



Predictive microbiology

Annie Beaufort

EU RL for *Listeria monocytogenes*

What is predictive microbiology?

The microbial responses to the food environments by mathematical models.

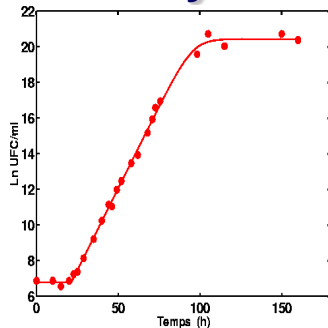
It is often use to assess the growth, the survival and the destruction of bacteria in foods.

Main software

Software	Admin Center	Applications	Growth	Survival	Heat destruction	Food application	Commercial software
Food MicroModel	MAFF (Agric. Minist. UK)	1st commercial software, Simulation in synthetic media (lab. broth) Food is not taken into account, This software was stopped	X	X	X		X
PMP	USDA	Simulation in synthetic media (broth), Food is not taken into account	X	X	X		
ComBase Predictor	IFR	Simulation in synthetic media (broth), Food could be taken into account by commercial IFR expertise.	X	X	X		
Seafood Spoilage and Safety Predictor	DIFRES	Specific software for sea food products, Growth simulation for pathogen and spoilage bacteria Sea food products are taken into account	X			X	
Sym'Previous	GIS Sym'Previous	Based on food and microbial parameters, All simulations takes food product into account	X	X	X	X	X

Predictive microbiology is based on primary models and secondary models

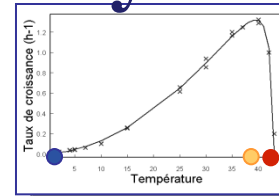
Primary models



Primary model parameters

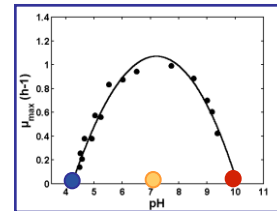
- μ_{\max} : growth rate
- lag : lag phase
- Log No : Initial population
- Log N_{max}: max population

different T°



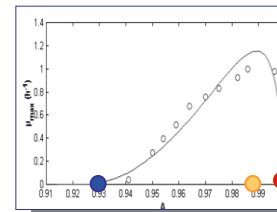
T_{\min} T_{opt} T_{\max}

different pH



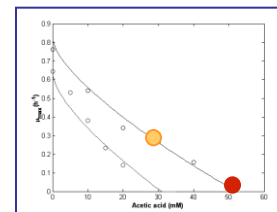
pH_{\min} pH_{opt} pH_{\max}

different a_w



$a_{w\min}$ $a_{w\text{opt}}$ $a_{w\max}$

different acid concentration



alpha MIC

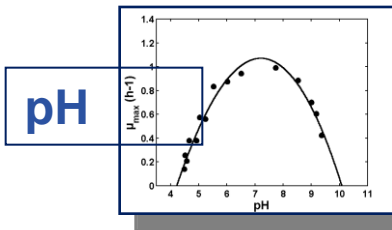
➤ A primary model describes the evolution of microbial population according to the time in a given environment.

➤ A secondary model expresses the evolution of parameters according to environmental factors: they link λ and μ_{\max} to environmental factors (temperature, pH, ...).

Primary models

$$\begin{aligned} \text{Gompertz} \quad \ln(N(t)) &= \ln(N_0) + A \exp\left(-\exp\left(\frac{\mu e}{A}(\text{lag} - t) + 1\right)\right) \\ \text{logistique} \quad \ln(N(t)) &= \ln(N_0) + \frac{A}{1 + \exp\left(\frac{4\mu}{A}(\text{lag} - t) + 2\right)} \end{aligned}$$

Secondary model



$$\mu_{\max} = \mu_{opt} \cdot \gamma_{pH}$$

$$\gamma(pH) = \frac{(pH - pH_{\min})(pH - pH_{\max})}{(pH - pH_{\min})(pH - pH_{\max}) - (pH - pH_{opt})^2}$$

Combase software

4 applications

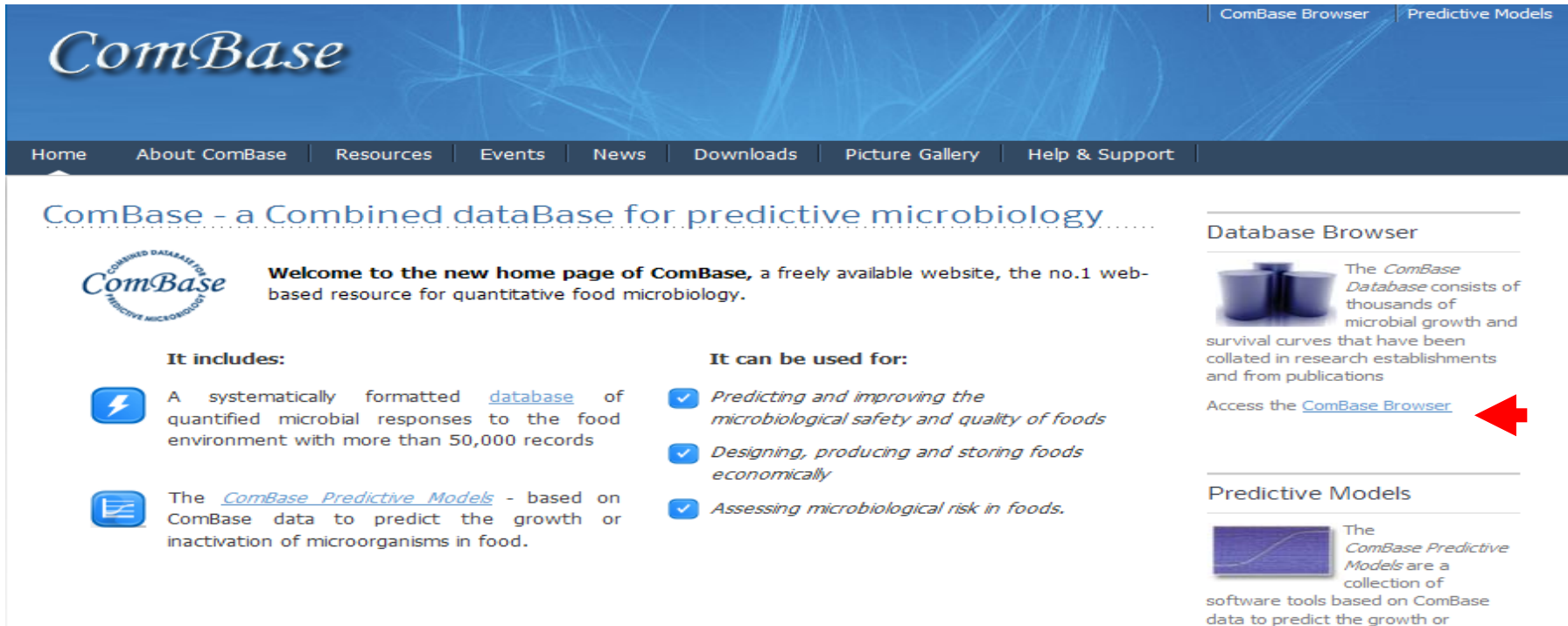
- ❖ **Combase: the data base**
- ❖ **Combase predictor**
- ❖ **Combase: Perfringens predictor**
- ❖ **Combase: growth interface**

First application

ComBase: database

ComBase: access on database

ComBase is a two-part system including a database and predictive models. In this first part, we will work on the database.




ComBase



ComBase Browser | Predictive Models

Home | About ComBase | Resources | Events | News | Downloads | Picture Gallery | Help & Support




ComBase - a Combined dataBase for predictive microbiology.....

 **Welcome to the new home page of ComBase**, a freely available website, the no.1 web-based resource for quantitative food microbiology.


It includes:


-  A systematically formatted [database](#) of quantified microbial responses to the food environment with more than 50,000 records
-  The [ComBase Predictive Models](#) - based on ComBase data to predict the growth or inactivation of microorganisms in food.

