The "Sym'Previous" software, a tool to support decisions to the foodstuff safety

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Abstract

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

1 Introduction

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

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

Research in predictive microbiology has been pursued throughout a FLAIR research project funded by EU and carried out in 1990-93 (Peck et al. 1994). Research teams from 12 European countries participated in this project, whose co-ordinator was Dr T. Roberts, from IFR. Afterwards the project was followed by a COST project (914) aiming to organise dissemination and exchanges of findings among a large number of laboratories, particularly on the validation of models on real food products. Another European project, named PREMIUM, directed by Prof. Dr. Jan Van Impe from the Katholieke Universiteit Leuven, was implemented and funded in the 4th Framework. Its main objectives were to elaborate a unified modelling system, and to validate it on real food products as well.

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

- several French scientific teams had participated in the European projects named above, and found them promising; especially a leader of the food industry who developed an application based on cardinal models (Rosso, 1995), and used it in real conditions, in plants manufacturing fresh dairy products.
- the French government was very interested in the opportunity of implementing an expertise in the domain of pathogens, in order to improve the general security level of foodstuffs; moreover, a further application of such a tool in Quantitative Risk Assessment was considered as well.
- The French food industry were interested also in participating in the building of a common software, to share their expertise in food safety and their data (challenge-tests, models, bacterial strains...).

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

2 The software facilities

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

2.1 A relational database of food microbiology

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

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

2.2 Predictive models in order to simulate growth kinetics

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

2.2.1 Microbial growth in food, in case of contamination

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

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

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

2.2.2 Software facilities

The starting assumption of this tool of simulation is that the user does not know which particular strain could contaminate his/her product. In this way the specific parameters (cardinal values) of this strain are ignored. It is probably more interesting to provide a "mean" response of the species completed by an interval confidence (Huet et al., 1996) than to describe the behaviour of a specific strain unknown by the user. To illustrate the global behaviour of the five pathogenic species studied during the Sym'Previus program, a specific group was in charge of selecting among a large collection of strains (more than 1000) the more representative and of determining their cardinal values (Membré et al., 2002, Membré et al., 2003).

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

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

2.3 Expertise in food microbiology

The major interest of Sym'Previus is not only to provide a database and mathematical models but to combine information and to supply an analysis done by a group of experts (microbiologists, statisticians) in order to summarise the knowledge. Figures 4 and 5 illustrate what is done with a request such as “which is the behaviour of *Escherichia coli* O157:H7 in beef meat in a range of temperatures from refrigerated to room values ?”. In the first time the database is scanned about the association beef meat / *Escherichia coli* O157:H7 under the influence of the temperature effect through the MIEL. Raw kinetics were extracted at different levels (Figure 4). The first interest is to bring an accurate idea of the bacterial behaviour on a product including variability due to different sources of data (different authors and laboratories). Thus, from each kinetic a growth rate was estimated, plotted versus the temperature and compared to these obtained in liquid medium (Figure 5). A difference of growth rates is observed, between data obtained in the food matrix and the data established in liquid medium. To fit the model to the beef meat data, the food dependent parameter, μ_{opt}, is adjusted (Eq. 1). Hence, the specific growth rate values of *Escherichia coli* on beef meat are available in the software, without carrying out any new experiment.

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

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

5. The Future of Sym'Previus

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

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

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

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

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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

