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Development and validation of a tertiary simulation model for predicting the growth of the food microorganisms under dynamic and static temperature conditions

Antonios N. Psomas[a,b], George-John Nychas[a], Serkos A. Haroutounian[b], Panagiotis N. Skandamis[a,*]

[a] *Department of Food Science & Technology, Laboratory of Food Hygiene and Quality Control, Agricultural University of Athens, Iera Odos 75, Athens 11855, Greece*
[b] *Department of Sciences, Laboratory of Chemistry, Agricultural University of Athens, Iera Odos 75, Athens 11855, Greece*

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ABSTRACT

The use of predictive modeling software may markedly contribute to the better understanding of the microbial behavior in foods. In this paper, the development and validation of a tertiary model, which provides predictions of microbial growth in foods under dynamic or static temperature conditions, is presented. In particular, the UGPM (Unified Growth Prediction Model) software applies the Baranyi and Roberts (1994) primary model, coupled to a secondary temperature model, in order to simulate growth of a given microorganism during storage of a specific food or food category. The software, intended to be used by both expert and non-expert users, may be a valuable decision support tool for the food industry, by assisting in the management of foods based on their actual shelf-life and microbial safety, thereby limiting the deterministic "best-by" practice for the determination of shelf-life. The latter is commonly based solely on empirical observations and has high uncertainty. This in turn, may result in the rejection of large quantities of unspoiled or safe foods, or even in the distribution of spoiled and unsafe foods, due to ignorance of the effect of temperature abuse on the microbial spoilage and safety of products.

1. Introduction

The application of predictive models has markedly assisted in modern food safety management (Gorris, 2005). Such models constitute mathematical tools, which are based on the product characteristics and the conditions occurring during processing or storage of foods, in order to accurately predict their microbial quality and safety. In this context, the ability to simulate the complex world of microbes constitutes a valuable methodology, which combines information from different scientific areas, such as chemistry, mathematics, biology, computer programming and statistics. Predictive microbiology can quantify the response of microorganisms in foods with the help of the various mathematical models. These models are mathematical expressions describing the inactivation or increase of microbial populations in foods as a function of the relevant intrinsic or extrinsic variables generally on a macroscopic scale (Marks, 2008). The mathematical models should also take into account the physiological state of microorganisms, which depends on the species and the '*history*' of exposure of microbial cells to various stresses during processing and distribution of foods (Tiganitas et al., 2009; Le Marc et al., 2010).

The models are classified into three categories: (i) the primary models, which are used to describe the changes of the microbial population density as a function of time using a limited number of kinetic parameters (e.g., lag time, growth or inactivation rate and maximum population density); (ii) the secondary models expressing the effect of environmental variables (e.g., temperature, NaCl, pH, etc.) on the kinetic parameters estimated by the primary models (McMeekin et al., 2006; Ross et al., 2000; Whiting, 1995); (iii) the tertiary models, which are computer tools that integrate the primary and secondary models into user-friendly units. The wider use of models in the food industry and research depends on the availability of user-friendly software, which encompass predictive models and allow different users to retrieve information from them in a rapid and convenient way (McMeekin and Ross, 2002; McMeekin et al., 2006).

Growth models are fundamental tools in predictive microbiology, especially for ready-to-eat (RTE) foods, since they may assess the exposure of consumers to the doses (levels) of pathogenic bacteria at the time of consumption (McMeekin et al., 2006). Several predictive modeling software have been developed in order to provide predictions of microbial responses in foods by controlling environmental and physicochemical factors and/or food additives (Baranyi and Tamplin, 2004). The most popular ones are: (i) the stand-alone Pathogen Modeling Program (PMP v.7.0) and the Online Pathogen Modeling Program (Online PMP) developed by the Eastern Regional Research Center, Agricultural Research

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* Corresponding author. Tel.: +30 210 5294684; fax: +30 210 5294684.
E-mail address: pskan@aua.gr (P.N. Skandamis).