It can be used for:

-  *Predicting and improving the microbiological safety and quality of foods*
-  *Designing, producing and storing foods economically*
-  *Assessing microbiological risk in foods.*

Database Browser

 The *ComBase Database* consists of thousands of microbial growth and survival curves that have been collated in research establishments and from publications

Access the [ComBase Browser](#) 

Predictive Models

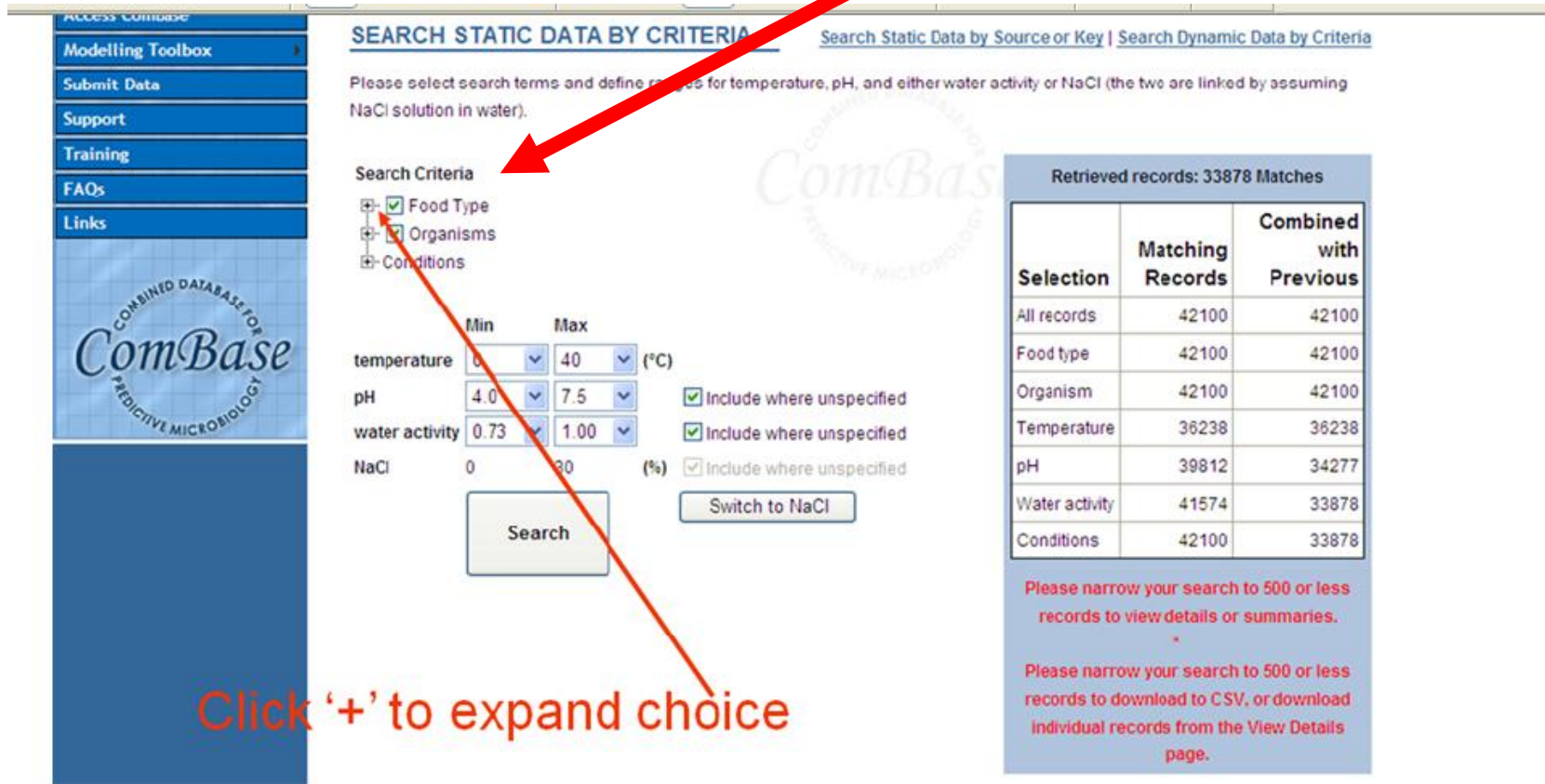
 The *ComBase Predictive Models* are a collection of software tools based on ComBase data to predict the growth or

Click on Access the ComBase Browser

You will be directed to the data base by criteria.

Search static data by criteria

Assuming that you are interested in the growth of *Salmonella* in poultry at refrigeration temperature, select the following



The screenshot shows the ComBase search interface. On the left is a navigation menu with links to 'Access ComBase', 'Modelling Toolbox', 'Submit Data', 'Support', 'Training', 'FAQs', and 'Links'. The main content area is titled 'SEARCH STATIC DATA BY CRITERIA' and includes instructions to select search terms and define ranges for temperature, pH, and either water activity or NaCl. The search criteria section has three expandable categories: 'Food Type', 'Organisms', and 'Conditions'. The 'Food Type' category is expanded, showing a 'Search' button. Below this are input fields for 'temperature' (0 to 40 °C), 'pH' (4.0 to 7.5), 'water activity' (0.73 to 1.00), and 'NaCl' (0 to 30 %). There are also checkboxes for 'Include where unspecified' for each parameter and a 'Switch to NaCl' button. A table on the right shows 'Retrieved records: 33878 Matches' with columns for 'Selection', 'Matching Records', and 'Combined with Previous'. A red arrow points from the text above to the '+' icon next to 'Food Type' in the search criteria section. Another red arrow points from the text 'Click '+ to expand choice' to the '+' icon.

SEARCH STATIC DATA BY CRITERIA [Search Static Data by Source or Key](#) | [Search Dynamic Data by Criteria](#)

Please select search terms and define ranges for temperature, pH, and either water activity or NaCl (the two are linked by assuming NaCl solution in water):

Search Criteria

- Food Type
- Organisms
- Conditions

temperature: Min 0 Max 40 (°C)

pH: 4.0 7.5 Include where unspecified

water activity: 0.73 1.00 Include where unspecified

NaCl: 0 30 (%) Include where unspecified

Retrieved records: 33878 Matches

Selection	Matching Records	Combined with Previous
All records	42100	42100
Food type	42100	42100
Organism	42100	42100
Temperature	36238	36238
pH	39812	34277
Water activity	41574	33878
Conditions	42100	33878

Please narrow your search to 500 or less records to view details or summaries.

Please narrow your search to 500 or less records to download to CSV, or download individual records from the View Details page.

Click '+' to expand choice

Example of search

HOME > Browser Home > Search Options > Search

SEARCH STATIC DATA BY CRITERIA [Search Static Data by Source or Key](#) | [Search Dynamic Data by Criteria](#)

Please select search terms and define ranges for temperature, pH, and either water activity or NaCl (the two are linked by assuming NaCl solution in water).

