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Seafood Spoilage Predictor—development and distribution of a product specific application software

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Abstract

To allow shelf-life prediction of a range of products, the Seafood Spoilage Predictor (SSP) software has been developed to include both kinetic models for growth of specific spoilage microorganisms and empirical relative rates of spoilage models. SSP can read and evaluate temperature profile data of different formats and in this way the software is a flexible device for electronic time–temperature integration. Predicted values of microbial growth and of remaining product shelf life can be exported from SSP as graphs and tables in ASCII, HTML and eXtensible Mark-up Language (XML) formats and this allows SSP to be used in combination with other programmes. More than 300 people have downloaded SSP and distribution of this software from the internet has been efficient in stimulating the application of predictive microbiology and of mathematical seafood shelf-life models within industry, research, seafood inspection and teaching. © 2002 Elsevier Science B.V. All rights reserved.

Keywords: Predictive microbiology application software; Shelf-life prediction; Time–temperature integration

1. Introduction

Numerous mathematical models have been generated within the field of predictive food microbiology but relatively few of these models are included in available application software. This is unfortunate as application software allows experts as well as people without detailed insight in the mathematics of predictive microbiology to obtain information from models in a rapid and convenient way. For pathogenic microorganisms some models of growth, survival or inactivation have been included in application software that is available commercially or gratis. For food safety evaluation, Pathogen Modeling Programme (Buchanan, 1993) and Food Micromodel (Anonymous, 1997) have illustrated the potential of predictive microbiology to wide groups of users. Application software with kinetic models for growth of food spoilage microorganisms have also been developed (Zwietering et al., 1992; Schellekens et al., 1994; Avery et al., 1996; Anonymous, 1997, 1998; Wijtzes et al., 1998). Growth models for *Brochothrix thermosphacta*, *Lactobacillus plantarium, Saccharomyces cerevisiae* and *Zygosaccharomyces bailii* are included in Food Micromodel

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(Anonymous, 1997) and the Food Spoilage Predictor (Anonymous, 1998), which is another commercially available application software, contains a model for growth of psychrotolerant pseudomonas (Neumeyer et al., 1997). The remaining programmes with kinetic spoilage models does not seem available and software with models for growth of important seafood spoilage bacteria like *Shewanella putrefaciens* and *Photobacterium phosphoreim* has not previously been developed.

Compared to the kinetic responses of pathogenic microorganisms, spoilage reactions in food are complicated and dynamic in the sense that spoilage reactions and spoilage microorganisms may change as a function of product characteristics and storage conditions. Therefore, the development of kinetic models for shelf-life prediction requires knowledge about the specific spoilage organisms (SSO) responsible for product deterioration as well as about the spoilage domain of these microorganisms, i.e. the range of product characteristics and storage conditions where a given SSO causes product spoilage (Dalgaard, 1995; Dalgaard et al., 1997). Clearly, development of spoilage models for prediction of shelf life is no easy task and various approaches to model development have been used.

The objectives of the present paper are to describe the development and distribution of the Seafood Spoilage Predictor (SSP) software as well as approaches used in modelling of seafood spoilage. The SSP software contains both kinetic models for growth of SSO and empirical relative rates of spoilage models. The software has been distributed via the internet and experiences with this type of software distribution are reported.

2. Approaches to modelling of seafood spoilage

Models for growth of pathogenic microorganisms have been developed mainly by using the general predictive modelling approach. This means data are generated in large experiments using standard liquid growth media. These data are then modelled and predictions compared to growth responses in various foods (Fig. 1; McMeekin et al., 1993; McClure et al., 1994). This approach has the advantage that kinetic parameters can be determined conveniently in liquid growth media, e.g. by absorbance measurements (Dalgaard and Koutsoumanis, 2001). However, with SSO from seafood growth rates in standard liquid media and in products may differ as much as by a factor of two. Furthermore, shelf life can be overestimated several folds if a kinetic model is applied outside of the spoilage domain of the SSO (Dalgaard, 1995; Dalgaard et al., 1997). An iterative approach for development of kinetic spoilage models was suggested to overcome these problems (Fig. 1). The basic idea behind the iterative approach is to validate individual components in the modelling process, e.g. growth medium, SSO and spoilage domain, before large amounts of data is generated. The influence of these components on kinetic models remain relatively little studies but seem quantitatively more important

