# *Predictive microbiology*

**Annie Beaufort**

**EU RL for *Listeria monocytogenes***

# What is predictive microbiology?

The microbial responses to the food environments by mathematical models.

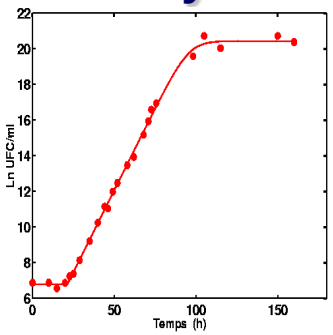
It is often use to assess the growth, the survival and the destruction of bacteria in foods.

# Main software

| Software | Admin Center | Applications | Growth | Survaival | Heat destruction | Food application | Commercial software |
|---|---|---|---|---|---|---|---|
| Food MicroModel | **MAFF (Agricult. 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'Previus | **GIS Sym'Previus** | 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

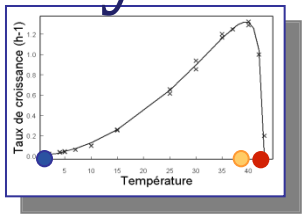
## Primary models




*Primary model parameters*

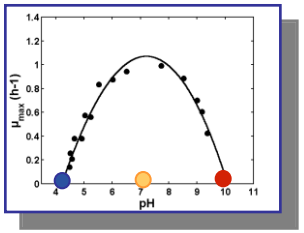
**$\mu_{max}$: growth rate**
**lag : lag phase**
**Log No : Initial population**
**Log $N_{max}$: max population**

**different T°**



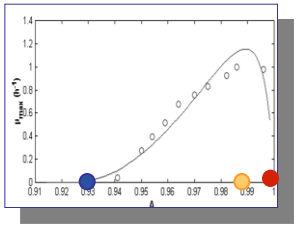

**$T_{min}$ $T_{opt}$ $T_{max}$**

**different pH**



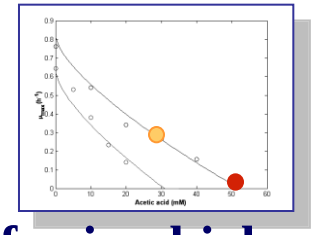

**$pH_{min}$ $pH_{opt}$ $pH_{max}$**

**different $a_w$**



**$a_{wmin}$ $a_{wopt}$ $a_{wmax}$**

**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 $\mu_{max}$ to environmental factors (temperature, pH, …).**

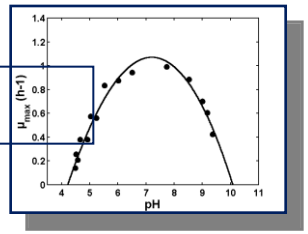
# Primary models

Gompertz $$\ln(N(t)) = \ln(N_0) + A \exp\left(-\exp\left(\frac{\mu e}{A}(lag - t) + 1\right)\right)$$

logistique $$\ln(N(t)) = \ln(N_0) + \frac{A}{1 + \exp\left(\frac{4\mu}{A}(lag - t) + 2\right)}$$

# Secondary model

pH




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

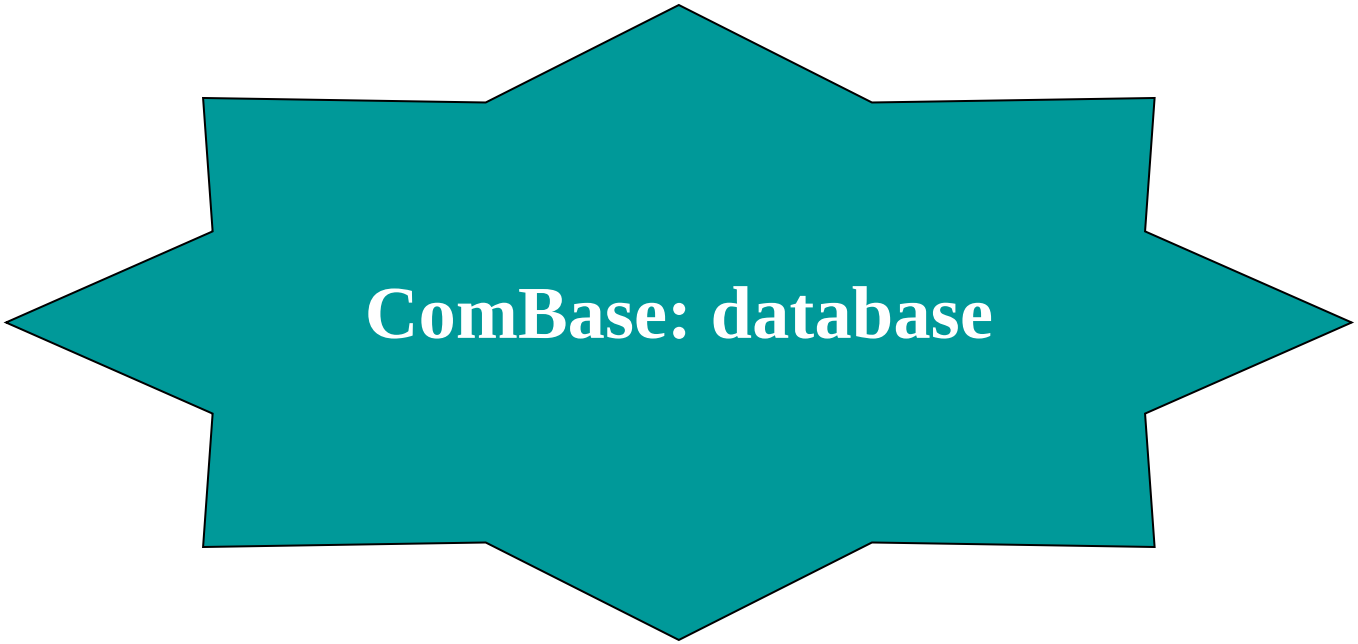
$$\gamma(pH) = \frac{(pH - pH_{min})(pH - pH_{max})}{(pH - pH_{min})(pH - pH_{max}) - (pH - pH_{opt})^2}$$