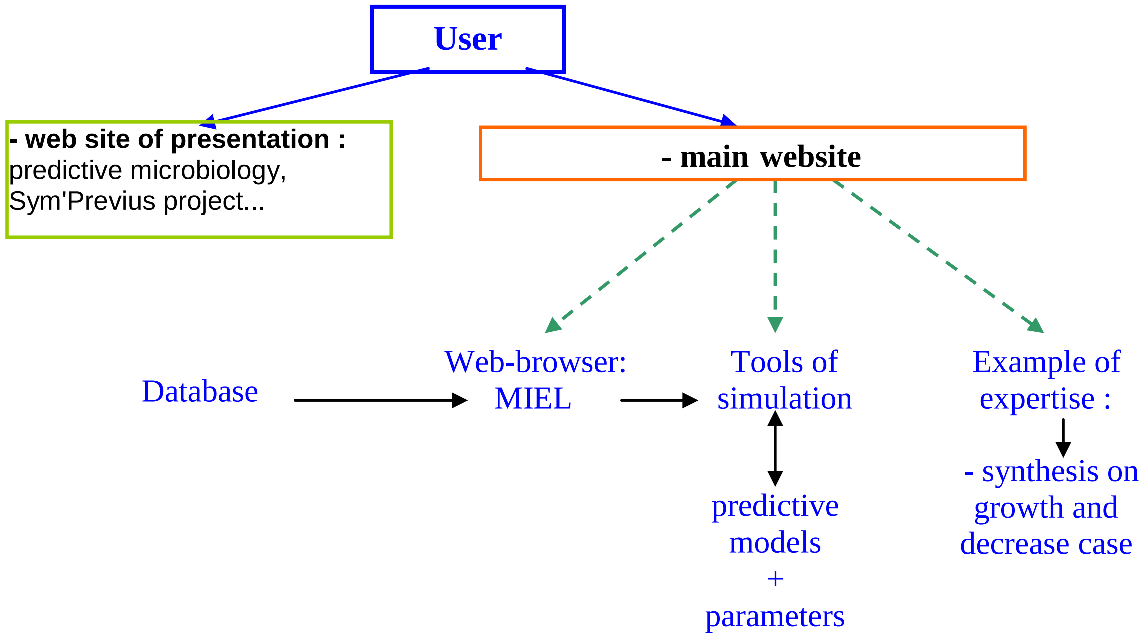
Figure 1: description of the Sym'Previus units.

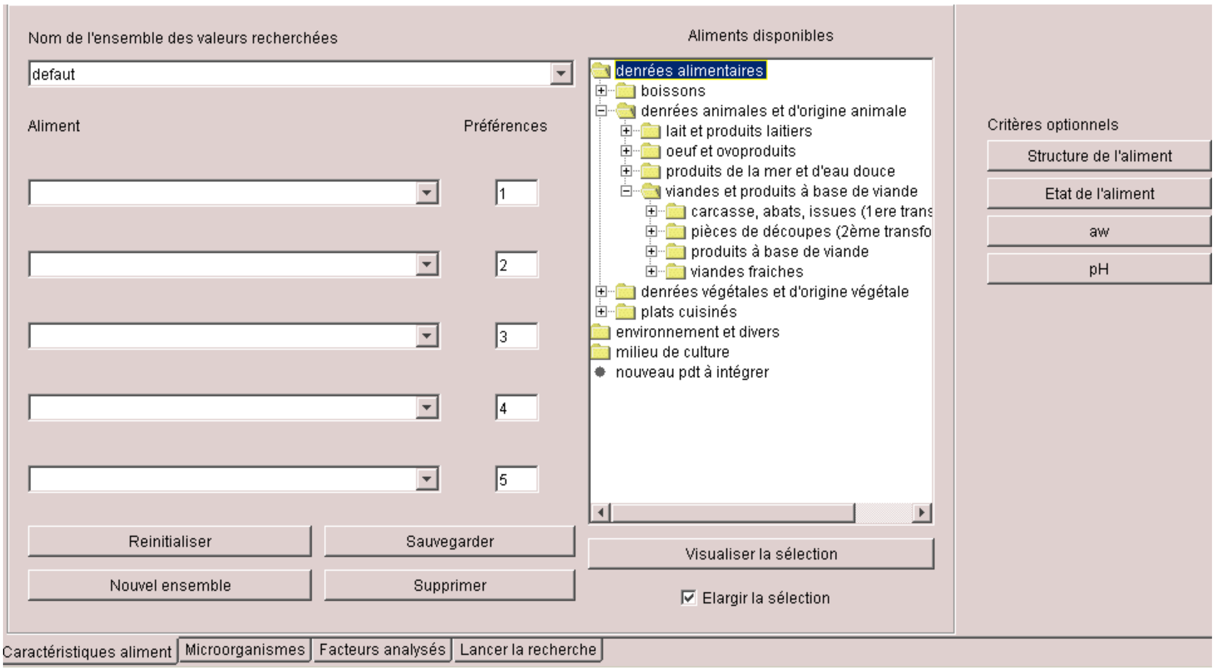
Figure 2: view of the web-browser: MIEL.