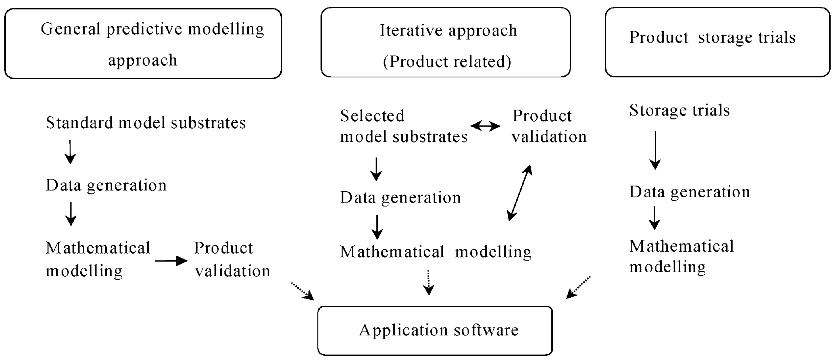

Fig. 1. Approaches used in the development of mathematical shelf life models for seafood (modified from Dalgaard, 1996).

than, e.g. selection between particular equations as primary and secondary growth models. Growth rates estimated from experimental data by the modified Gompertz model and by the Logistic model may differ by 10–20%, i.e. a factor of 0.1–0.2, and for the effect of temperature on growth rates the difference between the square root and the Arrhenius models is of the same magnitude (McMeekin et al., 1993; Dalgaard, 1996).

Clearly, the selection of an appropriate liquid growth medium, for development of kinetic models, can be circumvented by studying growth in storage trials with naturally contaminated food (Fig. 1). This approach has been used recently to develop kinetic models for prediction of shelf life of Mediterranean fish at different temperatures (Taoukis et al., 1999; Koutsoumanis and Nychas, 2000). These experiments further documented modelling of microbial growth in naturally contaminated food does not eliminate the importance of identifying SSO and their spoilage domain (Koutsoumanis and Nychas, 2000).

Over several decades, data from product storage trials have been used to develop empirical relative rate of spoilage (RRS) models to predict shelf life at different storage temperatures. RRS is defined as shelf life at 0 °C divided by shelf life at T °C. A model for the effect of temperature on RRS has the advantage that it allows shelf life to be predicted at different storage temperatures if only shelf life of a product has been determined by sensory evaluation at a single known storage temperature (Spencer and Baines, 1964; Olley and Ratkowsky, 1973). RRS models do not rely on kinetics of any identified spoilage reaction and the ranges of applicability of these models therefore can be wider than, e.g. the spoilage domain of a particular SSO. Furthermore, it is most likely that RRS models can be developed for numerous seafoods where spoilage reactions remain unknown. A single RRS model can be used for products with different shelf life, e.g. for various species of fishes, but different models are required for the groups of products where deterioration kinetics differ markedly. This is important because the apparent activation energy (E_a) for the effect of temperature on shelf life of seafood vary from as little as ~ 20 kJ mol^{-1} for hot smoked cod and mackerel over ~ 60 to ~ 80 kJ mol^{-1} for most fresh seafoods to > 100 kJ mol^{-1} for cooked and brined shrimps stored in modified atmosphere packaging (Dalgaard and Jørgensen, 2000). Due to this very wide range for the effect of temperature on shelf life of seafood the choice of appropriate apparent activation energies or corresponding temperature characteristics like T_{min} or Q_{10} is likely to be more important than the choice between different equations for the effect of temperature on RRS. It has been shown for fresh fish from temperate waters that the square root spoilage model developed by Ratkowsky et al. (1982) was more appropriate than the previously suggested Linear and Arrhenius spoilage models (Spencer and Baines, 1964; McMeekin et al., 1993, pp. 269–286). Furthermore, for the effect of temperature on RRS of fresh tropical fish and of some lightly preserved seafoods the Exponential and the Arrhenius models were more appropriate than the square root model (Dalgaard and Huss, 1997; Dalgaard and Jørgensen, 2000). Nevertheless, a comparison of the quantitative differences between the typically used mathematical models for the effect of temperature on RRS of various types of seafood remain to be presented.