Search Criteria

- Food Type
 - Beef (2713)
 - Bread (236)
 - Cheese (640)
 - Culture medium (27358)
 - Dessert food (258)
 - Egg or egg product (665)
 - Infant_food (257)
 - Juice, beverage (118)
 - Milk (1226)
 - Other or unknown type of dairy (526)
 - Other or unknown type of meat (510)
 - Other, mixed, uncategoryed or unknown type of food (1275)
 - Pork (1371)
 - Poultry (1774)
 - Sauce/Dressing (76)
 - Sausage (740)
 - Seafood (1239)
 - Vegetable or fruit and their products (990)
 - Water (128)
- Organisms

Retrieved records: 33878 Matches

Selection	Matching Records	Combined with Previous
All records	42100	42100
Food type	42100	42100
Organism	42100	42100
Temperature	36238	36238
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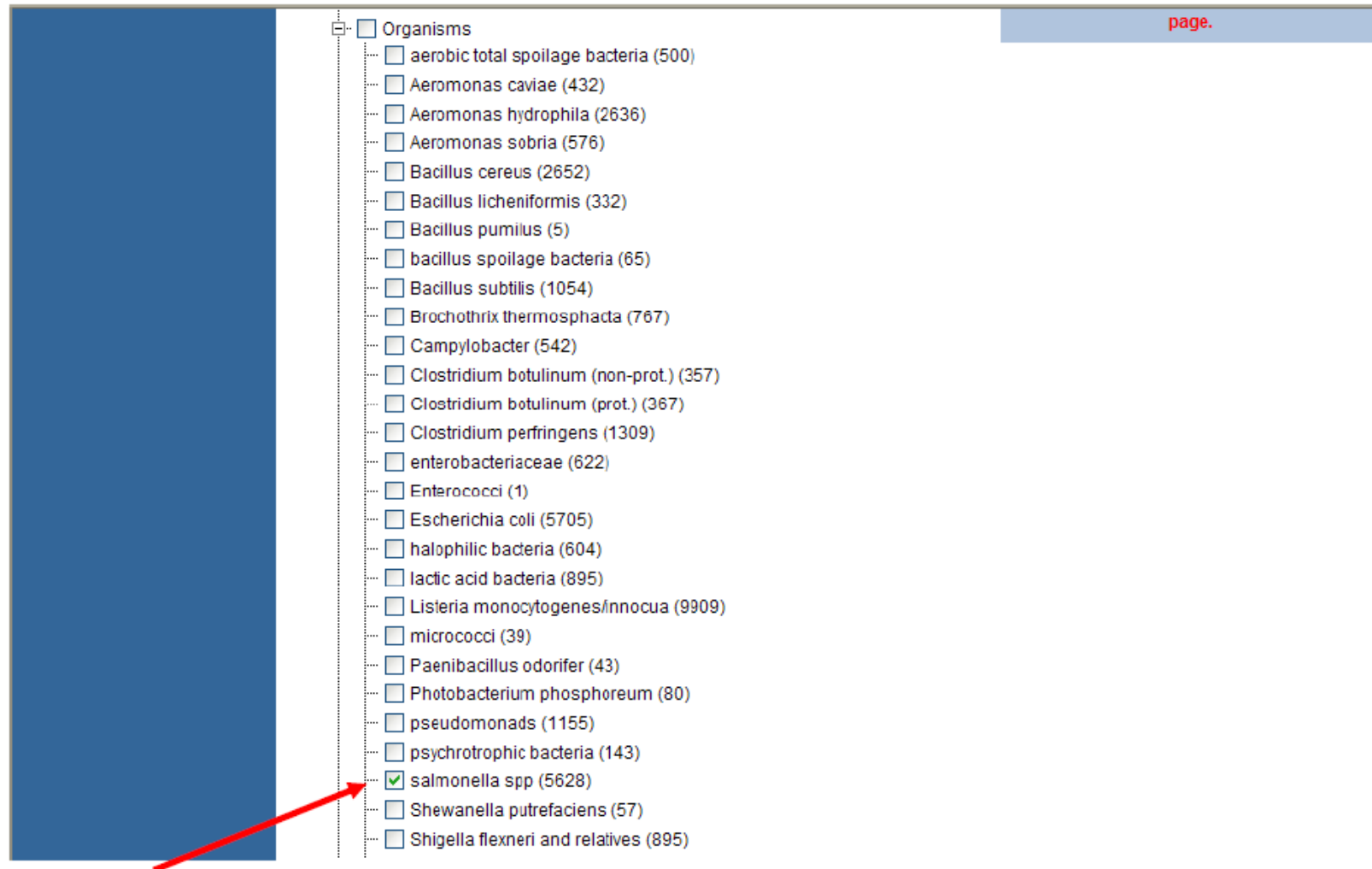
Please narrow your search to 500 or less records to view details or summaries.

Please narrow your search to 500 or less records to download to CSV, or download individual records from the View Details page.

Click '+' to expand choice and choose *Poultry*.

Example of search

In the "Organism" group, select *Salmonella spp*;



The screenshot shows a search interface with a list of organisms. A red arrow points to the 'salmonella spp' entry, which is marked with a green checkmark. The list includes various bacterial species and their counts in parentheses. A 'page.' label is visible in the top right corner of the interface.

Organism	Count
Organisms	
<input type="checkbox"/> aerobic total spoilage bacteria	(500)
<input type="checkbox"/> Aeromonas caviae	(432)
<input type="checkbox"/> Aeromonas hydrophila	(2636)
<input type="checkbox"/> Aeromonas sobria	(576)
<input type="checkbox"/> Bacillus cereus	(2652)
<input type="checkbox"/> Bacillus licheniformis	(332)
<input type="checkbox"/> Bacillus pumilus	(5)
<input type="checkbox"/> bacillus spoilage bacteria	(65)
<input type="checkbox"/> Bacillus subtilis	(1054)
<input type="checkbox"/> Brochothrix thermosphacta	(767)
<input type="checkbox"/> Campylobacter	(542)
<input type="checkbox"/> Clostridium botulinum (non-prot.)	(357)
<input type="checkbox"/> Clostridium botulinum (prot.)	(367)
<input type="checkbox"/> Clostridium perfringens	(1309)
<input type="checkbox"/> enterobacteriaceae	(622)
<input type="checkbox"/> Enterococci	(1)
<input type="checkbox"/> Escherichia coli	(5705)
<input type="checkbox"/> halophilic bacteria	(604)
<input type="checkbox"/> lactic acid bacteria	(895)
<input type="checkbox"/> Listeria monocytogenes/innocua	(9909)
<input type="checkbox"/> micrococci	(39)
<input type="checkbox"/> Paenibacillus odorifer	(43)
<input type="checkbox"/> Photobacterium phosphoreum	(80)
<input type="checkbox"/> pseudomonads	(1155)
<input type="checkbox"/> psychrotrophic bacteria	(143)
<input checked="" type="checkbox"/> salmonella spp	(5628)
<input type="checkbox"/> Shewanella putrefaciens	(57)
<input type="checkbox"/> Shigella flexneri and relatives	(895)

Choose *Salmonella sp*;

Example of search



- Food Type
- Organisms
- Conditions
 - Atmosphere
 - Glycerol monolaurate (emulsifier) in the environment of the cells (2305)
 - Nisin in the environment of the cells (2260)
 - Nitrogen in the environment of the cells (2417)
 - Oxygen (aerobic conditions) in the environment of the cells (2057)
 - Sodium chloride in the environment of the cells (183)
 - Sodium or potassium nitrite in the environment of the cells (1228)
 - With the indigenous flora in the environment of the cells (but not counted) (81)
 - Preparation
 - Smoked food (3312)
 - Sorbic acid (possibly as salt) in the environment of the cells (103)
 - Sterilised before inoculation (120)
 - Sucrose in the environment of the cells (2136)
 - Sugar in the environment of the cells (814)
 - Thyme essential oil in the environment of the cells (1957)
 - Vacuum-packed (350)
 - Microbial flora
- Additives
 - Acetic acid (possibly as salt) in the environment of the cells (781)
 - Allyl isothiocyanate (84)
 - ALTA fermentation product in the environment of the cells (133)
 - Anaerobic environment (30)
 - Ascorbic acid (possibly as salt) in the environment of the cells (103)
 - Benzoic acid (possibly as salt) in the environment of the cells (0)
 - Carbon-dioxide in the environment of the cells (61)
 - Chitosan in the environment of the cells. (6)
 - Citric acid (possibly as salt) in the environment of the cells (46)
 - Cut (minced, chopped, ground, etc) (372)
 - Dried food (470)
 - Ethanol in the environment of the cells (2524)
 - Ethylenediaminetetraacetic acid in the environment of the cells (148)

Then, click on the search button, and you get the records found.

Result of search

COMBASE SEARCH RESULT SUMMARY

[View Details](#)

Please exclude any records not of interest by clicking on the appropriate checkbox. You may need to page through the results by clicking on the page numbers at the end of the list. Clicking on a heading will sort by that column. Clicking again will sort in reverse order.