# Combase software

**4 applications**

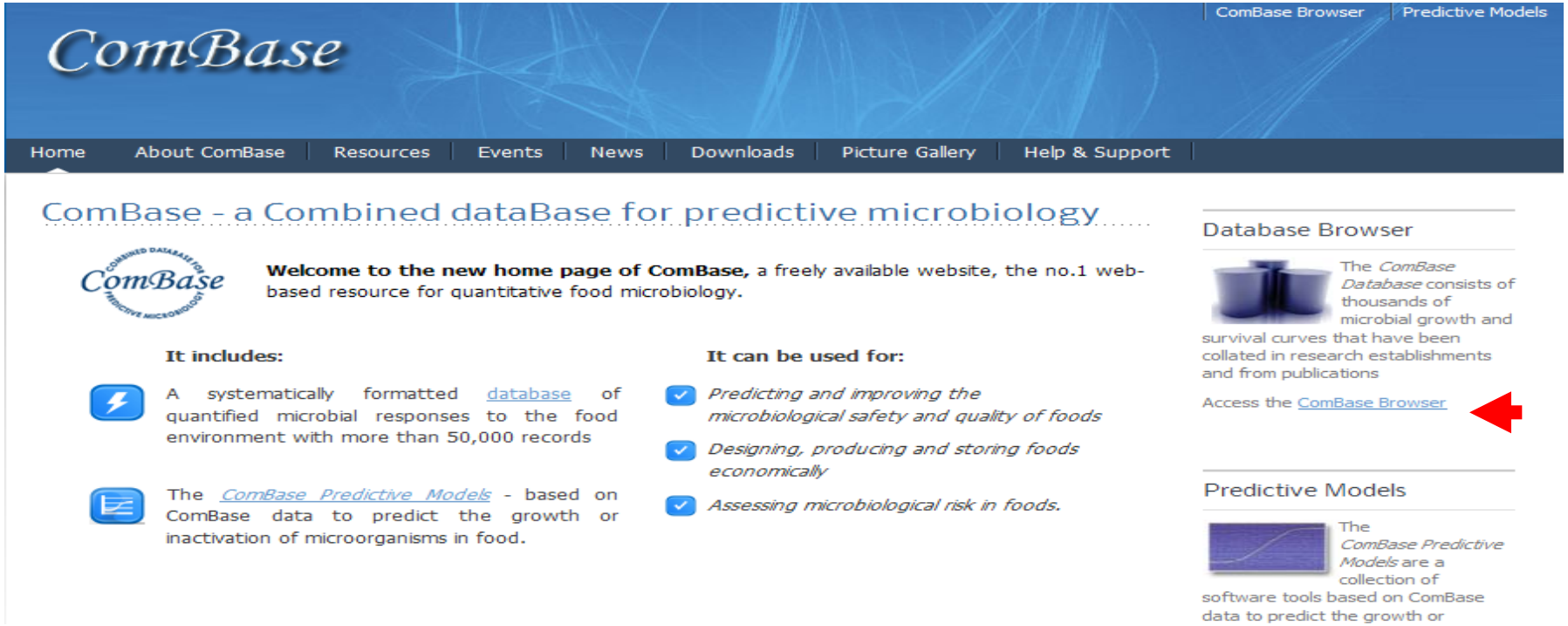
- **Combase: the data base**
- **Combase predictor**
- **Combase: Perfringens predictor**
- **Combase: growth interface**