Seafood RRS models have been combined with linear relations between indices of quality and storage time (Spencer and Baines, 1964; Branch and Vail, 1985; Gibson, 1985; Dalgaard, 1998). In this way determination of quality attribute by sensory or instrumental methods, enables shelf-life prediction of products at different temperatures. Clearly, the linear relation between an index of quality and storage time must be valid at the different temperature of prediction. For the sensory quality index method (QIM, Bremner, 1985) numerous studies have obtained linear relations between QIM scores and storage time at 0 °C but only very few studies have been carried out at higher temperatures (Bremner et al., 1985). Consequently, use of the QIM method for shelf-life prediction at different temperatures is still limited (see Dalgaard, 2000a for a recent review) and these models have not yet been included in the SSP software.

The complexity of seafood spoilage has resulted in numerous approaches for development of shelf-life models as mentioned above. For practical shelf-life prediction to be possible it seems most likely that application software must reflect this complexity and therefore need to contain different types of successfully validated spoilage models (Fig. 1).

3. Seafood Spoilage Predictor (SSP) software

The SSP software has been developed to predict and illustrate the effect of constant and fluctuating temperatures on growth of SSO and on remaining shelf life of seafood. Delphi v. 4.0 (Borland® Inprise, Scotts Valley, CA, USA, www.inprise.com) was selected for programming SSP v. 1.1 and this has allowed the software to be flexible and addition of new shelf life model to be convenient. SSP v. 1.1 contains two kinetic models for growth of SSO and two RRS models. The *S. putrefaciens* model, developed by using the general predictive modelling approach, includes only the effect of temperatures (Dalgaard, 1993). In SSP v. 1.1, the range of applicability of this model is indicated as 0–10 °C. The *P. phosphoreum* model was developed by the iterative approach and includes the effect of temperature (0–15 °C) and carbon dioxide levels (0–100%) (Dalgaard et al., 1997). Successful validation of the kinetic models included in SSP has relied on the ability of models to predict shelf life of naturally contaminated seafood with an accuracy of ± 25%. The bias factor (Ross, 1996) calculated from growth rates (BF-μ_{max}) has been used as part of the validation process ($0.75 <$ BF-$\mu_{max} < 1.25$) and to define the range of applicability of models (Dalgaard, 1999).

The two RRS models included in SSP v. 1.1 are: (i) the square root spoilage model (Ratkowsky et al., 1982) for the effect of temperatures from − 3 to + 15 °C on shelf life of fresh seafood from cold and temperate waters and (ii) an exponential RRS model (Dalgaard and Huss, 1997) for shelf life of fresh tropical seafood stored between 0 °C, i.e. in ice, and 30 °C (Eq. (1)).

$$\text{Shelf life at } T\ (^{\circ}\text{C}) = \frac{\text{Shelf life at } T_{\text{ref}}\ (^{\circ}\text{C})}{\exp[0.12 \times (T - T_{\text{ref}}\ (^{\circ}\text{C}))]} \tag{1}$$

The inclusion of different types of spoilage models in SSP allowed the software to be applicable for shelf-life prediction of many seafoods but each model has a specific range of applicability with respect to product characteristics and storage conditions. This range of applicability is indicated in the SSP-help function and the software provides warnings if a model is used at temperatures outside of this range.

The SSP software allows growth of SSO and remaining shelf life to be predicted at constant storage temperatures, for simple temperature profiles that can be entered manually within the software, and for temperatures profiles as collected by different data loggers. Predictions at constant temperatures or for simple temperature scenarios are useful to answer what-if questions like what will be the effect if (i) the degree of product contamination for an SSO was reduced, (ii) chill storage conditions were changed, or (iii) a different concentration of carbon dioxide was used in modified atmosphere packaging. The ability of SSP to read temperature profiles, as collected by data loggers, and to predict their effect on remaining product shelf life can be applied directly, e.g. in evaluation of chill chains in industry and within research. This type of electronic time–temperature integration relying on recorded temperature profiles has the advantage, as compared to visual TTI systems based, e.g. enzymatic reactions, that it is possible to see exactly the time at which changes in temperature occur. Fig. 2 shows an example where SSP was used to predict growth of *P. phosphoreum* and remaining shelf life of modified atmosphere packed cod (*Gadus morhua*) fillets. In this example, the initial level of the SSO was 10 CFU g^{-1} and product temperatures fluctuated between 0 and 10 °C. In Fig. 2, the lower graph to the right shows remaining shelf life at 0 °C (top curve), 5 °C (middle curve) and 10 °C (bottom curve). These curves indicate remaining shelf life predicted under the assumption that seafood samples at a given time are kept at each of the three constant temperatures until spoilage occur. Product shelf life corresponding to given temperature profile corresponds to the point in time when the three remaining shelf-life curves intersect. When users of SSP point on curves for a temperature profile, a microbial growth curve or remaining shelf life then the software provide numerical values of microbiological numbers, remaining shelf life and temperature at that particular time in the bar at the bottom to the output window (Fig. 2).