Record Count: 122/122

[Download to CSV \(Save Changes First\)](#)

Exclude All

Save Changes

List of Current Matches

Page: 1 2

<u>Organism</u>	<u>Food Type</u>	<u>in_on</u>	<u>Temp</u>	<u>pH</u>	<u>water activity</u>	<u>conditions</u>	<u>Source</u>	<u>Key</u>	<u>Exclude</u>
salmonella spp	Poultry	In: chicken breast	4	6.3		raw, lactic_acid(ppm): 20000	Anang_07	Anang_10_10S	<input type="checkbox"/>
salmonella spp	Poultry	In: chicken breast	4	6.3		raw, lauricidin(ppm): 0	Anang_07	Anang_10_1S	<input type="checkbox"/>
salmonella spp	Poultry	In: chicken breast	4	6.3		raw, lauricidin(ppm): 5000	Anang_07	Anang_10_2S	<input type="checkbox"/>
salmonella spp	Poultry	In: chicken breast	4	6.3		raw, lauricidin(ppm): 10000	Anang_07	Anang_10_3S	<input type="checkbox"/>
salmonella spp	Poultry	In: chicken breast	4	6.3		raw, lauricidin(ppm): 15000	Anang_07	Anang_10_4S	<input type="checkbox"/>
salmonella spp	Poultry	In: chicken breast	4	6.3		raw, lauricidin(ppm): 20000	Anang_07	Anang_10_5S	<input type="checkbox"/>
salmonella	Poultry	In: chicken breast	4	6.3		raw, lactic acid(ppm): 0	Anang_07	Anang_10_6S	<input type="checkbox"/>

Then, choose a record you are interested in.

Here is the record you are interested in

COMBASE SEARCH RESULT DETAILS FOR RECORD ID: GMW_0278

[View Summary](#)

[First](#) [Back 10](#) [Previous](#) [Next](#) [Forward 10](#) [Last](#)

[60/122 matches]

[Download GMW_0278 to CSV](#)

Record Details

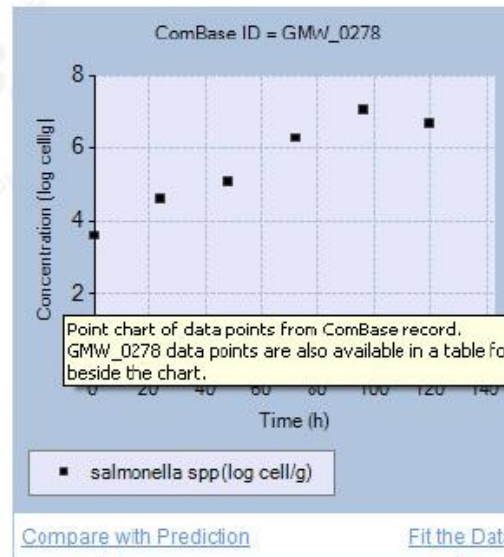
Organism: *salmonella* spp
Food type: Poultry (In: chicken breast)
Temperature: 10 °C
pH: Not reported
Water activity: Not reported
NaCl: Not reported
Maximum Rate (log₁₀(CFU/h)): See data

Conditions:

Modified atmosphere environment essential oil in the environment of the cells, Sodium chloride in the environment of the cells

Source:

Nissen (et al.), 2001: Survival and growth of *Escherichia coli* O157:H7, *Y. enterocolitica* and *Salmonella enteritidis* on decontaminated and untreated meat. *International of Food Microbiology*, 57, 291-298.



Record Data (GMW_0278)

Time (h)	log cell/g
0.00	3.600
24.00	4.600
48.00	5.100
72.00	6.300
96.00	7.100
120.00	6.700

You can estimate the μ_{\max} (growth rate): click on « Fit the data ».

A fitting tool (primary model)

DMFit

Food Research to allow microbiologists to fit log counts vs. time data and extract parameters such as growth/death rate and lag time/shoulder.
For further information on DMFit web edition, [click here](#).

Input your data in the textbox below

0.00	3.68
24.00	6.18
48.00	6.32
72.00	7.18
120.00	7.38
168.00	7.23

Show me how!

Choose a model:

Baranyi and Roberts	Linear, biphasic or trilinear models
<input type="radio"/> Complete model	<input type="radio"/> Trilinear
<input checked="" type="radio"/> No lag	<input type="radio"/> Biphasic (No lag)
<input type="radio"/> No asymptote	<input type="radio"/> Biphasic (No asymptote)
	<input type="radio"/> Linear

Display data

Fit

Convergence

R-square SE of Fit

Estimated parameters and standard errors

Initial value		Maximum rate	
<input type="text" value="4.0105"/>	<input type="text" value="0.5106"/>	<input type="text" value="0.0604"/>	<input type="text" value="0.0197"/>
Final value			
<input type="text" value="7.2344"/>	<input type="text" value="0.3198"/>		

time fitted value

0.00	4.01
3.36	4.21
6.72	4.42
10.08	4.62
13.44	4.82

You get :

- the experimental data
- the fitted growth curve
- the μ_{\max}

Second application

ComBase Predictor
(tool for growth)

Models

Organism	env.factors	Remarks
<i>Aeromonas hydrophila</i>	(temp, pH, aw)	
<i>Bacillus cereus</i>	(temp, pH, aw)	
<i>Bacillus cereus</i> + CO ₂	(temp, pH, aw, CO ₂)	
<i>Bacillus licheniformis</i>	(temp, pH, aw)	
<i>Bacillus subtilis</i>	(temp, pH, aw)	
<i>Brochothrix thermosphacta</i>	(temp, pH, aw)	
<i>Clostridium botulinum</i> (non.prot)	(temp, pH, aw)	
<i>Clostridium botulinum</i> (prot)	(temp, pH, aw)	
<i>Clostridium perfringens</i>	(temp, pH, aw)	
<i>Escheria coli</i> 0157	(temp, pH, aw)	
<i>Escheria coli</i> 0157 + CO ₂	(temp, pH, aw, CO ₂)	
<i>Listeria monocytogenes</i>	(temp, pH, aw)	
<i>Listeria monocytogenes</i> + CO ₂	(temp, pH, aw, CO ₂)	
<i>Listeria monocytogenes</i> + Nitrite	(temp, pH, aw, NaNO ₂)	
<i>Listeria monocytogenes</i> + Lactic	(temp, pH, aw, Lactic)	
<i>Listeria monocytogenes</i> + Acetic	(temp, pH, aw, acetic acid)	
<i>Staphylococcus aureas</i>	(temp, pH, aw)	
<i>Saccharomyces cerevisiae</i>	(pH,aw)	
Salmonellae	(temp, pH, aw)	
Salmonellae + CO ₂	(temp, pH, aw, CO ₂)	
Salmonellae + Nitrite	(temp, pH, aw, NaNO ₂)	
<i>Yersinia enterocolitica</i>	(temp, pH, aw)	
<i>Yersinia enterocolitica</i> + CO ₂	(temp, pH, aw, CO ₂)	
<i>Yersinia enterocolitica</i> + Lactic	(temp, pH, lact)	NaCl=0.5 const
<i>Yersinia enterocolitica</i> + Acetic	(temp, pH, acet)	NaCl=0.5 const
<i>Bacillus subtilis</i> (aw: with glycerol)	(temp, pH, aw)	
<i>Pseudomonads</i>	(temp, pH)	NaCl=0.5 const
<i>Brochothrix thermosphacta</i> death	(temp,pH)	FLAIR. NaCl had no effect between 0 and 2 %.

