

Predictive Food Microbiology: A Model to Achieving Shelf-Life Extension and Product Maximization

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ABSTRACT

Predictive food microbiology integrates traditional microbiological principles with mathematical modeling, statistics, and information technology to anticipate microbial behavior in foods. It aims to prevent food spoilage and food-borne illnesses by forecasting microbial growth, survival, or inactivation under varying conditions. The behavior of microorganisms is influenced by factors such as water activity, pH, temperature, relative humidity, and storage atmosphere. Using quantitative models, these effects can be predicted to estimate microbial population changes from production to consumption. Predictive models have significant practical applications in ensuring food safety, quality, and shelf-life extension. They enhance understanding of the microbial ecology of foods and serve as valuable decision-support tools in food safety management. Although these models simplify complex biological systems and thus have inherent limitations, they provide a strong basis for exposure assessment in Quantitative Microbial Risk Assessment (QMRA). When validated against performance criteria, predictive

models remain essential tools for improving microbial food safety through informed prediction and control of contamination risks.

Keywords: Food, Predictions, shelf-life, extension, microbes.

Introduction

Food preservation methods such as salting, drying, and fermentation have been practiced for thousands of years, representing early empirical strategies for controlling microbial populations in food. These traditional techniques continue to be employed by indigenous communities and are also evident in certain artisanal products from technologically advanced societies. Early applications of scientific principles to food preservation can be traced to Pasteur's pioneering studies on the specificity of undesirable fermentations in wine, and to Hansen's introduction of defined lactic starter cultures in Denmark at the end of the 19th century.

While much of the fermentation industry has adopted quantitative approaches—driven largely by large-scale production demands and the involvement of chemical engineers—many other sectors of food microbiology remain predominantly qualitative or semi-quantitative. Traditional “shake and plate” enumeration methods typically achieve precision within ± 0.5 log units, with detection limits often as high as 100 cfu/g. Similarly, the most probable number (MPN) technique yields broad confidence intervals, and enrichment methods can confirm presence but not necessarily absence of specific microorganisms. Moreover, sampling procedures themselves may be insufficient to accurately reflect the true prevalence or concentration of target organisms within an entire product lot [1].

Worldwide, food safety protocols have evolved significantly to protect consumers at a large scale.

The recognition of the germ theory of disease in the 19th century marked a turning point, leading to improved sanitation practices and enhanced animal welfare standards. These developments resulted in stricter safety regulations, particularly in the dairy industry, which soon extended to other sectors of the food system [2]. The rise of industrialization and large-scale food processing further emphasized the need for comprehensive public health initiatives to ensure the safety of food products for consumers.

Today, rigorous screening procedures are implemented to minimize risks associated with microbial hazards (including pathogenic microorganisms, toxins, and mycotoxins), chemical contaminants (such as heavy metals, pesticides, and carcinogens), as well as physical hazards like foreign objects [3]. Among these, biological hazards pose the most significant threat, often leading to severe foodborne outbreaks [4]. According to a review by Lee and Yoon [5], norovirus accounts for the highest global incidence of foodborne illnesses, followed by *Campylobacter*, *Salmonella*, and *Listeria monocytogenes*. Furthermore, a World Health Organization (WHO) report confirmed that bacterial foodborne infections occur more frequently than viral or parasitic diseases [6].

Efforts to mitigate these threats encompass both immediate interventions—focused on addressing urgent knowledge gaps—and long-term strategic initiatives aimed at improving preparedness and prevention capabilities [7]. Strengthening research in this domain enhances the ability to respond rapidly to emerging microbial threats and supports proactive measures to anticipate and prevent their occurrence.

Central to this proactive approach is the collection of quantitative data on microbial behavior in foods (predictive microbiology) and a deeper understanding of microbial physiology [8].

