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1 The “Sym’Previus” software, a tool to support decisions to the  
2 foodstuff safety.

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## 1 **Abstract**

2 Describing the Sym'Previus project, the software and its deliverable facilities is the aim of  
3 this present paper. This software concerns all the partners of the food industry who are  
4 involved in the management of food safety and allows food borne pathogen behaviour in food  
5 to be predicted, as function of the environment (nature of the food, manufacturing process,  
6 conditions of conservation). This analysis of microbial behaviour has been possible thanks to  
7 the progress made in predictive microbiology since the 80's. Sym'Previus offers to food  
8 industry professionals and their partners the possibility of applying this progress, by giving  
9 access to a database, to simulation systems and expertise.

## 10 **1 Introduction**

11 The objective of the first release of the Sym'Previus software is to be able to answer queries  
12 concerning the food safety and particularly the behaviour of bacteria on a food matrix in case  
13 of contamination (Table 1).

14 Over the past few years, several attempts have been made to launch tools similar to  
15 Sym'Previus. The first one was Food MicroModel, a software package developed by MAFF  
16 from United Kingdom, and marketed by Leatherhead Food Research Association. The second  
17 one, named Pathogen Modelling Program (PMP), has been developed in the USA by the  
18 USDA, and is now downloadable from the Internet  
19 (<http://www.arserrc.gov/mfs/pathogen.htm>).

20 Research in predictive microbiology has been pursued throughout a FLAIR research project  
21 funded by EU and carried out in 1990-93 (Peck et al. 1994). Research teams from 12  
22 European countries participated in this project, whose co-ordinator was Dr T. Roberts, from  
23 IFR. Afterwards the project was followed by a COST project (914) aiming to organise  
24 dissemination and exchanges of findings among a large number of laboratories, particularly

1 on the validation of models on real food products. Another European project, named  
2 PREMIUM, directed by Prof. Dr. Jan Van Impe from the Katholieke Universiteit Leuven,  
3 was implemented and funded in the 4<sup>th</sup> Framework. Its main objectives were to elaborate a  
4 unified modelling system, and to validate it on real food products as well.

5 The origins of the Sym'Previous project can be situated in accordance with a number of  
6 factors:

7 - several French scientific teams had participated in the European projects named  
8 above, and found them promising; especially a leader of the food industry who  
9 developed an application based on cardinal models (Rosso, 1995), and used it in real  
10 conditions, in plants manufacturing fresh dairy products.

11 - the French government was very interested in the opportunity of implementing an  
12 expertise in the domain of pathogens, in order to improve the general security level of  
13 foodstuffs; moreover, a further application of such a tool in Quantitative Risk  
14 Assessment was considered as well.

15 - The French food industry were interested also in participating in the building of a  
16 common software, to share their expertise in food safety and their data (challenge-  
17 tests, models, bacterial strains...).

18 All these conditions lead to the building of a network, including industry, research, technical  
19 centres, the Ministry of Agriculture and the Ministry of Research, funded by governmental  
20 grants and financial contribution of the participants (Leporq et al., 2003).

## 21 **2 The software facilities**

22 To collect information on bacterial behaviour in food, the users can obtain data from three  
23 different units : i) a database, ii) a simulation system and iii) a data analysis tool (expertise),  
24 as shown in Figure 1.

## 1 2.1 *A relational database of food microbiology*

2 The database was built in order to integrate food, bacteria and environmental characteristics  
3 (formulation, pH,  $a_w$ , culture condition, manufacturing process, condition of conservation ...)  
4 on microbial behaviour (growth, inactivation, survival...) concerning pathogenic germs able  
5 to contaminate food, and also epidemiological data (prevalence or level of contamination in  
6 food). The database contains data stemming from various sources, like scientific publications  
7 (more than 700 selected for their interest in food microbiology), industrial partners and R&D  
8 laboratories. The use of these data can be divided into different groups. Firstly, growth rates  
9 can be used directly by comparing the correspondence between the growth rate predicted by  
10 the simulation software and to the data extracted from the database. Secondly, growth kinetics  
11 could be used, either to estimate primary models parameters (such as growth rate), or to be  
12 confronted to kinetics simulations. Moreover, these data bring information on microbial  
13 behaviour in food under a specific combination of environmental factors, and then complete  
14 information when the corresponding model is not yet available (for example, the impact of the  
15 packaging, or the incidence of thermal stress on lag time).