Access to ComBase Predictor

ComBase

ComBase Browser | Predictive Models

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Predictive Models



The **ComBase Predictive models** are a collection of software tools based on ComBase data to predict the growth or inactivation of microorganisms. Currently available predictive tools include the following on line applications:

- ✓ [ComBase Predictor](#), a set of 23 growth models and 6 thermal death models for predicting the response of many important foodborne pathogenic and spoilage microorganisms to key environmental factors. An Excel version of this web application can also be found in the *ComBase Excel Demo* downloadable [here](#)
- ✓ [Perfringens Predictor](#), an application specially designed for predicting the growth of *Clostridium perfringens* during the cooling of meats. An [Excel AddIn version](#) of the program can also be found in the Downloads section of this web site

 [Access the ComBase Predictive Models](#)



Predictive Models

[PREDICTIVE MODELS](#)
[COMBASE PREDICTOR](#)
[PERINGENS PREDICTOR](#)

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To access these programs you must first register and then provide your username and password with each login

Access to ComBase Predictor

Growth Predictor

Growth Predictor version 1.0



Developed at the Institute of Food Research under the funding of the Food Standards Agency, UK

The models in Growth Predictor are based on the same data as the previous UK predictive modelling software, Food MicroModel. However, the models have been improved and contain new features. A similar predictive package, Pathogen Modeling Program, based on data generated under the funding of the Agricultural Research Service of the USDA, can be downloaded from

By clicking on the "Accept" button, you agree with the following:
All rights of ownership in Copyright and other Intellectual Property Rights in Growth Predictor and the program documentation shall at all times remain vested in the Food Standards Agency and the Institute of Food Research and no such rights have been or will be transferred to you.
The Food Standards Agency and Institute of Food Research have taken due care in the design of the models, their validation and implementation in the software. However, you acknowledge that your use or application of Growth Predictor is beyond the control of either body. The implementation of microbiological predictions from Growth Predictor requires expert interpretation and you are responsible for ensuring that

Accept **Exit**

ComBase Predictor

 Growth model

 Thermal inactivation model

 Non thermal survival model

Temperature input

 Static

 Changing temperature

Water activity

 NaCl

 Aw

Observation duration

Time (h)

add a row

Aeromonas hydrophila

Initial level <=7	Phys.state [0-1]	T (°C) [2-37]	pH [4.6-7.5]	NaCl (%) [0.0-4.5]	Max.rate (log.conc/h)	Dbl.time (h)
<input type="text" value="3"/>	<input type="text" value="0.001836"/> Help	<input type="text" value="20"/>	<input type="text" value="7"/>	<input type="text" value="0.5"/>	<input type="text" value="0.44"/>	<input type="text" value="0.69"/>

Aeromonas hydrophila

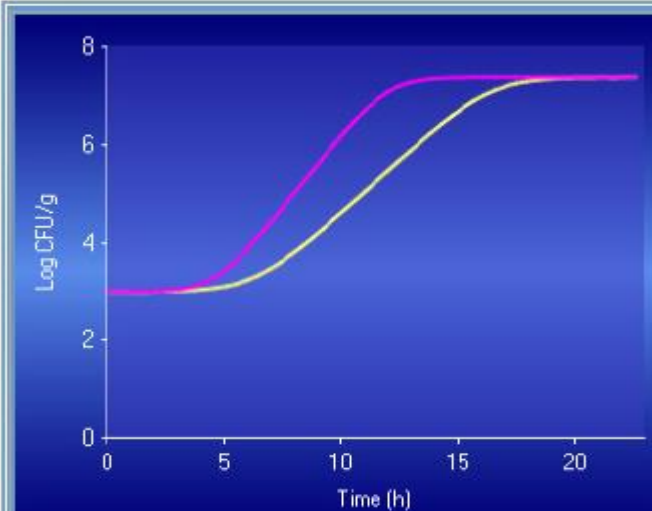
Initial level <=7	Phys.state [0-1]	T (°C) [2-37]	pH [4.6-7.5]	NaCl (%) [0.0-4.5]	Max.rate (log.conc/h)	Dbl.time (h)
<input type="text" value="3"/>	<input type="text" value="0.001836"/> Help	<input type="text" value="25"/>	<input type="text" value="7"/>	<input type="text" value="0.5"/>	<input type="text" value="0.60"/>	<input type="text" value="0.50"/>

remove last row

Predict

Predictions

time (h)	conc. (Log10 cells/g)
0.00	3.00
0.00	3.00
0.46	3.00
0.92	3.00
1.38	3.00
1.84	3.01
2.30	3.01
2.76	3.01
3.22	3.02
3.68	3.03



Third application

ComBase: *Clostridium*
perfringens

Access to Perfringens Predictor

ComBase

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Predictive Models



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Predictive Models

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To access these programs you must first register and then provide your username and password with each login


Access to Perfringens Predictor

PerfringensPredictor


Perfringens Predictor

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ACCEPT  **EXIT**

 **FOOD STANDARDS AGENCY**

Developed at the Institute of Food Research of Norwich under the funding of the FSA, UK


At the leading edge of food research

The predictive model describes the growth of *C. perfringens* in bulked meat during cooling after heating (final heating temperature: in the range 65-90°C)
Growth model: Baranyi, J. and Roberts, T. A. (1994): A dynamic approach to predicting bacterial

Use of Perfringens Predictor from Excel file

The screenshot shows the Microsoft Excel interface with the Perfringens Predictor add-in. A dialog box titled "Perfringens Predictor Add temperature profile" is open, providing instructions for selecting a temperature profile. The background spreadsheet contains a "DATA PROFILE" table and three data tables.

Perfringens Predictor Add temperature profile

Select a temperature profile in the current Excel Workbook.
Highlight the data only (without headings).

Data must be organized in columns:
Time (in hours) must be in the first column of the selection.
Temperature records data (in Celsius degrees) must be in the second column of the selection.

The table should start with a record at 0 hours.

Press OK when selected.

DATA PROFILE

54.4-->7.2 C in 15 h	54.4-->6.2 C in 12 h	54.4-->7.2 C in 12h
----------------------	----------------------	---------------------

0	54.4
1	46.4
2	39.6
3	33.9
4	29.1
5	25
6	19.6
7	18.7
8	16.2
9	14.2
10	12.5
11	11.1
12	9.8
13	8.8
14	7.8
15	7.2

0	54.4
1	44.6
2	36.6
3	30.2
4	25
5	20.8
6	17.4
7	14.7
8	12.5
9	10.7
10	9.3
11	8.1
12	7.2

9	7.8
10	7.2
11	6.7
12	6.2

Use of Perfringens Predictor

PerfringensPredictor

Prediction

Legend: (Sim. profile1) — 1 log increase — (T. profile1)

Buttons:

- Select a new T-Profile
- Interpretation advice
- Change Chart Properties
- Clear all Chart Objects
- Save results in a Sheet
- Save Chart as Bitmap File

PerfringensPredictor

Based on a review of previous research, the Food Standards Agency advises that the cooling of meat should be sufficiently rapid as to ensure that growth from heat resistant spores of *Clostridium perfringens* is minimal (i.e. allows no more than a one-log increase).

T. profile1 | T. profile2 | T. profile3

For this curve, there is a 2.92 log increase during cooling. The cooling curve therefore does not comply with Food Standards Agency advice. Please also note that the Food Standards Agency advises that meats are cooled to below 5°C.

OK

Office

	N	O
1		
2h		
	54.4	
	44.6	
	36.6	
	30.2	
	25	
	20.8	
	17.4	
	14.7	
	12.5	
	10.7	
	9.3	
	8.1	
	7.2	