Predictive microbiology applies quantitative research on microbial ecology to anticipate how microorganisms respond to environmental conditions. It is based on the principle that microbial responses to specific environmental factors are consistent and measurable. By characterizing these factors—such as temperature, pH, water activity, and atmospheric conditions—historical data can be used to forecast microbial behavior under similar circumstances. Consequently, the term *quantitative microbial ecology* has been proposed as an alternative to *predictive microbiology* [9].

After a significant period of development, predictive microbiology (which encompasses the quantitative microbial ecology of foods) has emerged as a vital component of contemporary food microbiology. This discussion will explore the evolution of predictive microbiology, particularly in relation to interfaces. The term interface carries multiple meanings, describing not only the boundaries of scientific inquiry, such as the growth/no growth interface, but also the intersections between different disciplines that have resulted in important conceptual and technological progress.

The idea of predictive microbiology is relatively new in its application, although it has existed for some time. Esty and Meyer [10] utilized mathematical methods to assess the survival rates of microorganisms. Additionally, modeling the growth of microbes has been a practice in industrial microbiology since Monod's work in 1949. Nonetheless, it is important for food microbiology to develop its own set of models rather than replicating those from industrial microbiology, as their goals differ [1].

Predictive microbiology focuses on understanding how microbial growth responds to various environmental factors, which is encapsulated in equations or mathematical models. A database could be created to house raw data and models, allowing for the retrieval of information that can help interpret how processing and transportation methods impact microbial growth [7]. The development, validation, and application of predictive microbiology have been thoroughly examined over the past few decades [11].

Initially, modeling studies primarily focused on the thermal inactivation of pathogenic bacteria. However, subsequent studies shifted their attention to understanding how various constraints affect microbial growth (as opposed to survival or death). These studies often employed a kinetic model approach instead of probability modeling, frequently highlighting temperature as either the sole controlling factor or one among several.

For instance, the temperature dependence model for the growth of *Clostridium botulinum* showed a strong correlation with the data. Nevertheless, the authors cautioned that "care must be taken at extremes of growth, as no growth may be registered in a situation where growth is indeed possible but has a low probability" [12].

Fundamentals of Predictive Microbiology

The fundamental concept of predictive microbiology is based on the understanding that we can simulate microbial growth and survival using mathematical models. Various criteria influence the effectiveness of these mathematical growth models. By minimizing the number of parameters being analyzed, we can achieve better resolution and predictive relevance.

Additionally, employing a mechanistic approach that focuses on a limited number of significant parameters enables us to encompass more stages of microbial growth, thereby enhancing the accuracy of the model [13].

a. Microbial Growth Models

The growth curve of most foodborne bacteria typically comprises four distinct phases: an initial lag phase, during which cells adapt to their environment with minimal detectable growth; an exponential (log) phase, characterized by rapid cell division; a stationary phase, where growth stabilizes as nutrients deplete and waste accumulates; and finally, a death phase, during which conditions become unfavorable and viable cell numbers decline [14]. Microbial models can be classified according to several criteria. Based on the expected microbial response, they are divided into *kinetic* and *probabilistic* models. According to the modeling approach, they may be *empirical* or *mechanistic*. Furthermore, depending on the type of dependent variable assessed, models are categorized as *primary*, *secondary*, or *tertiary* [15,16].

i. Primary Models

Primary models describe how bacterial populations change over time under specific environmental conditions. These models aim to represent microbial growth or inactivation behavior using the smallest possible number of parameters [17]. Depending on their focus, primary models may be empirical, growth rate-based, inactivation, or survival models—or a combination of these types. They typically incorporate a limited set of biologically meaningful parameters, such as the specific growth rate, initial population density, and maximum (asymptotic) population size, to characterize microbial responses quantitatively.

ii. Secondary Models

Secondary models examine the factors that influence the kinetic parameters identified by primary models. They describe the relationship between these parameters—such as growth rate or lag time—and both intrinsic (e.g., pH, water activity) and extrinsic (e.g., temperature, atmosphere) factors affecting microbial behavior [18]. While primary models focus on estimating microbial population changes over time, secondary models quantify how environmental and physicochemical variables modulate those changes (Perez-Rodriguez et al., 2013). Numerous secondary models have been developed to analyze the effects of one or more environmental factors on key parameters such as lag phase duration and specific growth rate [19].

