of time compared to conventional methods. In the case of bioactive peptides, bioinformatics allows researchers to explore unknown bioactive sequences in databases using tools like BIOPEP, ExPASy PeptideCutter, and PeptideRanker; it also allows for the screening and matching of specific proteases and proteins that can be used for bioactive peptide studies without requiring the resources needed to do experiments. With regard to food safety, bioinformatics makes use of sequence analysis, proteomics, and transcriptomics techniques to aid in the detection of allergens, genetically modified foods, pathogens, and food additives. Moreover, bioinformatics also plays a vital role in crop improvement by using comparative and functional genomics to improve disease resistance and yield predictions.

Nevertheless, bioinformatics faces several challenges that reduce its effectiveness when applied in practical settings. First, the fact that *in silico* predictions cannot assure replication in the laboratory, especially considering the intricate dynamics of interaction between proteases and protein under normal physiological conditions, makes one question the reliability of predictions from bioinformatics models. Second, existing bioactive peptides databases such as BIOPEP are infrequently updated; as a result, they could lose their relevance and not reflect recently discovered bioactive peptide sequences. Moreover, there is no ability for existing bioinformatics tools to forecast what exact bioactivity will be produced, its degree, and physiological circumstances of occurrence, making bioinformatics a less effective approach on its own. Concerning the food safety problem, the majority of the bioinformatics methods employed still require a sequence analysis, lacking integration in the mechanical processes. Besides, the genetic intricacy of various plants makes bioinformatics less effective in studying the pathogens' effect on crops.

Apart from technical aspects, the field of bioinformatics in the realm of food science also poses certain problems related to ethics, regulations, and privacy of genomic and proteomic data collected. Issues related to data ownership, consent, and potential abuse associated with biological data need to be addressed. Moreover, regulation in a number of countries fails to keep pace with the development of sophisticated bioinformatics techniques. When a food safety approval or health claim is based on results of *in silico* simulations, regulatory agencies face difficulties in controlling these processes due to the lack of experimental verification. In cases when proprietary software is involved, the results become less credible due to a lack of possibility to reproduce research results by other scientists and regulatory agencies. Finally, genetic engineering of crops and their analysis using bioinformatics tools may cause serious disputes concerning intellectual property rights associated with characterization of genetically engineered

organisms and disparities between high- and low-income countries in utilizing such technology.

6 conclusions

Bioinformatics, a key research area in contemporary food science, is an essential interdisciplinary field that provides unique possibilities to perform the rapid and accurate analysis of complex biological data using modern high throughput technologies. Bioinformatics is utilized in many fields of food science, including but not limited to allergen detection; evaluation of food safety; identification of microorganisms; plant breeding; personalization of nutrition; and multi-omics integration. Changes in computational techniques as well as the extensive use of artificial intelligence in food research have significantly changed the field of food science over the last thirty years by broadening and deepening the scope of food research. Cutting-edge software programs allow researchers to gain insight into molecular interaction patterns and their effects on microbial communities and metabolic tendencies, which ultimately impact the quality, safety, and nutritional composition of food products. Numerous barriers have prevented the use of bioinformatics in food research because biological entities comprise a high level of complexity, diversity, and difficulty to model. Additionally, existing databases and algorithms often lack sufficient information and/or functionality to meet the requirements of the bioinformatics decided process. To further the advancement of bioinformatics in food science, there are several requirements: (1) all databases used for food research should continuously be updated; (2) all *in silico* conclusions should be verified through experimentation; (3) preparation and analysis of studies should be conducted in conjunction with computational and experimental studies; and (4) ethical issues involved with the personalization of nutrition should be investigated.

Credit authorship contribution statement

Hanuman Anshiram Jadhav: Writing - review & editing, Writing - original draft. Kisore S: Writing - review & editing. Chandrasekar Veerapandian: Writing - review & editing, Supervision, Resources, Investigation. V. Eyarkai Nambi: Writing - review & editing, Supervision.

Declaration of competing interest

The authors declare that they have no known competing financial interest

Data availability

No data was used for the research described in the article.

References

1. Afgan E, Baker D, Batut B, Van Den Beek M, Bouvier D, Čech M, Chilton J, Clements D, Coraor N, Grüning BA. The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. *Nucleic Acids Res.* 2018;46(W1):W537-W544.
2. Akalin PK. Introduction to bioinformatics. *Mol Nutr Food Res.* 2006;50(7):610-619.
3. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. *J Mol Biol.* 1990;215(3):403-410.
4. Approaches B, Nutrition P. Bioinformatics approaches for personalized nutrition. 2022;3(5):12-16.