16 This database is enquired through the web-based browser called MIEL (Figure 2), a  
17 multicriterion system, specifically developed for this database and performing fuzzy querying  
18 thanks to an additional knowledge discussed in Buche et Loiseau (1999) and Buche et al.  
19 (2002). MIEL crosses the user demand about food, micro-organism and environmental  
20 factors. However, this basic query is not always satisfying, the nature of the data and their  
21 multiple providers render the database incomplete by nature. It is not realistic to think that this  
22 database contains experimental data for all food products, all pathogen germs, under all  
23 conditions. Therefore MIEL is a querying system which retrieves the nearest data compared  
24 to the selection criteria specified by the user.

## 1 2.2 Predictive models in order to simulate growth kinetics

2 Today, a large variety of primary and secondary models exists to describe the behaviour of  
3 micro-organisms in food, submitted to the influence of environmental factors. Sym'Previous  
4 does not reiterate the equations, advantages, disadvantages and connections between the  
5 models. A large literature is available on these subjects. Nevertheless, the most known and  
6 used models are presented through the free web site (<http://www.symprevious.org>).  
7 Concerning the scientific knowledge used in this software, the model called "delay and break"  
8 developed by Rosso et al., 1995, has been selected as primary model, and cardinal models  
9 including interpretable parameters ( $T_{\min}$ ,  $T_{\text{opt}}$ ,  $T_{\max}$ ,  $\text{pH}_{\min}$ ...) have been chosen as secondary  
10 models (Rosso et al., 1995) to describe the effect of the temperature, pH and  $a_w$  effect on  
11 growth rate. About lag time, more scientific results are needed before introducing them in  
12 simulations.

### 13 2.2.1 Microbial growth in food, in case of contamination

14 In order to simulate the behaviour of pathogenic bacteria in foodstuff, the modelling approach  
15 is based on the gamma concept (Eq.1) (Zwietering et al., 1992). Each unit,  $\tau(T)$ ,  $\rho(\text{pH})$  and  
16  $\alpha(a_w)$  was quantified by a cardinal secondary model (Rosso et al., 1995). The effects of each  
17 factor were combined and an extra parameter corresponding to the effect of the foodstuff on  
18 the growth rate, called  $\mu_{\text{opt}}$ , was added.

$$19 \quad \mu_{\max} = \mu_{\text{opt}} \cdot \tau(T) \cdot \rho(\text{pH}) \cdot \alpha(a_w) \quad \text{Eq. 1}$$

20 This approach was successfully validated in foods (Pinon et al. 2004 ; Membré et al. 2004).

### 21 2.2.2 Software facilities

22 The starting assumption of this tool of simulation is that the user does not know which  
23 particular strain could contaminate his/her product. In this way the specific parameters  
24 (cardinal values) of this strain are ignored. It is probably more interesting to provide a "mean"  
25 response of the species completed by an interval confidence (Huet et al., 1996) than to

1 describe the behaviour of a specific strain unknown by the user. To illustrate the global  
2 behaviour of the five pathogenic species studied during the Sym'Previous program, a specific  
3 group was in charge of selecting among a large collection of strains (more than 1000) the  
4 more representative and of determining their cardinal values (Membré et al., 2002, Membré et  
5 al., 2003).

6 Concerning the facilities developed in this tool, the simulation of the behaviour of growth of  
7 pathogenic bacteria on different families of foodstuffs is provided (Figure 3). The user has to  
8 i) select a food matrix and the associated micro organism (already tested among them), ii)  
9 check if the parameters of pH and water activity of the food matrix proposed by default  
10 correspond to their product (theses values extracted from the experiments done in  
11 Sym'Previous could be adjusted to the user product, in a defined range), finally iii) set the level  
12 of the temperature factor. Furthermore, the result of this simulation is reported on a graph and  
13 available in a table to be exported to a spreadsheet as well. Moreover, the user could confront  
14 results given by modelling to data obtained independently from his own laboratory or stored  
15 in a database by adding theses data to the graph. The comparison on the same graph of the  
16 influence of two temperature levels or two food matrix, is also possible.

17 Few bonus were included for users who would like to go further. Firstly, a table which  
18 summarises the three environmental factors and the food influences in order to appreciate the  
19 most preponderant factor modifying the growth rate (Eq. 1). Secondly, a graph presenting the  
20 data which have permitted to determine the model parameters (i.e. cardinal values and the  
21 interval confidence around the predicted values) is plotted.