iii. Tertiary Models

Tertiary models are computational tools that integrate primary and secondary models within a user-friendly graphical interface (GUI). These software-based systems employ algorithms to simulate and visualize microbial responses under various environmental conditions, thereby enhancing accessibility for users with limited modeling experience. Tertiary models are widely applied in both research and the food industry to consolidate insights derived from primary and secondary modeling approaches. A notable example is the Unified Growth Prediction Model (UGPM) software, which is based on the Baranyi and Roberts primary model and incorporates temperature-dependent secondary models to predict microbial behavior more accurately [20].

b. Empirical and Mechanistic Models

1. Empirical Models

Empirical models provide practical, structured frameworks in which relationships between variables are represented mathematically, often using first- or second-degree polynomial equations [7]. These models generate predictions based on observed data without explicitly accounting for the underlying physicochemical factors that may influence microbial behavior. A well-known example of this approach is the quadratic response surface model developed by Gibson et al. [21], which is frequently applied to describe the combined effects of environmental factors on microbial growth parameters.

2. Mechanistic or Deterministic Models

Mechanistic, or deterministic, models are grounded in established scientific principles and describe microbial responses based on known biological and physicochemical processes. Unlike empirical models, they emphasize causality by linking observable outcomes to underlying mechanisms. These models typically require fewer parameters, provide a closer fit to experimental data, and offer a more accurate representation of microbial behavior. Moreover, their strong theoretical foundation gives them superior extrapolation capabilities, making them generally more robust and reliable than empirical models [18].

C. Kinetic and Probabilistic Models

1. Kinetic Models

Kinetic models are developed to determine the expected rates of microbial responses, including both growth and inactivation processes. They are primarily used to predict concentration levels associated with specific microbial strains, thereby enabling the assessment of related risks such as infection or intoxication (Stavropoulou and Bezirtzoglou, 2019). Common examples include the Gompertz and square root models, which describe microbial parameters such as lag time, specific growth rate, and maximum population density. In addition, inactivation or survival models are employed to represent microbial destruction or persistence over time under various environmental conditions [22].

2. Probability Models

In contrast to kinetic models, probabilistic models focus solely on the likelihood of microbial growth or toxin production rather than the rate at which these events occur [23]. These models are particularly useful for identifying the absolute limits of microbial growth under specific environmental conditions. They also help to define stress threshold levels—conditions that may temporarily inhibit microbial proliferation but do not necessarily prevent it entirely [24]. By quantifying the probability of growth or toxin formation, probabilistic models provide valuable insights for risk assessment and food safety management, especially in scenarios where microbial behavior is influenced by variable or borderline environmental factors.

Applications of Predictive Microbiology in Food Safety

1. Quality Control of Food Products.

Predictive microbiology can be effectively employed to validate the efficacy of microbial inactivation techniques such as drying, heat treatment, and refrigeration. Food industries producing yogurt, milk, wine, and sous-vide products must adhere to strict refrigeration and heat treatment protocols to ensure microbiological safety [25].

However, these control methods are often inadequately applied or poorly managed, resulting in unwanted microbial proliferation. In the dairy sector, for instance, the limitations of heat treatments as the sole control measure against fungal spore germination have been well documented. Certain spore-forming fungal and bacterial species can survive pasteurization or even thrive at low storage temperatures. *Bacillus sporothermophilus*, for example, is known for its remarkable resistance to the high temperatures typically achieved during pasteurization [26].

Several studies have also identified widespread non-compliance with cold-chain regulations across distribution, retail, and storage stages, which can compromise food safety by the time products reach consumers. This highlights the urgent need for the implementation of quality control checkpoints throughout the food supply chain.