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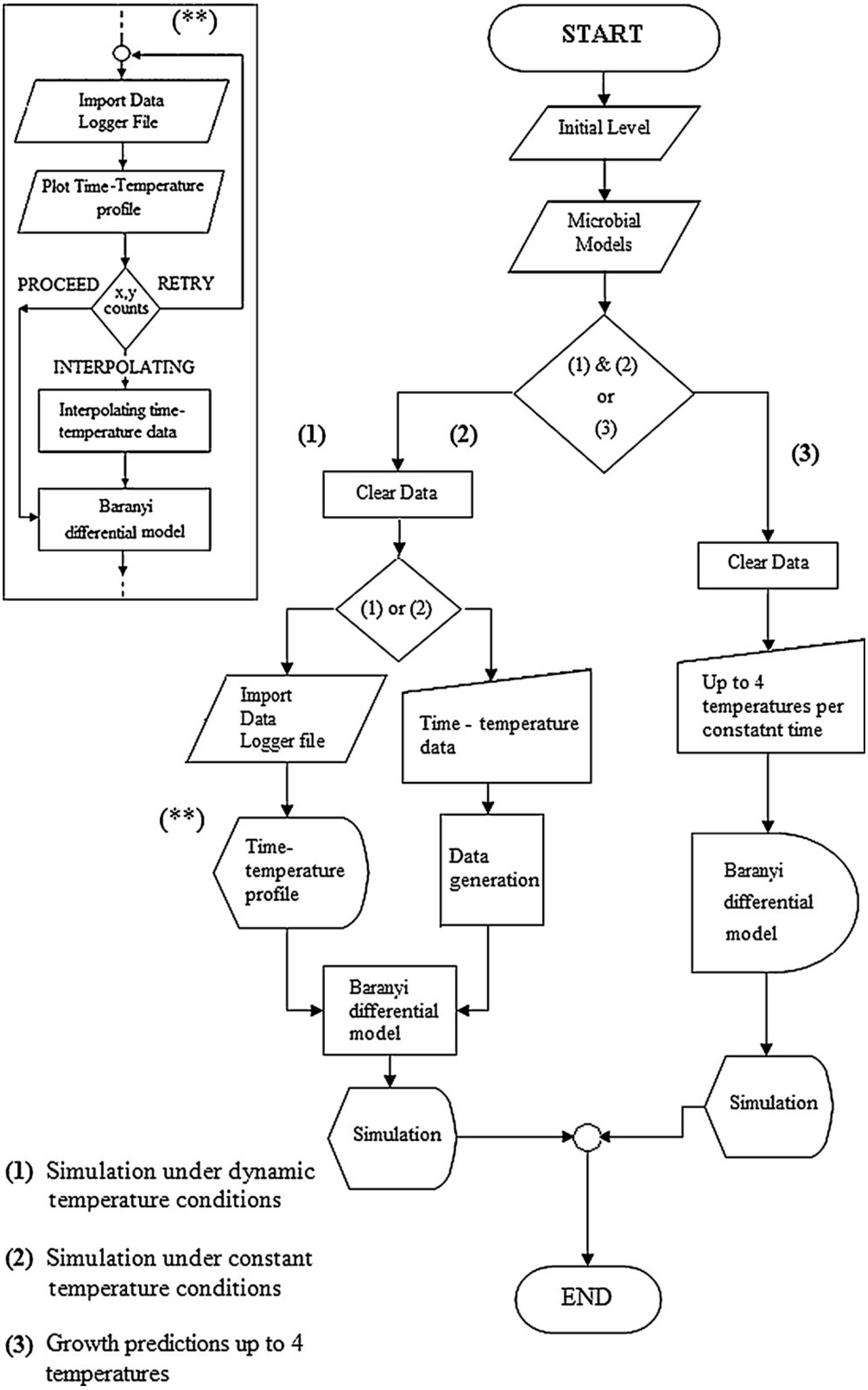

Fig. 1. Flowchart describing the UGPM software application layout.

Service, U.S. Department of Agriculture (USDA, 2009a,b); (ii) the Sym'Previous (Leporq et al., 2005); (iv) the Microbial Responses Viewer (Koseki, 2009); (v) the Pseudomonas predictor (Neumeyer et al., 1997); (vi) the Seafood Spoilage Predictor (Dalgaard et al., 2002); (vii) the ComBase Predictor which is a modified, augmented and improved web-version of the free of charge Growth Predictor stand-alone program (2003) (ComBase, 2007); (viii) the Perfrigens Predictor (Le Marc et al., 2008) which can be accessed through the modeling toolbox of Combase; (ix) the software for predicting growth/inactivation of *Salmonella* under dynamic conditions of temperature, pH and a_w (Pin et al., in press). Most of these programs are locked and the modification of their models or the addition of new models is not feasible or requires authorization. Furthermore, the embedded models are based mainly on data from laboratory