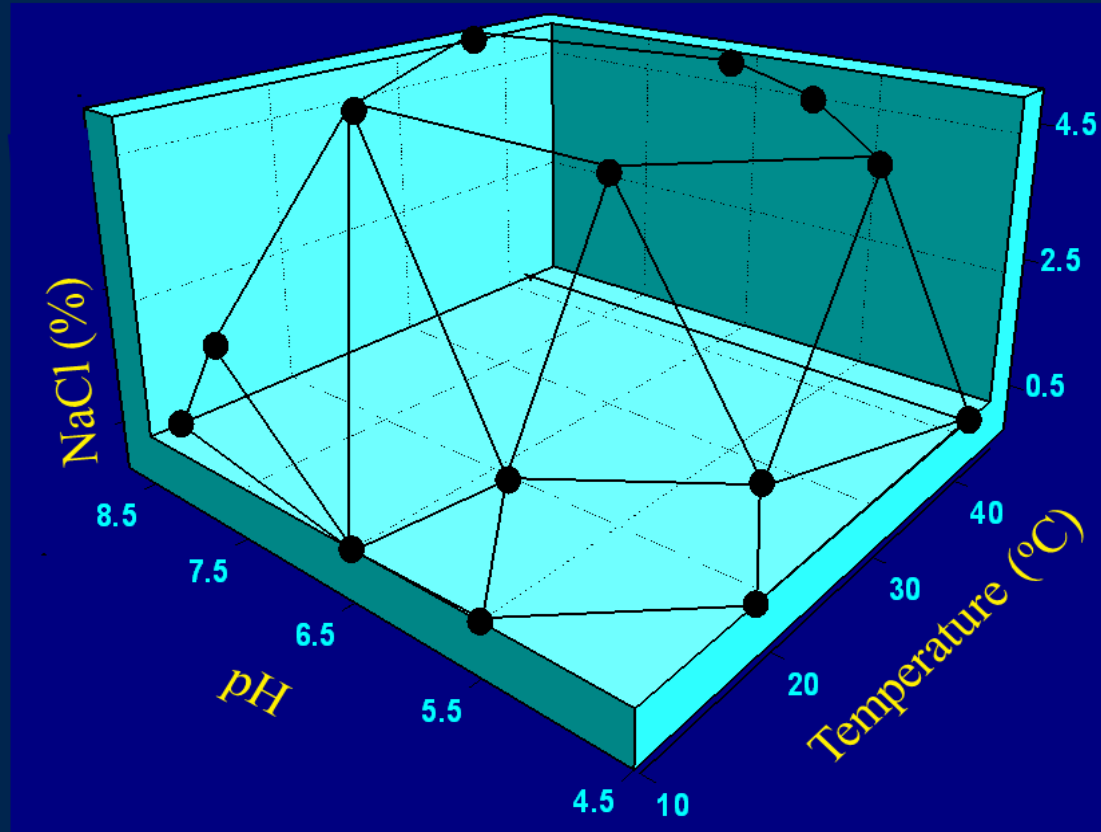
Sheet1 / Sheet2 / IFR test data /

Ready

Fourth application

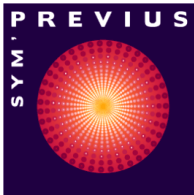
ComBase: growth interface

Strict interpolation region in 3 dimensions



The 2D interpolation region (Temp, pH) becomes smaller as salt concentration increases.

Sym'Previus :
System for prediction of
microbial behaviour in foods



Système de prévision
du comportement
des microorganismes
dans les aliments

Partners involved

- *Public research laboratories*
- *Technical centers ACTIA*
- *Industrials*
- *Public powers*

Tools package includes:

❖ **Database**

❖ **Growth / no growth boundary simulations**

❖ **Probabilistic simulations**

❖ **Heat destruction simulations**

Sym'Previus :

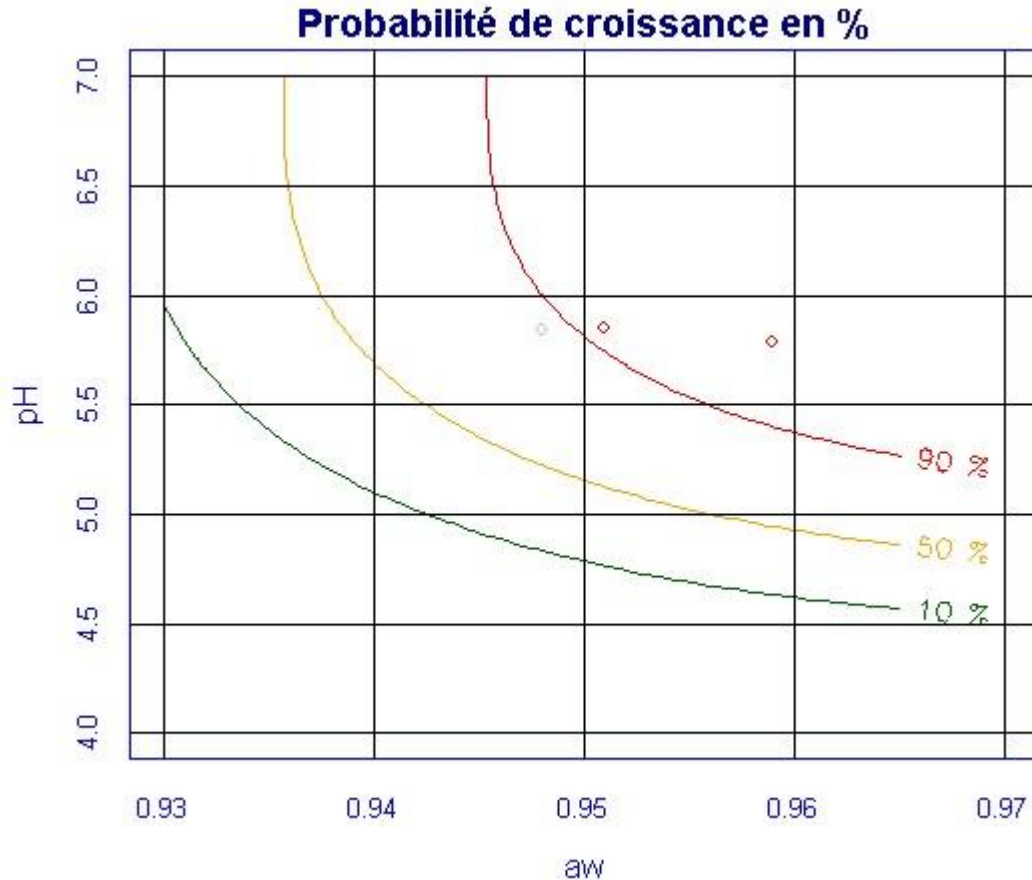
2 applications

- ❖ **Sym'Previus : growth interface**
- ❖ **Sym'Previus : probabilistic module**


First application

**Sym'Previus : growth
interface**

Sym'Previus shows "growth boundaries" according to 2 factors



L. monocytogenes
T = 8° C



**Sym'Previus : probabilistic
module**

Probabilistic software

- ❖ Growth simulation of a bacteria in a food taking into account **variabilities** related to :
 - strains
 - food
 - initial contaminations.

- ❖ The software can include challenge-tests data to take into account the food matrix (determination of the μ_{opt} parameter).

How to use the probabilistic software?

Microorganism

Food

Contamination

Simulation

Results

The present tool allows simulation of bacterial growth in food. Please fill in the first 4 forms before reaching the results of simulation.

Step 1 :

Choose a microorganism in the pop-up menu. Many bacterial species (pathogens, spoilage) are proposed. Information related to the biological variability is also specified, which is of great importance for result interpretation.

Otherwise enter your own bacterial species input growth parameters. These data will be saved in the system, but will remain confidential and will be available only with your personal login.

Pathogens ▾

Listeria monocytogenes ▾

12 strains of *Listeria monocytogenes* isolated from various food products have been studied and included in Sym'Previous simulation tool, in order to take microbiological variability into account.

Next

Use of probabilistic software

Microorganism

Food

Contamination

Simulation

Results

Step 2 :

In order to take into account all the food characteristics which could affect bacterial growth, all information data you have (growth rate, challenge-tests...) have to be entered in this step. For this, 4 choices are available :

- I know a growth curve of *Listeria monocytogenes* in this studied food. I use it as a "reference curve".
- I know a growth rate of *Listeria monocytogenes* in this studied food. I use it as "reference data".
- I know characteristic parameters of *Listeria monocytogenes* growth in this studied food (optimal growth rate μ_{opt}).
- I don't have any data on both *Listeria monocytogenes*/food. I wish to simulate growth on culture medium for my information.

Food name (facultative) :

Growth curve fitting

Input experimental data

Time	Population

?