### 22 2.3 *Expertise in food microbiology*

23 The major interest of Sym'Previous is not only to provide a database and mathematical models  
24 but to combine information and to supply an analysis done by a group of experts  
25 (microbiologists, statisticians) in order to summarise the knowledge. Figures 4 and 5 illustrate

1 what is done with a request such as “which is the behaviour of *Escherichia coli* O157:H7 in  
2 beef meat in a range of temperatures from refrigerated to room values?”. In the first time the  
3 database is scanned about the association beef meat / *Escherichia coli* O157:H7 under the  
4 influence of the temperature effect through the MIEL. Raw kinetics were extracted at  
5 different levels (Figure 4). The first interest is to bring an accurate idea of the bacterial  
6 behaviour on a product including variability due to different sources of data (different authors  
7 and laboratories). Thus, from each kinetic a growth rate was estimated, plotted versus the  
8 temperature and compared to these obtained in liquid medium (Figure 5). A difference of  
9 growth rates is observed, between data obtained in the food matrix and the data established in  
10 liquid medium. To fit the model to the beef meat data, the food dependent parameter,  $\mu_{opt}$ , is  
11 adjusted (Eq. 1). Hence, the specific growth rate values of *Escherichia coli* on beef meat are  
12 available in the software, without carrying out any new experiment.

13 In conclusion, this kind of expertise combines all the tools of Sym'Previous, and allows to  
14 improve the knowledge on an association of food and micro organism by combining different  
15 sources of information and statistical treatment. Thus, this group of experts will be able to  
16 provide information to users who have difficulties using the tools, or who observe a  
17 difference between their data and those provided by the software.

18 Therefore, the most important advantage is that Sym'Previous is not only a database and a  
19 group of mathematical models, but overall a network of expertise, gathering laboratories,  
20 technical centres and companies, all of them being well aware of the difficulties and the traps  
21 existing in the use of predictive microbiology. The objective is to provide a complete service,  
22 including consultation of the database, simulation of growth, a guide for interpretation, and  
23 the opportunity to contact experts.



## 1 **5. The Future of Sym'Previus**

2 A system like Sym'Previus necessitates a permanent updating and improvement of the service  
3 offered to users every time it is possible. It will be necessary to add data about new germs and  
4 continue to enrich the data on the pathogens already included in the database.

5 New research projects will also bring new data (some of them being already in progress) and  
6 create the possibility to improve the accuracy of simulations, for example a better estimation  
7 of lag phase, particularly on *Listeria monocytogenes*. In the future, some other research  
8 projects will have to be set up in order to take a better account of the diversity of food  
9 matrices and add factors to the models like organic acids, preservatives, or effects of different  
10 types of stress on micro organisms.

11 It would be probably very useful to implement links with other databases like ComBase so  
12 that we could share experience and knowledge with the other's European experts and in this  
13 way improve each other's performances in the field of food microbiology.

14 Since the beginning of 2004, the head laboratory of the Sym'Previus project has been moved  
15 from INRA (Villeneuve d'Ascq, France) to Adria (Quimper, France).

## 16 **3 Acknowledgements**

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18 was supported by French Departments of Research and Agriculture.

## 19 **4 References**

20 Buche, P., Loiseau S, 1999. Using Contextual Fuzzy Views to Query Imprecise Data. Lecture  
21 Notes in Computer Science 1677. Conference Proceedings DEXA'99 460-472.[Database  
22 and EXpert system Application, Florence (Italy), August 99].

23 Buche, P., Dervin C., Brouillaud-Delattre, A., Gnanou-Besse, N., 2002. Combining fuzzy  
24 querying of imprecise data and predictive microbiology using category-based reasoning