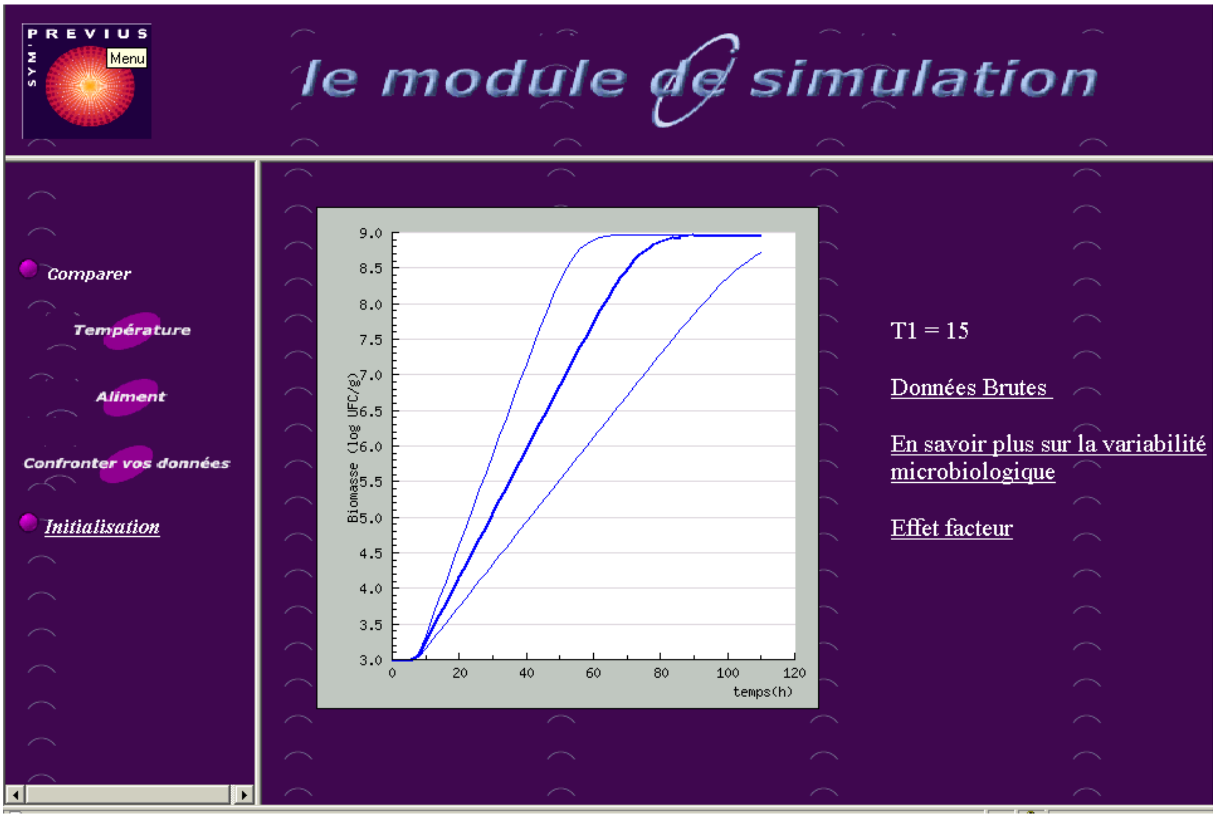
Figure 3: view of the simulation tool.