A study by Gougouli et al. [27] demonstrated that microbial growth in yogurt—evidenced by visible mycelial formation—is significantly influenced by factors such as storage temperature, duration, and the specific microbial strain present. Consequently, predictive models capable of simulating fungal growth under these conditions are highly valuable in the dairy industry. By integrating such models into final product testing, producers can enhance quality assurance and detect fungal contamination before market release. Predictive models also support the identification of optimal environmental conditions for various microbial species during end-product challenge testing.

It is essential to recognize that different microbial contaminants thrive under distinct environmental conditions. Therefore, selecting test conditions during challenge studies must be based on sound scientific evidence rather than arbitrary criteria, as inappropriate choices may yield false negatives and lead to the inadvertent distribution of contaminated products. Additional predictive modeling efforts within the dairy sector have evaluated how factors such as temperature, pH, water activity, and inoculum size influence the growth of *Listeria monocytogenes* in milk and *Yersinia enterocolitica* in Camembert-type cheese [28].

2. Risk Assessment and Management.

Risk assessment is a structured, scientific process used to evaluate the potential human health risks associated with exposure to foodborne hazards [29]. It comprises four sequential stages: hazard identification, exposure assessment, hazard characterization, and risk characterization. Data generated through Microbial Risk Assessment (MRA) are fundamental in shaping policies and regulations addressing major foodborne pathogens [30].

Traditional approaches to food risk assessment are predominantly deterministic [31]. These methods assume that estimated parameters remain constant, disregarding the inherent variability and uncertainty present in real-world conditions. Consequently, discrepancies between challenge tests and laboratory results can lead to erroneous conclusions when deterministic methods are used in isolation. To overcome these limitations, more dynamic and sensitive techniques—such as predictive modeling—should be incorporated into the risk assessment process.

Predictive models enable the estimation of microbial hazards throughout the entire food chain, from production to consumption (Membre and Guillou, 2016). The insights derived from these models support science-based decision-making by

defining acceptable levels of microbial exposure and guiding the development of effective risk mitigation strategies for consumer protection [33].

3. HACCP (Hazard Analysis and Critical Control Point) Systems.

The Hazard Analysis and Critical Control Point (HACCP) system is a preventive food safety framework designed to identify, evaluate, and control potential hazards throughout all stages of food production, processing, distribution, and consumption. It employs a systematic approach to detect pathogenic microorganisms in raw materials and during processing, implement effective control measures for their elimination or reduction, and prevent contamination or deterioration in the final product due to improper handling.

Predictive food microbiology plays a pivotal role in supporting the implementation and optimization of the HACCP system. The integration of Quantitative Microbial Risk Assessment (QMRA) within hazard analysis enhances the identification of Critical Control Points (CCPs) and the establishment of appropriate Critical Limits (CLs) by quantifying potential microbial risks within the food chain. Predictive models can be designed to simulate and evaluate systems used to monitor CCPs, thereby validating the overall effectiveness of HACCP-based control strategies.

Moreover, predictive testing models are capable of forecasting CCPs by determining threshold values for parameters that influence microbial growth. These models also provide estimations of microbial behavior under varying conditions, enabling the establishment of scientifically justified limits for food safety management. Consequently, the integration of HACCP with predictive modeling offers a powerful, data-driven framework for proactive decision-making and continuous improvement in food safety assurance [34].

4. Shelf-Life Determination.

Traditional microbiological methods used for determining food shelf life are often labor-intensive and time-consuming, as they require substantial microbial growth before visible spoilage indicators appear. Conversely, modern analytical techniques, while faster and more precise, often rely on advanced and expensive instrumentation. Predictive modeling of microbial behavior offers a practical and scientifically sound alternative by providing the foundation for developing intelligent monitoring tools capable of estimating shelf life throughout storage, transportation, distribution, and retail phases.