- 1 for prediction of the possible microbial spoilage in foods: application to *Listeria*  
2 *monocytogenes*. *International Journal of Food Microbiology* 73, 171-185.
- 3 Huet, S., Bouvier, A., Gruet M.A., Jolivet E., 1996. *Statistical tools for non linear regression*.  
4 Springer Verlag, New York, USA.
- 5 Leporq, B., Membré, J.-M., Zwietering, M., Dervin, C., Buche, P., Guyonnet J.P., 2003. The  
6 "Sym'Previous" software, a tool to support decisions to the foodstuff safety. In : J.F.M.  
7 Van Impe, A.H. Geeraerd, I. Leguérinel and P.Mafart (Eds), *Predictive modelling in food*  
8 – Conference Proceedings, 55-57, Société française de Microbiologie, 347pp. (ISBN 90-  
9 5682-400-7) [4<sup>th</sup> International Conference, Quimper (France), June 15-19,2003].
- 10 Membré, J.-M., Leporq, B., Vialette, M., Mettler, E., Perrier, L., Zwietering, M.H., 2002.  
11 Experimental protocols and strain variability of cardinal values (pH and  $a_w$ ) of bacteria  
12 using Bioscreen C: microbial and statistical aspects. In: L. Alexon, E.S. Tronrud and K.J.  
13 Merok (Eds), *Microbial adaptation to changing environments - Conference Proceedings*,  
14 143-146, Matforsk Norwegian food research institute, 405pp. (ISBN NR:82-90394-88-8)  
15 [18th symposium of the International Committee on Food Microbiology and Hygiene,  
16 Lillehammer (Norway), August 18-23, 2002]
- 17 Membré, J.-M., Leporq, B., Vialette, M., Mettler, E., Perrier, L., Thuault, D., Zwietering,  
18 M.H., 2003. Temperature effect on bacterial growth rate : quantitative microbiology  
19 approach including cardinal values and variability estimates, to perform growth  
20 simulations on/in food. In: J.F.M. Van Impe, A.H. Geeraerd, I. Leguérinel and P. Mafart  
21 (Eds.), *Predictive modelling in foods - Conference Proceedings*. Katholieke Universiteit  
22 Leuven / BioTeC, Belgium.
- 23 Membré, J.-M., Kubaczka, M., Dubois, J., and Chèné, C. 2004. Temperature effect on  
24 *Listeria monocytogenes* growth in the event of contamination of cooked pork products.  
25 *Journal of Food Protection*, 67, 463-469.

- 1 Peck, M.W., Roberts, T.A., Sutherland, J.P., Walker, S.J.,1994. Modelling the growth,  
2 survival and death of microorganisms in foods: the UK Food Micromodel approach.  
3 *International Journal of Food Microbiology* 23, 265-275.
- 4 Pinon, A., Zwietering, M. H., Perrier, L., Membré, J.-M., Leporq, B., Mettler, E., Thuault, D.,  
5 Coroller, L., Stahl, V., & Vialette, M. 2004. Development and Validation of Experimental  
6 Protocols for Use of Cardinal Models for Prediction of Microorganism Growth in Food  
7 Products. *Applied and Environmental Microbiology* 70, 1081-1087.
- 8 Rosso L., 1995. Modélisation et Microbiologie Prévisionnelle : élaboration d'un nouvel outil  
9 pour l'agro-alimentaire, Thèse de doctorat, présentée devant l'Université Claude Bernard -  
10 Lyon (France).
- 11 Rosso, L., Lobry, J.R., Bajard, S., Flandrois J.P., 1995. Convenient Model To Describe the  
12 Combined Effects of Temperature and pH on Microbial Growth. *Applied and*  
13 *Environmental Microbiology* 61 (2), 610-616.
- 14 Zwietering, M.H., Wiltjes, T., De Wit, J.C., Van'T Riet, K., 1992. A decision support system  
15 for prediction of the microbial spoilage in foods. *Journal. of Food Protection* 55 (12), 973-  
16 979.

Table 1 The software deliveries.

User	Aim	Query
Industrial Companies	Challenge test	Which information can be deducted from this experiment? Which germs are concerned for my product? Which product families behave in the same way?
	New product conception	Which impact of pH, sugar, organic acids or thermal treatment on growth or survival of related pathogens ?
Distributor	Comparison of shelf life conditions	Growth occurring for real thermal profile with regard to standard temperature
Governmental Organisations	Hazard incidence on a given product	Simulation of behaviour according to contamination, product characteristics and shelf life conditions