5. Aung MM, Chang YS. Traceability in a food supply chain: Safety and quality perspectives. *Food Control*. 2014; 39:172-184.
6. Balali-Mood M, Naseri K, Tahergorabi Z, Khazdair MR, Sadeghi M. Toxic mechanisms of five heavy metals: mercury, lead, chromium, cadmium, and arsenic. *Front Pharmacol*. 2021; 12:643972.
7. Bansal S, Rodriguez CZ, Thompson-Witrick KA, Wang Y, Taft DH, Zhang B. Machine learning-powered multi-omics for food microbiology and smarter food safety. *Trends Food Sci Technol*. 2025; 163:105145. DOI: 10.1016/j.tifs.2025.105145.
8. Bayat A. Science, medicine, and the future: Bioinformatics. *BMJ*. 2002;324(7344):1018-1022.
9. Bennetzen JL, Kellogg EA, Lee M, Messing J. A plant genome initiative. *Plant Cell*. 1998;10(4):488-493. DOI:10.1105/tpc.10.4.488.
10. Besemer J, Lomsadze A, Borodovsky M. GeneMarkS: a self-training method for prediction of gene starts in microbial genomes. Implications for finding sequence motifs in regulatory regions. *Nucleic Acids Res*. 2001;29(12):2607-2618.
11. Bolyen E, Rideout JR, Dillon MR, Bokulich NA, Abnet CC, Al-Ghalith GA, Alexander H, Alm EJ, Arumugam M, Asnicar F. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nat Biotechnol*. 2019;37(8):852-857.
12. Boutanaev AM, Moses T, Zi J, Nelson DR, Mugford ST, Peters RJ, Osbourn A. Investigation of terpene diversification across multiple sequenced plant genomes. *Proc Natl Acad Sci USA*. 2015;112(1):E81-E88.
13. Brul S, Schuren F, Montijn R, Keijser BJF, Van der Spek H, Oomes S. The impact of functional genomics on microbiological food quality and safety. *Int J Food Microbiol*. 2006;112(3):195-199.
14. Buckley M, Reid A. Global food safety: keeping food safe from farm to table. Washington (DC): American Academy of Microbiology; 2010.
15. Carvalho FP. Pesticides, environment, and food safety. *Food Energy Secur*. 2017;6(2):48-60.
16. da Silva Anastacio V. Nutrigenetics & nutrigenomics and its clinical application [dissertation]. London: St Mary's University; 2024.
17. DeSesso JM. Future of developmental toxicity testing. *Curr Opin Toxicol*. 2017; 3:1-5. DOI: 10.1016/j.cotox.2017.04.001.
18. Desiere F, German B, Watzke H, Pfeifer A, Saguy S. Bioinformatics and data knowledge: the new frontiers for nutrition and foods. *Trends Food Sci Technol*. 2001;12(7):215-229. DOI:10.1016/S0924-2244(01)00089-9.
19. Ding H, Tian J, Yu W, Wilson DI, Young BR, Cui X, Xin X, Wang Z, Li W. The application of artificial intelligence and big data in the food industry. *Foods*. 2023;12(24):4511.
20. Dong D, Jones G, Zhang S. Dynamic evolution of bitter taste receptor genes in vertebrates. *BMC Evol Biol*. 2009;9:1-9.
21. Dotson CD, Zhang L, Xu H, Shin YK, Vignes S, Ott SH, Elson AET, Choi HJ, Shaw H, Egan JM. Bitter taste receptors influence glucose homeostasis. *PLoS One*. 2008;3(12):e3974.
22. Feng C, Teuber S, Gershwin ME. Histamine (scombroid) fish poisoning: A comprehensive review. *Clin Rev Allergy Immunol*. 2016;50(1):64-69.