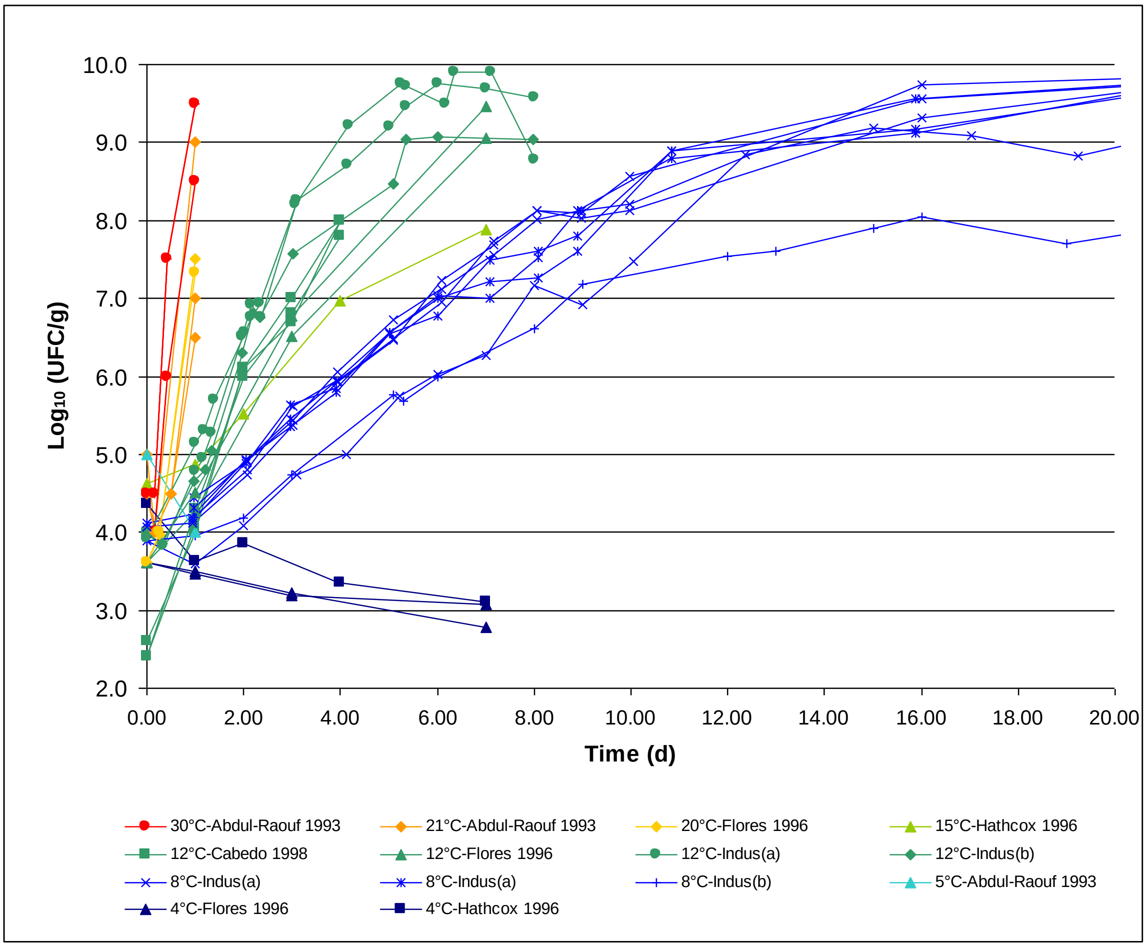
Figure 4: kinetics of *Escherichia coli* O157:H7 on ground beef meat, at various temperature levels, extracted from the database. The raw data refereed to x-names, x =temperature level, names = first author of the paper and year of the publication, or industrial Sym'Previus partner source.

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.