## Figures

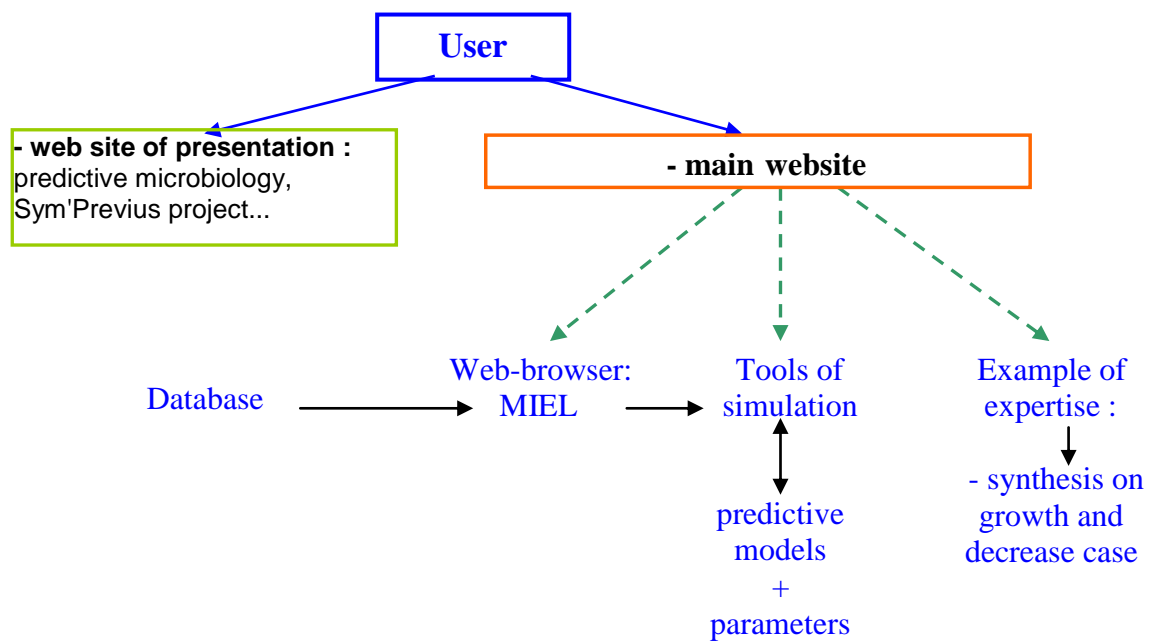
Figure 1: description of the Sym'Previous units.

Figure 2: view of the web-browser: MIEL.

Figure 3: view of the simulation tool.

Figure 4: kinetics of *Escherichia coli* O157:H7 on ground beef meat, at various temperature levels, extracted from the database. The raw data referred to x-names, x =temperature level, names = first author of the paper and year of the publication, or industrial Sym'Previous partner source.

Figure 5: example of exploitation of data by the model. The open squares correspond to growth rate values obtained on liquid medium as function of the temperature level, and circles to growth rates determined on ground beef meat. The thin continuous line represents the fitting on the mean value completed by the interval confidence in dotted lines (Huet et al.,1996). The bold line is the “final” fitting corresponding to the growth on the food product.



Nom de l'ensemble des valeurs recherchées

Aliments disponibles

- denrées alimentaires
  - boissons
  - denrées animales et d'origine animale
    - lait et produits laitiers
    - oeuf et ovoproduits
    - produits de la mer et d'eau douce
    - viandes et produits à base de viande
      - carcasse, abats, issues (1ère trans)
      - pièces de découpes (2ème transfo)
      - produits à base de viande
      - viandes fraîches
  - denrées végétales et d'origine végétale
  - plats cuisinés
  - environnement et divers
  - milieu de culture
  - nouveau pdt à intégrer

Aliment:  Préférences:

Reinitialiser    Sauvegarder    Visualiser la sélection

Nouvel ensemble    Supprimer     Elargir la sélection

Critères optionnels

Structure de l'aliment

Etat de l'aliment

aw

pH

Caractéristiques aliment    Microorganismes    Facteurs analysés    Lancer la recherche



# le module de simulation

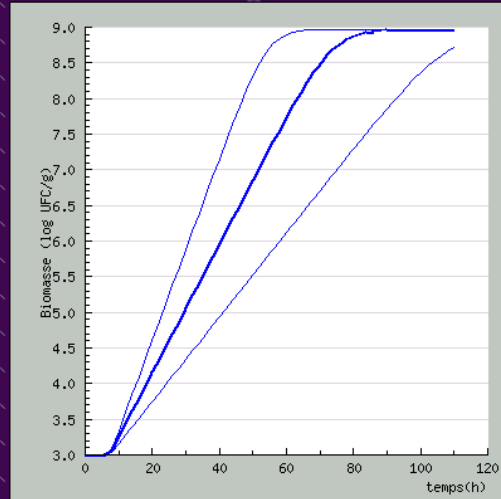
Comparer

Température

Aliment

Confronter vos données

Initialisation



T1 = 15

Données Brutes

En savoir plus sur la variabilité  
microbiologique

Effet facteur