# First application



# ComBase: 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.

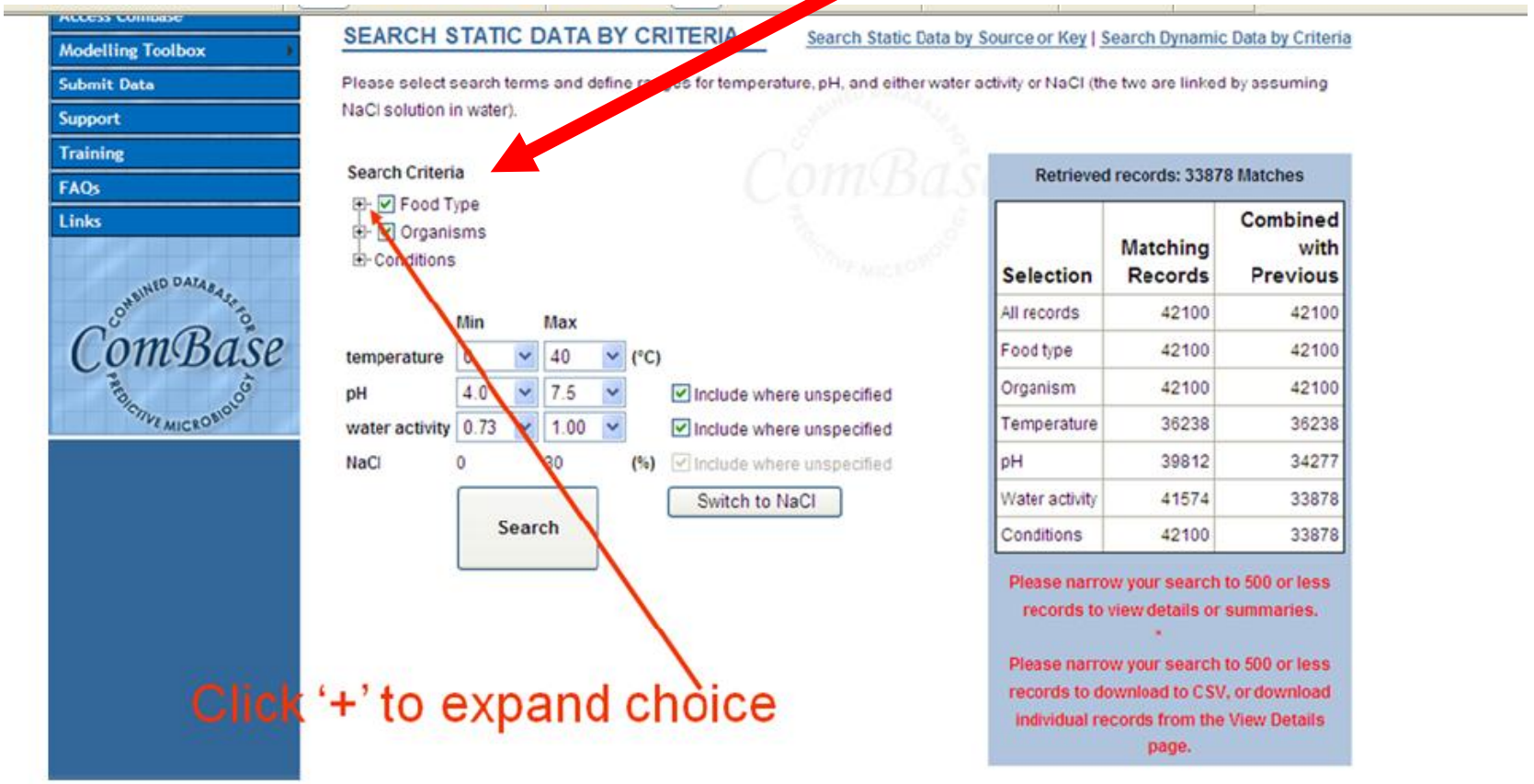