Time unit

hours

Population unit

Log UFC/g

Use of probabilistic software

Input experimental data

Time	Population
0	3.38
15	3.556
24	4.422
39	5.391
48	5.756

Time unit:

Population unit:

Initial Values for fitting (facultative) :

Initial contamination (log CFU/g):

Maximal contamination (log CFU/g):

Lag time (h):

growth rate (/h):

Environmental conditions :

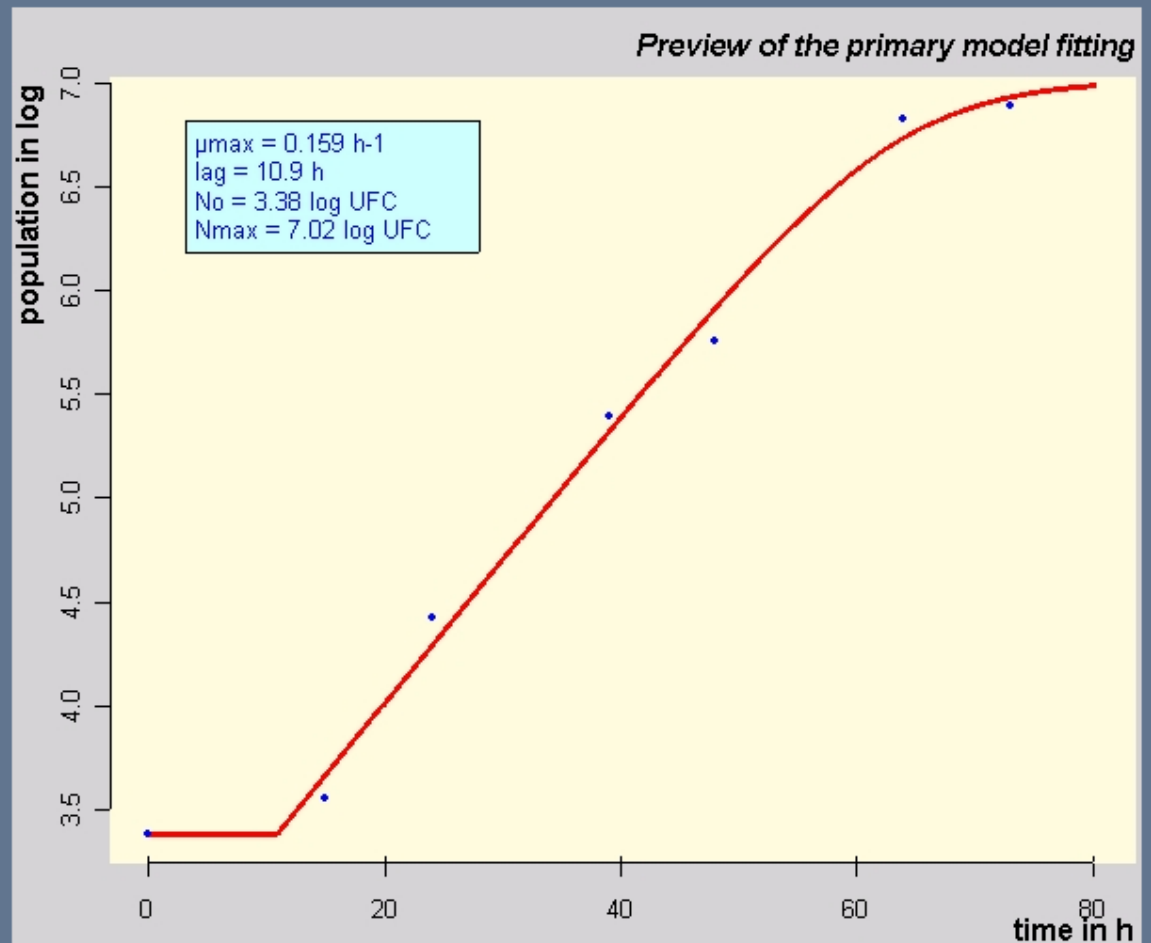
Temperature:

pH:

Water activity:

Lactic acid:

Organic acids unit:



Use of probabilistic software

Microorganism

Food

Contamination

Simulation

Results

Step 3 :

It is often difficult to evaluate the initial food contamination, because analyses can be affected by sampling, low prevalence, variability, etc... However, this contamination is very important to evaluate the risk during storage. For instance, lag time could be affected by low contamination.

This third step allows the estimating of contamination level of your product, based on your own data. If we suppose a gaussian distribution of this initial contamination, levels parameters will be calculated from your input.

3 options can be selected :



<input checked="" type="radio"/> Contamination (in log/g)	Mean	<input type="text" value="-1.2"/>
	Standard deviation	<input type="text" value="0.7"/>
<input type="radio"/> Autocontrol data (Presence / Absence)	Number of analysed samples	<input type="text"/>
	Number of positive samples	<input type="text"/>
	Weight of analysed sample (in g)	<input type="text"/>
<input type="radio"/> Autocontrol data (bacterial count)	Unit : <input type="radio"/> in CFU/g	
	Unit : <input type="radio"/> in log CFU/g	
How to fill in these data		<input type="text"/>
<input type="button" value="Cancel"/> <input type="button" value="Validate"/>		

Use of probabilistic software

Microorganism

Food

Contamination

Simulation


Results

Step 3 :

It is often difficult to evaluate the initial food contamination, because analyses can be affected by sampling, low prevalence, variability, etc... However, this contamination is very important to evaluate the risk during storage. For instance, lag time could be affected by low contamination.

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<input type="radio"/>	Contamination (in log/g)	Mean	<input type="text"/>
		Standard deviation	<input type="text"/>
 <input checked="" type="radio"/>	Autocontrol data (Presence / Absence)	Number of analysed samples	<input type="text" value="1000"/>
		Number of positive samples	<input type="text" value="50"/>
		Weight of analysed sample (in g)	<input type="text" value="25"/>
<input type="radio"/>	Autocontrol data (bacterial count)	Unit : <input checked="" type="radio"/> in CFU/g	
		Unit : <input type="radio"/> in log CFU/g	
		How to fill in these data	
		<input type="text"/>	
		<input type="button" value="Cancel"/>	<input type="button" value="Validate"/>

Use of probabilistic software

Microorganism

Food

Contamination

Simulation

Results

Step 4 :

Simulation step allows you to choose new environmental conditions (formulation, static or dynamic storage) in which you wish to evaluate microbial growth, and general information such as product shelf-life, its weight or the maximal contamination not to reach at the end of shelf life.

Max contamination level (not to reach at the end of shelf life, in log CFU/g)	2	
Shelf life (in days)	7	
Weight of final product (in gram)	Mean	120
	Standard deviation	10

Impose a lag time equal to 0 :

Temperature	<input type="radio"/> Static	Mean	<input type="text"/>												
	<input type="radio"/> dynamic ? (time in hours)	<table border="1"> <thead> <tr> <th>Time</th> <th>Temperature</th> </tr> </thead> <tbody> <tr><td> </td><td> </td></tr> <tr><td> </td><td> </td></tr> <tr><td> </td><td> </td></tr> <tr><td> </td><td> </td></tr> <tr><td> </td><td> </td></tr> </tbody> </table>		Time	Temperature										
	Time	Temperature													
<input type="radio"/> Preselected profiles	1/3 of shelf life at 4°C + 2/3 at 8°C														
	<input type="radio"/> static	Mean	<input type="text"/>												
		Standard deviation	<input type="text"/>												

Use of probabilistic software

Weight of final product (in gram)	mean	120
	Standard deviation	10

Impose a lag time equal to 0 :

Temperature	<input checked="" type="radio"/> Static	Mean	8												
	<input type="radio"/> dynamic ? (time in hours)	<table border="1"><thead><tr><th>Time</th><th>Temperature</th></tr></thead><tbody><tr><td></td><td></td></tr><tr><td></td><td></td></tr><tr><td></td><td></td></tr><tr><td></td><td></td></tr><tr><td></td><td></td></tr></tbody></table>		Time	Temperature										
	Time	Temperature													
<input type="radio"/> Preselected profiles	1/3 of shelf life at 4°C + 2/3 at 8°C														

pH	<input checked="" type="radio"/> static	Mean	6											
		Standard deviation	0											
	<input type="radio"/> Autocontrol	<table border="1"><thead><tr><th>Time</th><th>pH</th></tr></thead><tbody><tr><td></td><td></td></tr><tr><td></td><td></td></tr><tr><td></td><td></td></tr><tr><td></td><td></td></tr></tbody></table>		Time	pH									
	Time	pH												
<input type="radio"/> dynamic ? (time in hours)	<table border="1"><thead><tr><th>Time</th><th>pH</th></tr></thead><tbody><tr><td></td><td></td></tr><tr><td></td><td></td></tr><tr><td></td><td></td></tr><tr><td></td><td></td></tr><tr><td></td><td></td></tr></tbody></table>		Time	pH										
Time	pH													
<input type="radio"/> Optimum for growth														



