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Identification of the significant factors in food quality using global sensitivity analysis and the accept-and-reject algorithm. Part I: Methodology

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ABSTRACT

Knowledge of the quality evolution of food products along the cold chain is of major importance to ensure safety and extend shelf-life. In order to study the evolution of food products, different sources of variability observed in practice such as food properties and product temperature in different links have to be considered. Different methods have been developed in the past to account, through modelling, for the variability of inputs on the output variance of a quality characteristic. The Monte-Carlo method, based on pseudo-random process, is the most widely used because of its simplicity and facility of implementation. The purpose of this study was to evaluate the product quality evolution along the cold chain considering both the variability of time–temperature profiles and product initial quality (colour, microbial load, etc.) by means of the Monte Carlo method. Two methodologies based on global sensitivity analysis and an accept-and-reject algorithm was proposed to identify in an elegant way the most influencing factors on the final product quality.

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1. Introduction

Low temperature storage of perishable products is essential to slow down quality deteriorating reactions and limit growth of pathogenic and spoilage microorganisms. However, though refrigeration is very important in extending the shelf life of perishable products, cold chain management is a tedious task because of numerous sources of variability in terms of temperatures and biological variability (initial quality). In this context, predictive modelling of food quality evolution has become an important tool because it helps food business operators and competent authorities to define shelf-life and to evaluate the impact of frozen and chilled logistics chain on final food product quality.

Kinetic models have been widely developed to study the different types of quality characteristics in various food products, for example, microbial load (Ratkowsky et al., 1982; Baranyi and Roberts, 1994; Rosso et al., 1996; Geeraerd et al., 2004; Cornu et al., 2006; Mejlholm et al., 2010; Stahl et al., 2012), firmness of apples (Gwanpua et al., 2012), vitamin C in vegetables (Giannakourou and Taoukis, 2003; Gonçalves et al., 2011; Dermesonluoglu et al., 2012), ice recrystallization in ice cream (Ben-Yoseph and Hartel, 1998; Dermesonluoglu et al., 2012). As recommended by Van Boekel (2008), the effect of biological variability has to be taken into account in the model if we want to obtain realistic results. Such variability was widely studied: weight loss during ripening of cheese (Baudrit et al., 2009), colour of tomatoes (Hertog et al., 2009), shelf-life of tomatoes (De Ketelaere et al., 2004), stem length of Belgian endives (Hertog et al., 2007b) and firmness of apples (Gwanpua et al., 2013).

However, most of these models are time and temperature dependent and thus, accurate knowledge of the logistic chain is required to properly predict the quality evolution of food products

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Nomenclature

I	itinerary	y_0	initial product quality
j	link index	y_{end}	product quality at the end of the chain
J	number of links	S_i	individual effect index
K	number of factors	St_i	total effect index
N	number of samples	$t_{rs,j}$	residence time link j days
P_{nc}	probability of non-compliance with the safety criterion	T_j	product temperature in link j °C
p	model parameter		

along the cold chain. Flick et al. (2012) proposed a general methodology that combines deterministic models for the refrigeration equipment and stochastic models to take into account different sources of variability in the cold chain (sequence of the equipment, ambient conditions and thermostat-setting temperature). This approach allows the prediction of the evolution of product state such as temperature and quality criteria along the cold chain (water content, microbial load, colour, etc.). This methodology was then applied by Hoang et al. (2012b) for pre-packaged meat cold chain using the data of the survey carried out by Cemagref, (2004). Others approaches that combine both the variability of time temperature profile and biological parameters were also proposed (Afchain et al., 2005; Hertog et al., 2007a; Couvert et al., 2010; Koutsoumanis et al., 2010; De Cesare et al., 2013).