Click on Access the ComBase Browser

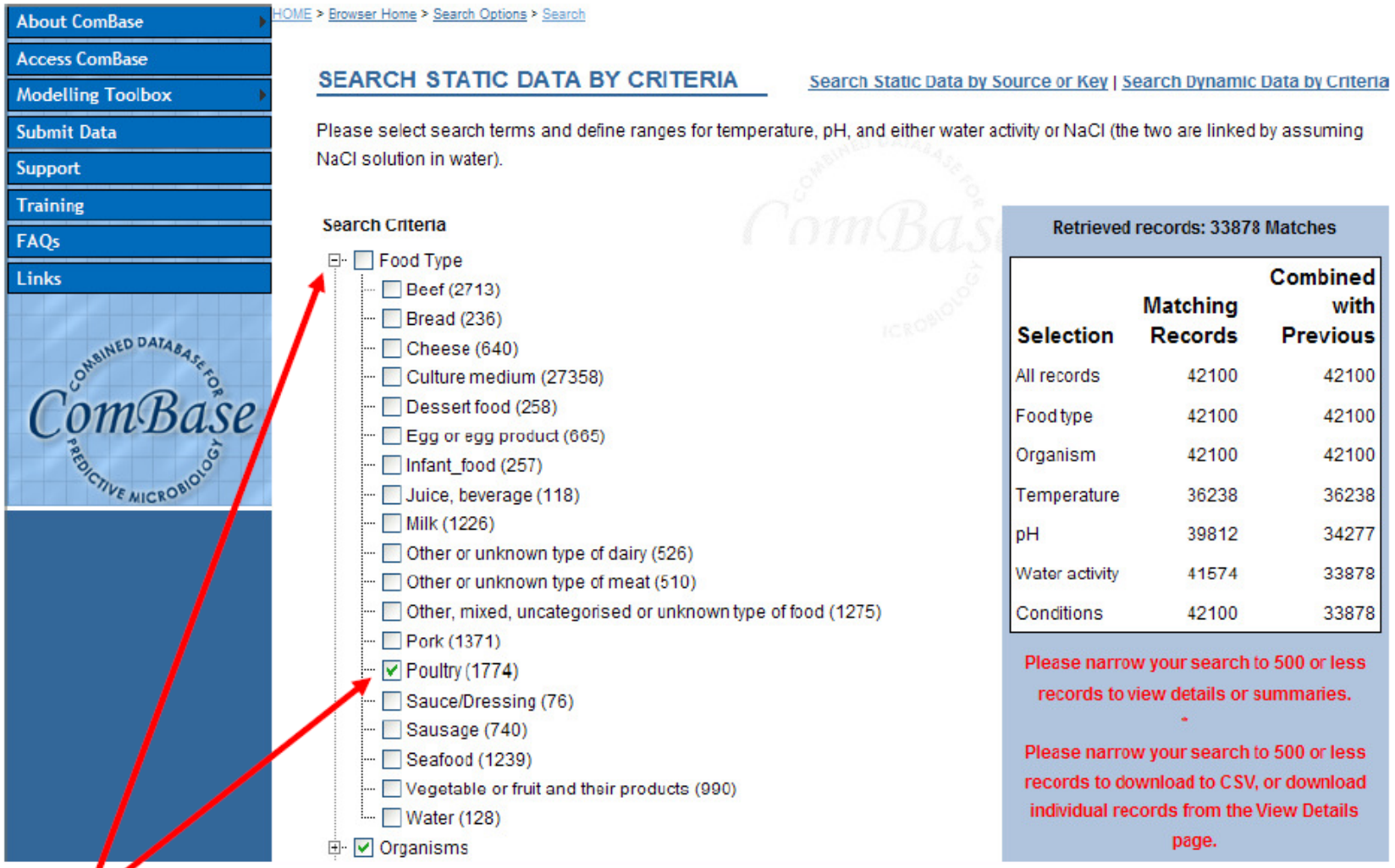
You will be directed to the data base by criteria.