23. Ferrocino I, Rantsiou K, Cocolin L. Microbiome and -omics application in food industry. *Int J Food Microbiol*. 2022; 377:109781. DOI: 10.1016/j.ijfoodmicro.2022.109781.
24. Fiers MWEJ, Kleter GA, Nijland H, Peijnenburg AACM, Nap JP, van Ham RCHJ. Allermatch™: A webtool for the prediction of potential allergenicity according to current FAO/WHO Codex alimentarius guidelines. *BMC Bioinformatics*. 2004; 5:133. DOI:10.1186/1471-2105-5-133.
25. Fiers MWEJ, Kleter GA, Nijland H, Peijnenburg AACM, Nap JP, Van Ham RCHJ. Allermatch™: A webtool for the prediction of potential allergenicity according to current FAO/WHO Codex alimentarius guidelines. *BMC Bioinformatics*. 2004;5(1):133.
26. Fung F, Wang HS, Menon S. Food safety in the 21st century. *Biomed J*. 2018;41(2):88-95.
27. Gallo M, Ferrara L, Calogero A, Montesano D, Naviglio D. Relationships between food and diseases: What to know to ensure food safety. *Food Res Int*. 2020; 137:109414.
28. Gbashi S, Njobeh PB. Enhancing food integrity through artificial intelligence and machine learning: A comprehensive review. *Appl Sci*. 2024;14(8):3421.
29. Ge Z, Song Z, Ding SX, Huang B. Data mining and analytics in the process industry: The role of machine learning. *IEEE Access*. 2017;5:20590-20616.
30. Gendel SM. Sequence databases for assessing the potential allergenicity of proteins used in transgenic foods. *Food Chem Toxicol*. 1998;36(11): S1-S2.
31. Gendel SM. Bioinformatics and food allergens. *J AOAC Int*. 2004;87(6):1417-1422. DOI:10.1093/jaoac/87.6.1417.
32. Gendel SM, Jenkins JA. Allergen sequence databases. *Mol Nutr Food Res*. 2006;50(7):633-637.
33. Hao DC, Xiao PG. Genomics and evolution in traditional medicinal plants: Road to a healthier life. *Evol Bioinform*. 2015;11: EBO-S31326.
34. Healy MJ, Tong W, Ostroff S, Eichler HG, Patak A, Neuspiel M, Deluyker H, Slikker W. Regulatory bioinformatics for food and drug safety. *Regul Toxicol Pharmacol*. 2016; 80:342-347. DOI: 10.1016/j.yrtph.2016.05.021.
35. Holton TA, Vijayakumar V, Khaldi N. Bioinformatics: Current perspectives and future directions for food and nutritional research facilitated by a Food-Wiki database. *Trends Food Sci Technol*. 2013;34(1):5-17. DOI: 10.1016/j.tifs.2013.08.009.
36. Iqbal N, Kumar P. From data science to bioscience: Emerging era of bioinformatics applications, tools and challenges. *Procedia Comput Sci*. 2023; 218:1516-1528.
37. Ivanciuc O, Schein CH, Braun W. SDAP: Database and computational tools for allergenic proteins. *Nucleic Acids Res*. 2003;31(1):359-362.
38. Jeevanandam J, Agyei D, Danquah MK, Udenigwe C. Food quality monitoring through bioinformatics and big data. In: *Future Foods*. Amsterdam: Elsevier; 2022. p. 733-744.
39. Jenkins JA, Griffiths-Jones S, Shewry PR, Breiteneder H, Mills ENC. Structural relatedness of plant food