A kinetic model, as shown in Fig. 2, allows the initial level of an SSO to be taken into account when shelf life is predicted. This can be most useful for seafood where levels of contamination may vary substantially. However, to benefit from this property of kinetic models the initial level of SSO in a lot needs to be (i) determined by a rapid microbiological meth-

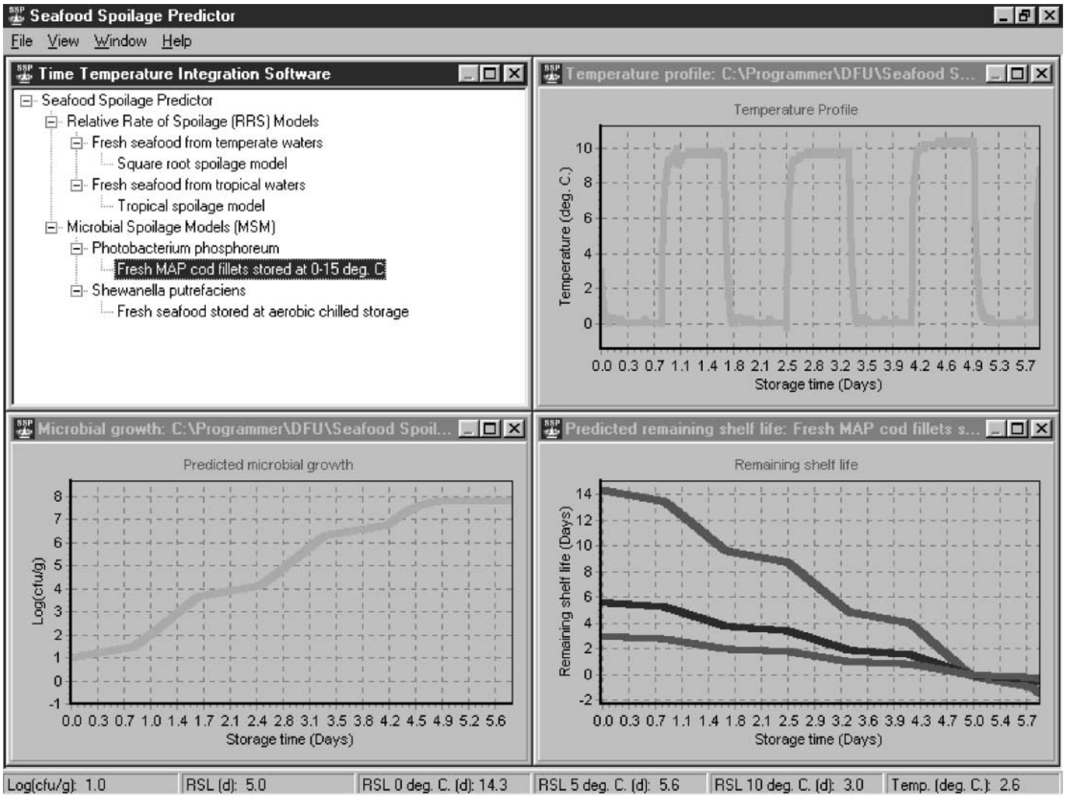

Fig. 2. Output from Seafood Spoilage Predictor (SSP) software showing the effect of a temperature profile on growth of *P. phosphoreum* and on remaining shelf life of modified atmosphere packed cod fillets at 0 °C (top curve), 5 °C (middle curve) and 10 °C (bottom curve).

ods or (ii) know as a function of factors like season, catch area and handling practices. For determination of *P. phosphoreum* and *S. putrefaciens* in seafood, specific enumeration methods are available. However, for these as well as for other seafood SSO further research to improve enumeration methods and to expand our quantitative understanding of how different biological and technological factors influence levels of SSO in seafood is still needed.