# Search static data by criteria

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



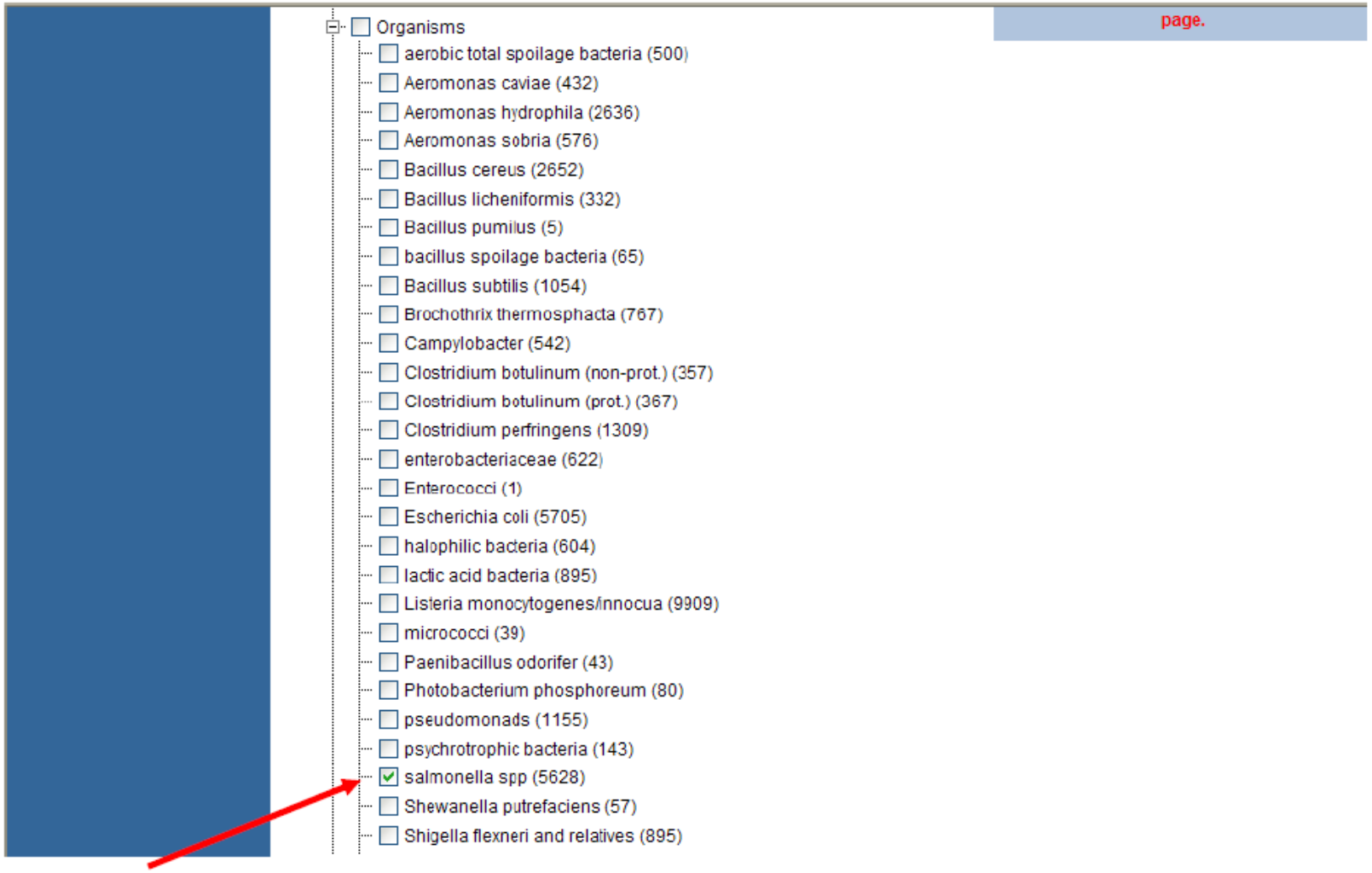
# Example of search




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

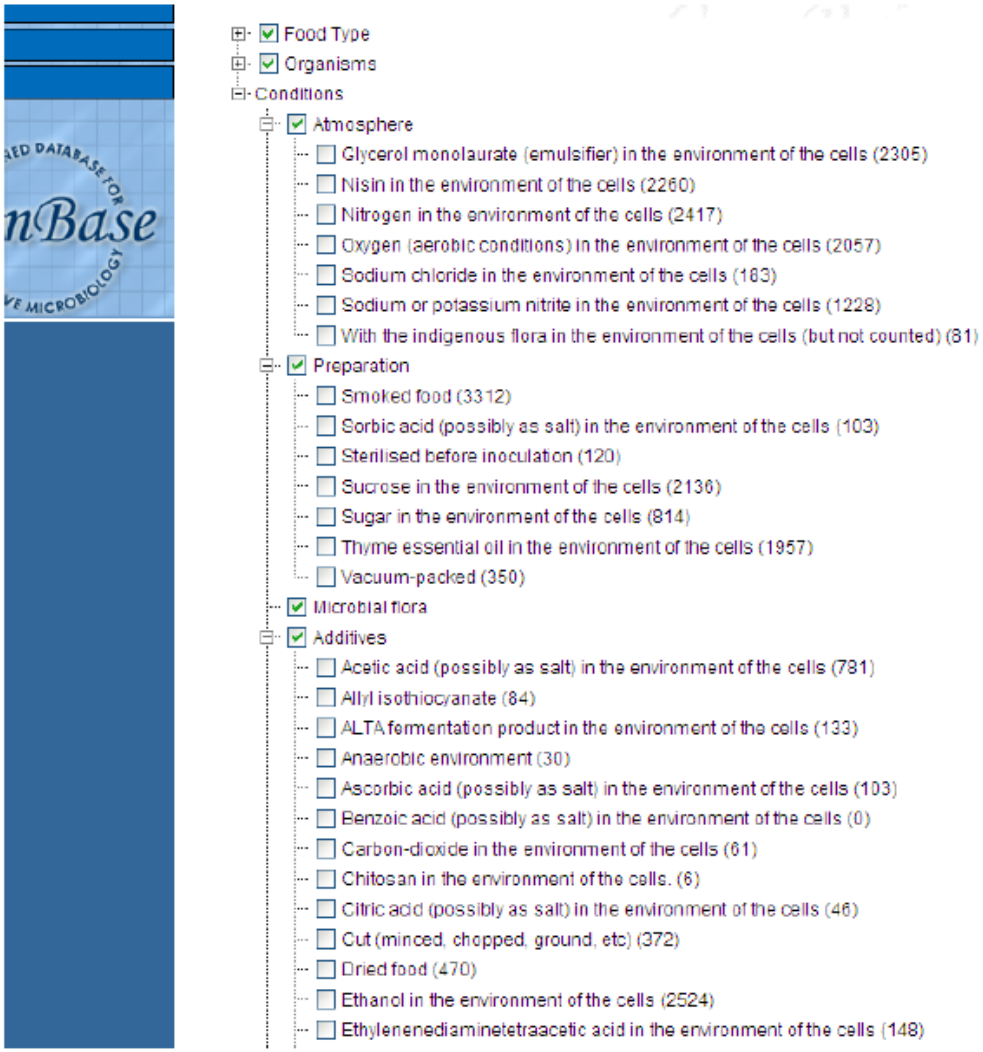
# Example of search

In the “Organism” group, select *Salmonella spp;*




Choose *Salmonella sp;’*

# Example of search




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

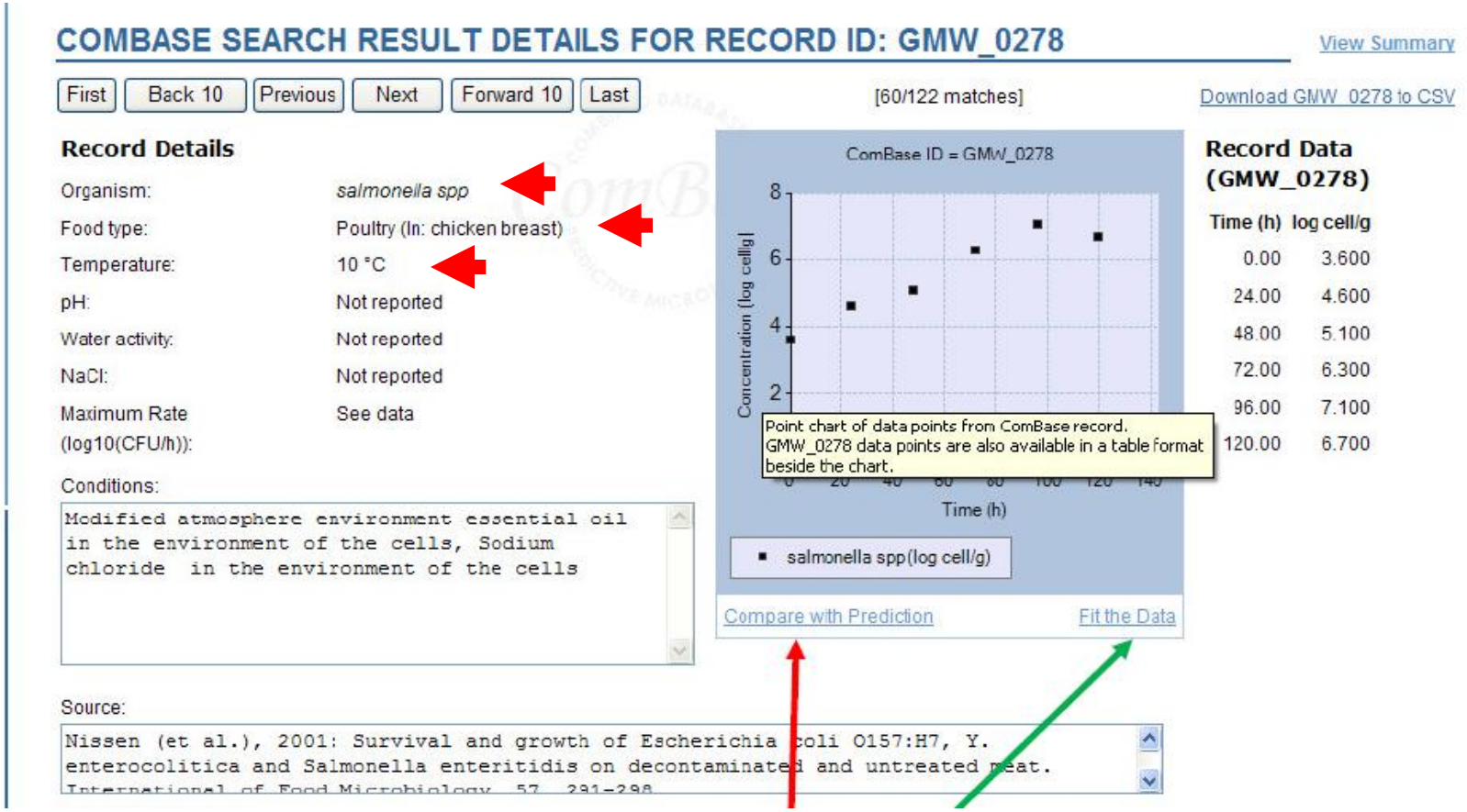
**List of Current Matches**

Page: 1 2