- allergens with specific reference to cross-reactive allergens: An in silico analysis. *J Allergy Clin Immunol.* 2005;115(1):163-170.
40. Joint FAO/WHO. Evaluation of allergenicity of genetically modified foods: Report of a Joint FAO/WHO Expert Consultation on Allergenicity of Foods Derived from Biotechnology, 22-25 January 2001. Rome: Food and Agriculture Organization of the United Nations; 2001.
 41. ordan MI, Mitchell TM. Machine learning: Trends, perspectives, and prospects. *Science.* 2015;349(6245):255-260.
 42. Jumper J, Evans R, Pritzel A, Green T, Figurnov M, Ronneberger O, Tunyasuvunakool K, Bates R, Židek A, Potapenko A, *et al.* Highly accurate protein structure prediction with AlphaFold. *Nature.* 2021;596(7873):583-589.
 43. Kanehisa M, Furumichi M, Sato Y, Kawashima M, Ishiguro-Watanabe M. KEGG for taxonomy-based analysis of pathways and genomes. *Nucleic Acids Res.* 2023;51(D1):D587-D592.
 44. Kendall P, Medeiros LC, Hillers V, Chen G, Dimascola S. Food handling behaviors of special importance for pregnant women, infants and young children, the elderly, and immune-compromised people. *J Am Diet Assoc.* 2003;103(12):1646-1649.
 45. Lemay DG, Zivkovic AM, German JB. Building the bridges to bioinformatics in nutrition research. *Am J Clin Nutr.* 2007;86(5):1261-1269. DOI:10.1093/ajcn/86.5.1261.
 46. Lin J, Bruni FM, Fu Z, Maloney J, Bardina L, Boner AL, Gimenez G, Sampson HA. A bioinformatics approach to identify patients with symptomatic peanut allergy using peptide microarray immunoassay. *J Allergy Clin Immunol.* 2012;129(5):1321-1328.e5. DOI: 10.1016/j.jaci.2012.02.012.
 47. Malik S, Muhammad K, Waheed Y. Artificial intelligence and industrial applications: A revolution in modern industries. *Ain Shams Eng J.* 2024;15(9):102886.
 48. Manzoor Waidha K, Kaur R, Singh D, Neetu J, Jabalia N, Jha A. Bioinformatics approaches in food industry: An overview. National Conference on [conference details unavailable]. 2015 Nov:1-4. DOI:10.13140/RG.2.2.27961.77926.
 49. Mari A, Scala E, Palazzo P, Ridolfi S, Zennaro D, Carabella G. Bioinformatics applied to allergy: Allergen databases, from collecting sequence information to data integration. The Allergome platform as a model. *Cell Immunol.* 2006;244(2):97-100.
 50. Mathers C. The global burden of disease: 2004 update. Geneva: World Health Organization; 2008.
 51. Mehta A, Hasija Y. Bioinformatics approaches for genomics and post-genomics applications of anticancer plants. In: *Anticancer Plants: Mechanisms and Molecular Interactions.* Vol. 4. Cham: Springer; 2018. p. 283-317.
 52. Mohammad AM, Chowdhury T, Biswas B, Absar N. Food poisoning and intoxication: A global leading concern for human health. In: *Food Safety and Preservation.* Amsterdam: Elsevier; 2018. p. 307-352.
 53. Molitor C. A bioinformatics and genotyping approach exploring personalised nutrition [dissertation]. 2021.
 54. Muh HC, Tong JC, Tammi MT. AllerHunter: A SVM-pairwise system for assessment of allergenicity and allergic cross-reactivity in proteins. *PLoS One.* 2009;4(6):e5861.
 55. Nap B, Weston B, Brandt A, Wodak MF, Bergheim I, Thiele I. The Nutrition Toolbox permits in silico generation, analysis, and optimisation of personalised diets through metabolic modelling. 2026:1-6.
 56. Nayak J, Vakula K, Dinesh P, Naik B, Pelusi D. Intelligent food processing: Journey from artificial neural network to deep learning. *Comput Sci Rev.* 2020; 38:100297.
 57. Nerkar PM, Shinde SS, Liyakat KKS, Desai S, Kazi SSL. Monitoring fresh fruit and food using IoT and machine learning to improve food safety and quality. *Tuijin Jishu/J Propul Technol.* 2023;44(3):2927-2931.
 58. Noronha A, Modamio J, Jarosz Y, Guerard E, Sompairac N, Preciat G, Daniëlsdóttir AD, Krecke M, Merten D, Haraldsdóttir HS, *et al.* The Virtual Metabolic Human database: Integrating human and gut microbiome metabolism with nutrition and disease. *Nucleic Acids Res.* 2019;47(D1):D614-D624.
 59. Nourazarain A, Vaziri Y. Nutrigenomics meets multi-omics: Integrating genetic, metabolic, and microbiome data for personalized nutrition strategies. *Genes Nutr.* 2025.
 60. Ordovas JM, Corella D. Nutritional genomics. *Annu Rev Genomics Hum Genet.* 2004;5(1):71-118. Radauer, C., Bublin, M., Wagner, S., Mari, A., & Breiteneder, H. (2008). Allergens are distributed into few protein families and possess a restricted number of biochemical functions. *Journal of Allergy and Clinical Immunology*, 121(4), 847-852.
 61. Raspor P. Total food chain safety: How good practices can contribute? *Trends Food Sci Technol.* 2008;19(8):405-412.
 62. Sayers EW, Beck J, Bolton EE, Bourexis D, Brister JR, Canese K, Comeau DC, Funk K, Kim S, Klimke W, *et al.* Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res.* 2021;49(D1):D10-D17.
 63. Schein CH, Ivanciuc O, Braun W. Bioinformatics approaches to classifying allergens and predicting cross-reactivity. *Immunol Allergy Clin North Am.* 2007;27(1):1-27. DOI: 10.1016/j.iac.2006.11.005.
 64. Seemann T. Prokka: Rapid prokaryotic genome annotation. *Bioinformatics.* 2014;30(14):2068-2069.
 65. Shi P, Zhang J. Contrasting modes of evolution between vertebrate sweet/umami receptor genes and bitter receptor genes. *Mol Biol Evol.* 2006;23(2):292-300.
 66. Soroushianfar M, Asgari G, Afzali F, Falahat A, Soroush M, Baghahi M, Haratizadeh MJ, Khalili-Tanha G, Nazari E. Application of bioinformatics and machine learning tools in food safety. *Curr Nutr Rep.* 2025;14(1). DOI:10.1007/s13668-025-00657-w.
 67. Stoesser G, Baker W, van den Broek A, Garcia-Pastor M, Kanz C, Kulikova T, Leinonen R, Lin Q, Lombard V, Lopez R. The EMBL nucleotide sequence database: Major new developments. *Nucleic Acids Res.* 2003;31(1):17-22.
 68. Syaiful Khoiri, Moussango VD. A short review on harnessing bioinformatics for food safety: Computational approaches to detecting foodborne