Use of probabilistic software



aw	<input checked="" type="radio"/> static	Mean	<input type="text" value="0.991"/>									
		Standard deviation	<input type="text" value="0"/>									
	<input type="radio"/> Autocontrol	<input type="text"/>										
	<input type="radio"/> dynamic ? (time in hours)	<table border="1"><thead><tr><th>Time</th><th>aw</th></tr></thead><tbody><tr><td></td><td></td></tr><tr><td></td><td></td></tr><tr><td></td><td></td></tr><tr><td></td><td></td></tr></tbody></table>		Time	aw							
Time	aw											
<input type="radio"/> Optimum for growth												



Lactic acid	<input checked="" type="radio"/> static	Mean	<input type="text" value="0"/>									
		Standard deviation	<input type="text" value="0"/>									
	<input type="radio"/> Autocontrol	<input type="text"/>										
	<input type="radio"/> dynamic ? (time in hours)	<table border="1"><thead><tr><th>Time</th><th>Lactic acid</th></tr></thead><tbody><tr><td></td><td></td></tr><tr><td></td><td></td></tr><tr><td></td><td></td></tr><tr><td></td><td></td></tr></tbody></table>		Time	Lactic acid							
Time	Lactic acid											
<input type="radio"/> Optimum for growth												

Cancel

Validate

Result of one example

Growth simulation of *Listeria monocytogenes* in Food

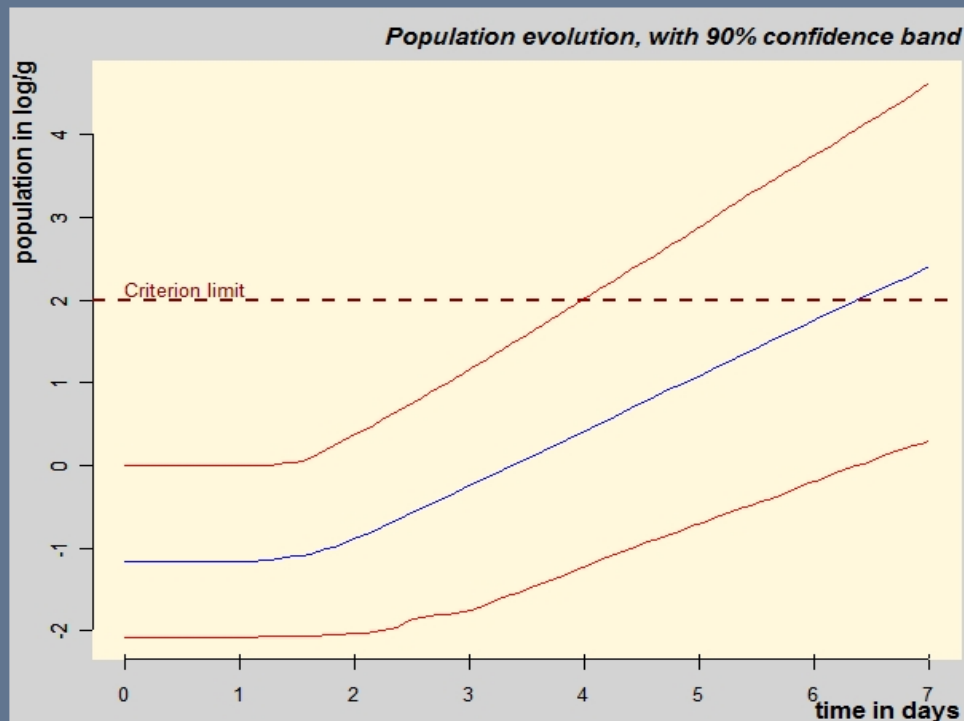
Probability than a food unit is contaminated is 95%. For these contaminated units, growth simulations are presented below :

Simulated parameters values

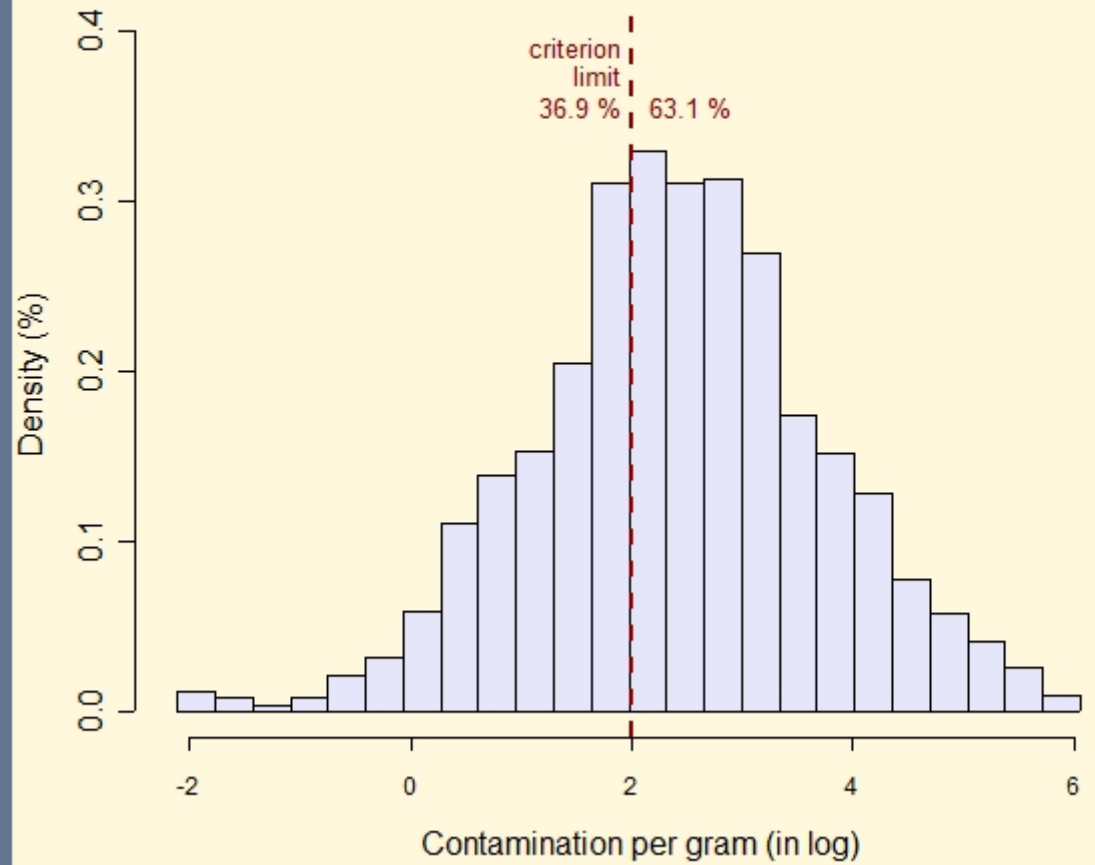
	Median	Quantiles at 5% / 95%
Growth rate (/h)	0.0641	0.042 / 0.09
Generation time (h)	10.8	7.71 / 16.6
Lag time (h)	41	25.5 / 74.5
Initial population (log)	-1.16	-2.08 / -0.00435
Maximal population (log)	5.83	5.75 / 5.9

Physico-chemical factors

Factors	Value	Standard deviation
Temperature	8	1
pH	6	0
aw	0.991	0



Contamination density at 7 days



Conclusion related to probalistic approach

Sym'Previus allows to estimate the shelf life taking into account

- **industrial microbiological counts**
- **physical chemical variability measured.**



Food safety laboratory
Maisons-Alfort, France