| Organism | Food Type | in_on | Temp | pH | water activity | conditions | Source | Key | Exclude |
|---|---|---|---|---|---|---|---|---|---|
| salmonella spp | Poultry | In: chicken breast | 4 | 6.3 | | raw, lactic_acid(ppm): 20000 | Anang_07 | Anang_10_10S | ☐ |
| salmonella spp | Poultry | In: chicken breast | 4 | 6.3 | | raw, lauricidin(ppm): 0 | Anang_07 | Anang_10_1S | ☐ |
| salmonella spp | Poultry | In: chicken breast | 4 | 6.3 | | raw, lauricidin(ppm): 5000 | Anang_07 | Anang_10_2S | ☐ |
| salmonella spp | Poultry | In: chicken breast | 4 | 6.3 | | raw, lauricidin(ppm): 10000 | Anang_07 | Anang_10_3S | ☐ |
| salmonella spp | Poultry | In: chicken breast | 4 | 6.3 | | raw, lauricidin(ppm): 15000 | Anang_07 | Anang_10_4S | ☐ |
| salmonella spp | Poultry | In: chicken breast | 4 | 6.3 | | raw, lauricidin(ppm): 20000 | Anang_07 | Anang_10_5S | ☐ |
| salmonella | Poultry | In: chicken breast | 4 | 6.3 | | raw, lactic_acid(ppm): 0 | Anang_07 | Anang_10_6S | ☐ |

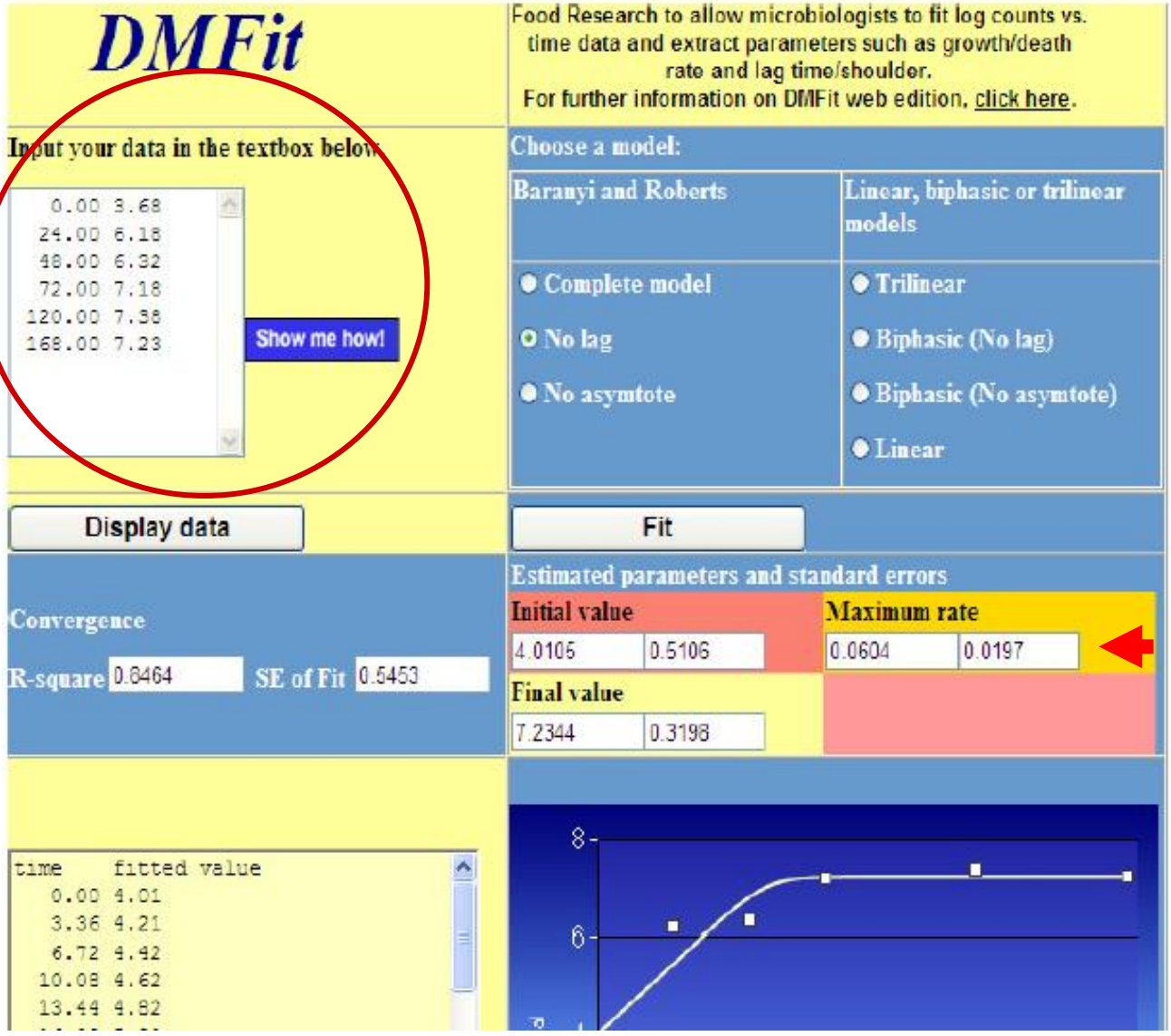
Then, choose a record you are interested in.