Effective shelf-life prediction models must satisfy several essential criteria. They should identify spoilage reactions (SRs)—including slime formation, discoloration, and the development of off-odors—while also recognizing the specific spoilage organisms (SSOs) responsible for these reactions. Additionally, such models must define the spoilage domain (SD), representing the environmental conditions that allow a particular SSO to grow and produce spoilage effects. Developing and validating a shelf-life prediction model involves experimental identification of SSOs, their spoilage reactions, and corresponding spoilage domains. Subsequently, modeling microbial behavior within these domains enables the determination of the minimum spoilage level, or the threshold concentration of SSOs at which a product becomes organoleptically unacceptable. Notably, it is not only the population density of spoilage organisms but also their metabolic activity that drives spoilage processes (Dalgaard and Huss, 2020).

A wide range of predictive models has been developed for shelf-life estimation across diverse food categories. For instance, Mataragas et al. [36] created a model for predicting the shelf life of yogurt; Limbo et al. [37] developed a similar model for minced beef; and Rasane [38] proposed a model for Nutri cereal-based baby food. Other studies have focused on identifying specific spoilage mechanisms, such as the impact of *Pseudomonas* species on pork and poultry (Bruckner et al. [39]) and the role of lactic acid bacteria in cooked ham (Kreyenschmidt [40]). Collectively, these predictive models contribute significantly to enhancing food quality assurance, safety management, and product shelf-life optimization by elucidating the microbial and environmental determinants of spoilage.

Major Limitations of Predictive Models

Predictive models provide valuable support in decision-making and risk management within the food industry. Nevertheless, it is essential to recognize that these models represent simplified abstractions of complex biological systems. Consequently, predictions derived from model outputs should be interpreted with caution and contextualized using prior empirical knowledge and ecological understanding of microbial behavior. A key limitation is that predictive models are generally reliable only within the experimental ranges for which they were developed—such as specific temperature or water activity conditions. This restriction arises because most models, particularly empirical models, are constructed by fitting observed data and may not accurately capture microbial responses outside their original experimental parameters. Fakruddin et al. [41] reported that certain models predict faster microbial growth rates than those observed in actual food systems. This discrepancy is largely attributed to the use of artificial laboratory media during model development, which limits their predictive accuracy under real food processing and storage conditions [42].

Moreover, food industry practitioners have emphasized that models calibrated under static environmental conditions often fail to reflect real-world scenarios, where temperature, pH, and water activity fluctuate continuously. As a result, the application of these models to dynamic food systems can produce misleading or overly optimistic results. Importantly, predictive models cannot fully account for the multifactorial nature of microbial growth and food spoilage. Most existing models consider only one or a limited number of parameters influencing microbial behavior, thereby reducing their comprehensiveness and general applicability [9, 43].

Challenges and Future Directions: Most existing microbial models are simplistic representations, primarily focusing on measurable responses to environmental changes. Although these models are effective in predicting parameters such as microbial growth and inactivation rates within optimal temperature ranges, their ability to describe complex phenomena—such as lag phases, adaptive responses, and stress-induced variability—remains limited. Consequently, there is a growing need for next-generation, mechanistic, and adaptable models that integrate cellular-level information to better elucidate the complexities of microbial behavior [44,45]. Emerging modeling approaches emphasize understanding the behavior of individual microbial cells as a means of improving population-level predictions. Recent studies have underscored the importance of cellular heterogeneity as a major source of variability within microbial populations [46].

Since food contamination events can originate from only a few pathogenic cells, comprehending the mechanisms governing individual cell responses is essential for accurate microbial risk assessment [47].

To address these challenges, researchers are increasingly adopting stochastic, single-cell modeling frameworks grounded in systems biology. These approaches reveal critical insights into intra-clonal variability and the intricate relationship between gene expression and phenotypic behavior [48]. Furthermore, next-generation models must account for intraspecies diversity, particularly among spore-forming bacteria, whose variable responses to environmental stressors carry significant implications for risk assessment and food safety management. This dimension remains underrepresented in current predictive modeling approaches and warrants focused research attention [49].

The combination of Predictive Microbiology with various other technologies.