This study describes a novel methodology to account for the different sources of variability and to identify and rank in an elegant way the significant factors determining final food product quality, by means of global sensitivity analysis (SA) and an accept-and-reject algorithm (AR). The results will, in a later stage, be part of a Quality, Energy and Environmental Assessment tool (QEEAT) (Gwanpua et al., 2014), a software for assessing refrigeration technologies, developed within the framework of the European Union FP7 project, FRISBEE (Food Refrigeration Innovations for Safety, consumers' Benefit, Environmental impact and Energy optimization along the cold chain in Europe). The objective is to provide a tool which could be used by food business operator to evaluate the food product quality along the cold chain according to chosen scenarios. Using comprehensive methods (i.e., global sensitivity analysis and accept and reject algorithm) help them to make decisions. Moreover, this methodology will be coded for numerous types of product (i.e. cooked ham, fruits, ice cream, and frozen spinach) and for numerous types of quality criteria (i.e. *Listeria monocytogenes*, firmness, colour, vitamin C, crystal size). The applications of this methodology is presented in the next articles for the growth of *L. monocytogenes* in cooked ham (Duret et al., 2014a) and for the evolution of the firmness and colour of apple (Duret et al., 2014b).

2. Application of the Monte Carlo method in cold chain logistics

Monte Carlo is the name of the computational method that relies on repeated pseudo-random sampling to compute resulting outputs. This method was used in this study to account for the variability of product temperature in each link of the cold chain and the biological variability of products (initial quality, variability of model parameters). To represent a real logistic chain, a high number of products of the same type was considered for the Monte Carlo simulation. For each product, the random variables (initial quality and temperature in each link) were sampled from statistical distributions which can be obtained by survey data such as those of Uyttendaele et al. (1999), Laguerre et al. (2002), Cemagref (2004), Marklinder et al. (2004), Azevedo et al. (2005), De Vriese et al. (2006), Garrido et al. (2009) and Hoang et al. (2012a). This methodology can be applied to all types of food products: chilled (apple, ready to eat (RTE) pork meal, salmon), superchilled (salmon) and frozen (spinach and ice cream) for numerous quality model (microbial growth, firmness, colour, vitamin C, etc.). The algorithm is presented in Fig. 1, in which three parts can be distinguished: in Section 1 the model inputs (i.e. temperature profile, initial quality and model parameters) are specified, in Section 2 the kinetic models are used to calculate the evolution of the quality attributes of the product, and in Section 3 indicators are derived which analyse the results and identify the most influencing factors (i.e. individual and total effect indices and probability of non-compliance with a quality criterion) Variables and symbols used in Fig. 1 will be further explained below.

2.1. Including time – temperature variability in cold chain logistic modelling

N number of products of the same type (fruit, cooked ham, ice cream, etc.) are introduced in the first link $j = 1$. The temperature T_j and the residence time $t_{rs,j}$ of the product are randomly sampled from a statistical distribution. This distribution is obtained by

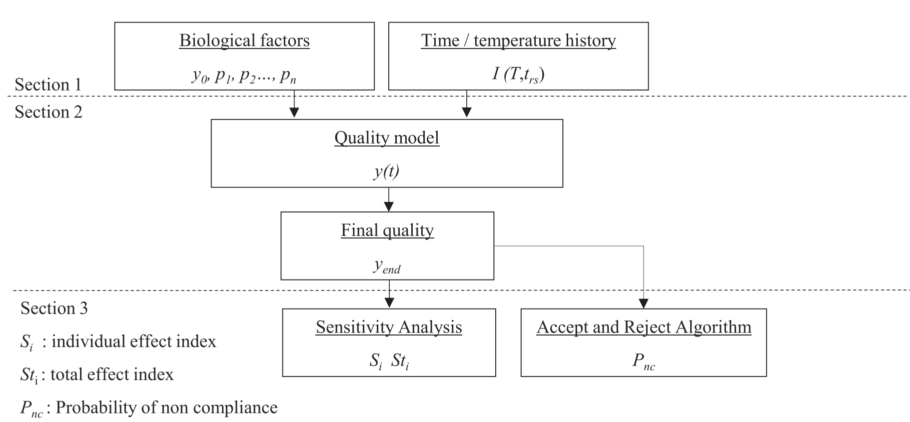

Fig. 1. Diagram used to estimate the sensitivity of the input factors on the final quality.

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