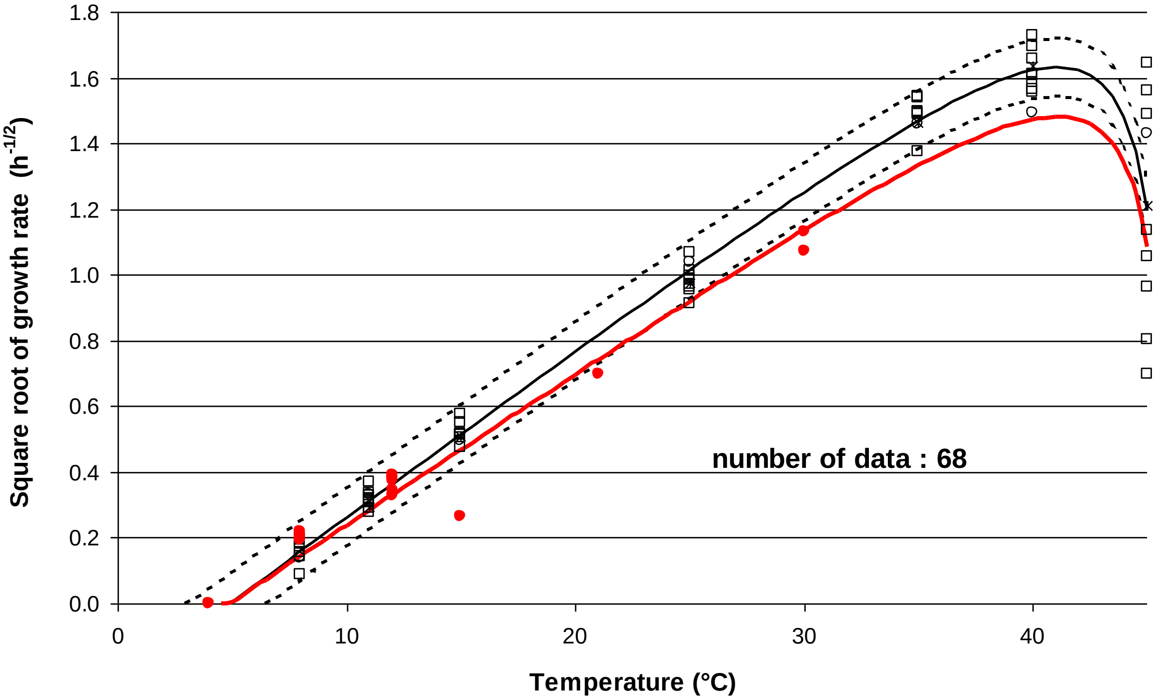

User
- web site of presentation :
predictive microbiology,
Sym'Previus project...
- main website
Database
Web-browser:
MIEL
Tools of
simulation
predictive
models
+
parameters
Example of
expertise :
- synthesis on
growth and
decrease case


Nom de l'ensemble des valeurs recherchées
defaut
Aliment
Préférences
1
2
3
4
5
Reinitialiser
Sauvegarder
Nouvel ensemble
Supprimer
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 (1ere trans
pièces de découpes (2ème transfo
produits à base de viande
viandes fraiches
denrées végétales et d'origine végétale
plats cuisinés
environnement et divers
milieu de culture
nouveau pdt à intégrer
Visualiser la sélection
Elargir la sélection
Critères optionnels
Structure de l'aliment
Etat de l'aliment
aw
pH
Caractéristiques aliment
Microorganismes
Facteurs analysés
Lancer la recherche


PREVIUS
SYM'
Menu
le module de simulation
Comparer
Température
Aliment
Confronter vos données
Initialisation
Biomasse (log UFC/g)
9.0
8.5
8.0
7.5
7.0
6.5
6.0
5.5
5.0
4.5
4.0
3.5
3.0
0
20
40
60
80
100
120
temps(h)
T1 = 15
Données Brutes
En savoir plus sur la variabilité microbiologique
Effet facteur



10.0
9.0
8.0
7.0
6.0
5.0
4.0
3.0
2.0
Log10 (UFC/g)
0.00
2.00
4.00
6.00
8.00
10.00
12.00
14.00
16.00
18.00
20.00
Time (d)
30°C-Abdul-Raouf 1993
21°C-Abdul-Raouf 1993
20°C-Flores 1996
15°C-Hathcox 1996
12°C-Cabedo 1998
12°C-Flores 1996
12°C-Indus(a)
12°C-Indus(b)
8°C-Indus(a)
8°C-Indus(a)
8°C-Indus(b)
5°C-Abdul-Raouf 1993
4°C-Flores 1996
4°C-Hathcox 1996


1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Square root of growth rate (h-1/2)
0
10
20
30
40
Temperature (°C)
number of data : 68