Recent advancements in Whole Genome Sequencing (WGS) technologies, coupled with innovations in genomics and metagenomics, are revolutionizing how pathogens are detected, characterized, and identified in the context of food safety. These developments have given rise to the emerging interdisciplinary field of foodomics, which integrates high-throughput omics technologies to provide a comprehensive understanding of food composition, safety, and functionality [50]. Furthermore, analytical tools derived from proteomics and metabolomics are increasingly applied to identify bacterial toxins and mycotoxins in food products, establishing omics-based approaches as indispensable components of risk assessment and food safety monitoring in the 21st century.

The integration of WGS into foodborne pathogen surveillance programs has already demonstrated success in tracing and mitigating outbreaks of Listeriosis and Salmonellosis, many of which may have otherwise remained undetected [51]. Within the framework of predictive microbiology, WGS provides critical insights into pathogen serotypes, virulence determinants, antimicrobial resistance genes, and genetic variations such as single-nucleotide polymorphisms (SNPs) [52]. This information enhances the precision of quantitative microbial risk assessment (QMRA) by enabling robust correlations between microbial genotypes and their clinical outcomes (Njage et al., 2019). For instance, *Shiga toxin-producing Escherichia coli* (STEC) strains are associated with a broad spectrum of illnesses, ranging from mild diarrhea to severe hemolytic uremic syndrome (HUS). The application of WGS in risk assessment facilitates the establishment of direct links between specific microbial hazards and corresponding clinical outcomes [53]. This approach was exemplified in the study by Pielat et al. [54], in which molecular data from WGS were used to characterize hazards associated with *E. coli* O157:H7 [55].

Beyond genomics, metagenomics has emerged as a powerful tool for exploring microbial interactions within complex communities [56]. Food-associated microbial ecosystems are inherently dynamic, where the behavior of one microorganism can profoundly influence the growth and activity of others. By applying metagenomic analyses to study these interactions, researchers can develop next-generation predictive models that more accurately represent the ecological dynamics of microbial populations in food systems.

In parallel, the integration of Artificial Intelligence (AI) and Machine Learning (ML) technologies presents transformative potential for predictive food microbiology.

The development and application of predictive models generate vast and complex datasets that often exceed the analytical capacity of traditional statistical methods. AI and ML algorithms can process these large datasets efficiently, uncovering hidden correlations, non-linear relationships, and predictive patterns that enhance model accuracy and reliability. Consequently, AI-driven modeling enables the creation of intelligent, adaptive, and data-rich predictive systems that account for multiple variables influencing microbial growth, inactivation, and survival, thereby advancing the precision and utility of predictive microbiology in food safety management.

Conclusion

This review underscores the extensive application of predictive models in food microbiology for analyzing and forecasting microbial growth dynamics in various food matrices. Despite their widespread use, these models continue to face challenges in accurately simulating the complex interactions that occur among diverse microbial communities, particularly within heterogeneous food environments.

The integration of cutting-edge technologies—including Whole Genome Sequencing (WGS), metagenomics, artificial intelligence (AI), and machine learning (ML)—has significantly improved the precision and adaptability of predictive modeling frameworks. Furthermore, the incorporation of advanced monitoring tools, such as robotics, the Internet of Things (IoT), and time-temperature indicators, has enhanced the real-time assessment of food safety and quality. In particular, machine learning-driven models have demonstrated exceptional potential for developing intelligent, data-rich predictive systems capable of capturing nonlinear and multifactorial microbial responses. Continued research and innovation in these domains are essential for improving model reliability, optimizing food processing systems, and minimizing the risk of microbial contamination.

Ensuring microbial food safety remains a shared priority among industry, government, and consumers—each expecting a secure and wholesome food supply as a core foundation of public health. Within this context, predictive microbiology serves as a cornerstone of modern food safety management. Its growing importance reflects advances in quantitative microbial ecology and its successful integration with complementary scientific fields. As the discipline continues to evolve, predictive microbiology is poised to become an even more powerful, rapid, and efficient tool for food processing, preservation, and product optimization—ultimately contributing to a safer and more sustainable global food system.

DECLARATION OF COMPETING INTEREST

I hereby declare that there is no conflict of interest in this review

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