For evaluation of product temperatures, SSP has been developed to read the temperature profile data in five different specific text formats that can be obtained from commonly used data loggers. However, the lack of an internationally accepted standard for temperature date, e.g. in an XML or ASCII format, still represent a practical problem for this type of electronic time–temperature integration. To facilitate communication between SSP and other software, temperature profiles and predicted values of microbial growth and remaining shelf life can be saved in the form of tabulated values and graphs. Users can chose ACSII, HTML or XML format for export of data from SSP.

The SSP software has been available for download, free of charge, since February 1999 at http://www.dfu.min.dk/micro/ssp/. Until the end of September 2000, the SSP software had been downloaded by 302 different people around the world. Major groups of users were working in research (41%), production and distribution of seafood (21%), seafood inspection (10%) and teaching (12%). In May 1999, the availability of SSP was announced on the seafood mailing list at UC Davis in the USA. This markedly increased the number of downloads (Fig. 3) as did a presentation of the software at the 3rd International Conference on Predictive Modelling in Foods in September 2000

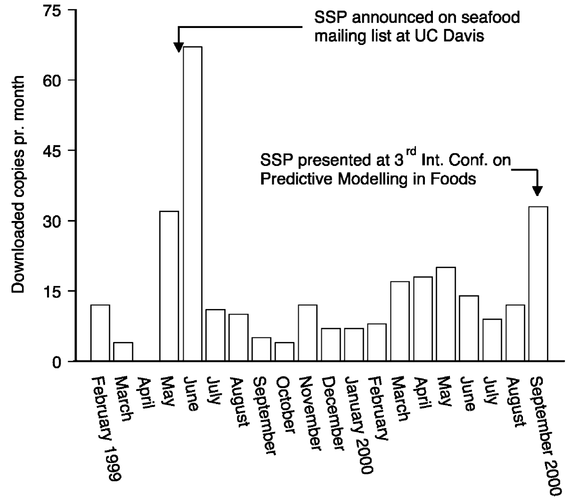

Fig. 3. Download of the SSP software from http://www.dfu.min.dk/micro/ssp/ between February 1999 and end of September 2000.

(Dalgaard, 2000b). With respect to users of SSP, it is interesting that people initially downloading the software almost exclusively worked in the field of research. In contrast, the percentage of users from production and distribution of seafood has increased steadily since SSP became available in February 1999.

To collect suggestions to improve SSP v. 1.1, a questionnaire was circulated to users of the programme in May 2000. The feedback indicated some users had problems with download and set-up of this software whereas other suggested inclusion of a larger number of shelf-life models as the most important aspect of the programme to be improved.

4. SSP on-line — an internet version of the seafood spoilage predictor software

To overcome computer compatibility problems resulting in difficulties with download and set-up of SSP v. 1.1, a new internet version called ‘SSP online’ has been developed (Dalgaard et al., 2000). SSP online is a simplified version of SSP v. 1.1 that has been available at the SSP homepage since June 2000 where it can be assessed directly. SSP online includes the same mathematical shelf-life models as SSP v. 1.1. However, only temperature profile data in an eXtensible Mark-up Language (XML) format can be evaluated by SSP online v. 1.0. The specific XML format used by SSP online is specified in the help function of the software. A XML format has been chosen as standard for temperature data because XML is a structured language that allows instructions for data handling and information on data structure to be included in simple text files. Consequently, it will be possible in the future to transform temperature logger files into a standard XML format.

For export of data, SSP online allows temperature profiles, microbial growth and remaining shelf-life data to be saved on hard disks of clients. Data are exported as graphs or tables in ASCII, HTML or XML formats. SSP online v. 1.0 was developed by using Active Server Pages (ASP) and implemented with Microsoft Visual InterDev 6.0 msdn.microsoft.com/vinterdev/) and AspChart 1.0 from ServerObjects (www.serverobjects.com).

5. Conclusion

Development of SSP and distribution of this application software from the internet has been an efficient way of stimulating the use of predictive microbiology and of mathematical seafood shelf-life models. Different groups of users have shown considerable interest in SSP and their feedback has indicated a need to expand this product specific application software with new shelf-life models, e.g. for lightly preserved seafoods. Furthermore, is seems relevant to combine shelf-life prediction and electronic time–temperature integration, as carried out by SSP, with information collected from the moment of catch of fish raw material, i.e. traceability systems and thereby obtain a tool to further improve product quality assurance in the seafood sector.

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