- pathogens. *J Adv Health Inform Res.* 2024;2(3):109-114. DOI:10.59247/jahir.v2i3.296.
69. Szklarczyk D, Gable AL, Nastou KC, Lyon D, Kirsch R, Pyysalo S, Doncheva NT, Legeay M, Fang T, Bork P, *et al.* The STRING database in 2021: Customizable protein-protein networks and functional characterization of user-uploaded gene/measurement sets. *Nucleic Acids Res.* 2021;49(D1):D605-D612.
70. Talevi A, Enrique AV, Bruno-Blanch LE. Anticonvulsant activity of artificial sweeteners: A structural link between sweet-taste receptor T1R3 and brain glutamate receptors. *Bioorg Med Chem Lett.* 2012;22(12):4072-4074.
71. Udenigwe CC. Bioinformatics approaches, prospects and challenges of food bioactive peptide research. *Trends Food Sci Technol.* 2014;36(2):137-143. DOI: 10.1016/j.tifs.2014.02.004.
72. UniProt: The universal protein knowledgebase in 2025. *Nucleic Acids Res.* 2025;53(D1):D609-D617.
73. Valdés A, Alvarez-Rivera G, Socas-Rodríguez B, Herrero M, Ibanez E, Cifuentes A. Foodomics: Analytical opportunities and challenges. *Anal Chem.* 2021;94(1):366-381.
74. Vashisht R, Thakral G. A comprehensive study of bioinformatics with machine learning. In: *Federated Learning and Privacy-Preserving in Healthcare AI*. Hershey (PA): IGI Global Scientific Publishing; 2024. p. 46-57.
75. Vora LK, Gholap AD, Jetha K, Thakur RRS, Solanki HK, Chavda VP. Artificial intelligence in pharmaceutical technology and drug delivery design. *Pharmaceutics.* 2023;15(7):1916.
76. Weston BR, Thiele I. A nutrition algorithm to optimize feed and medium composition using genome-scale metabolic models. *Metab Eng.* 2023;76:167-178.
77. Wheeler DL, Church DM, Federhen S, Lash AE, Madden TL, Pontius JU, Schuler GD, Schriml LM, Sequeira E, Tatusova TA, Wagner L. Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res.* 2003;31(1):28-33. DOI:10.1093/nar/gkg033.
78. World Health Organization. *Air Quality Guidelines for Europe*. 2nd ed. Copenhagen: WHO Regional Office for Europe; 2000.
79. Wooding S, Bufe B, Grassi C, Howard MT, Stone AC, Vazquez M, Dunn DM, Meyerhof W, Weiss RB, Bamshad MJ. Independent evolution of bitter-taste sensitivity in humans and chimpanzees. *Nature.* 2006;440(7086):930-934.
80. Wu CH, Yeh LS, Huang H, Arminski L, Castro-Alvear J, Chen Y, Hu Z, Kourtesis P, Ledley RS, Suzek BE, Vinayaka CR, Zhang J, Barker WC. The Protein Information Resource. *Nucleic Acids Res.* 2003;31(1):345-347. DOI:10.1093/nar/gkg040.
81. Xu W. Application of bioinformatics technology in food processing and food safety assessment. In: *2018 International Conference on Zoology, Botany and Ecology (ICZBE)*. 2018. p. 106-112. DOI:10.25236/iczbe.2018.023.
82. Yang C, Valerio LG, Arvidson KB. Computational toxicology approaches at the US Food and Drug Administration. *Altern Lab Anim.* 2009;37(5):523-531. DOI:10.1177/026119290903700509.