# Here is the record you are interested in




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

# A fitting tool (primary model)




You get :

- the experimental data
- the fitted growth curve
- the $\mu_{max}$

# Second application

# Models

| Organism | env.factors | Remarks |
|---|---|---|
| ***Aeromonas hydrophila*** | (temp, pH, aw) | |
| ***Bacillus cereus*** | (temp, pH, aw) | |
| ***Bacillus cereus*** **+ CO_2** | (temp, pH, aw,CO_2) | |
| ***Bacillus licheniformis*** | (temp, pH, aw) | |
| ***Bacillus subtilis*** | (temp, pH, aw) | |
| ***Brochothrix thermosphacta*** | (temp, pH, aw) | |
| ***Clostridium botulinum*** **(non.prot)** | (temp, pH, aw) | |
| ***Clostridium botulinum*** **(prot)** | (temp, pH, aw) | |
| ***Clostridium perfringens*** | (temp, pH, aw) | |
| ***Escheria coli*** **0157** | (temp, pH, aw) | |
| ***Escheria coli*** **0157 + CO_2** | (temp, pH, aw,CO_2) | |
| ***Listeria monocytogenes*** | (temp, pH, aw) | |
| ***Listeria monocytogenes*** **+ CO_2** | (temp, pH, aw, CO_2) | |
| ***Listeria monocytogenes*** **+ Nitrite** | (temp, pH, aw, NaNO_2) | |
| ***Listeria monocytogenes*** **+ Lactic** | (temp, pH, aw, Lactic) | |
| ***Listeria monocytogenes*** **+ Acetic** | (temp, pH, aw, acetic acid) | |
| ***Staphylococcus aureas*** | (temp, pH, aw) | |
| ***Saccharomyces cerevisiae*** | (pH,aw) | |
| **Salmonellae** | (temp, pH, aw) | |
| **Salmonellae + CO_2** | (temp, pH, aw, CO_2) | |
| **Salmonellae + Nitrite** | (temp, pH, aw, NaNO_2) | |
| ***Yersinia enterocolitica*** | (temp, pH, aw) | |
| ***Yersinia enterocolitica*** **+ CO_2** | (temp, pH, aw, CO_2) | |
| | | |
| ***Yersinia enterocolitica*** **+ Lactic** | (temp, pH, lact) | NaCl=0.5 const |
| ***Yersinia enterocolitica*** **+ Acetic** | (temp, pH, acet) | NaCl=0.5 const |
| ***Bacillus subtilis*** **(aw: with glycerol)** | (temp, pH, aw) | |
| ***Pseudomonads*** | (temp, pH) | NaCl=0.5 const |
| ***Brochothrix thermosphacta*** **death** | (temp,pH) | FLAIR. NaCl had no effect between 0 and 2 %. |

# Access to ComBase Predictor

ComBase

ComBase Browser | Predictive Models

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

You are here: Home ▸ Predictive Models

## Predictive Models

The ***ComBase Predictive models*** are a collection of software tools based on ComBase data to predict the growth or inactivation of microrganisms. 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 specically 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

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

Predictive Models

PREDICTIVE MODELS
COMBASE PREDICTOR
PERINGENS PREDICTOR

Search on the web site

Search...

Languages

English
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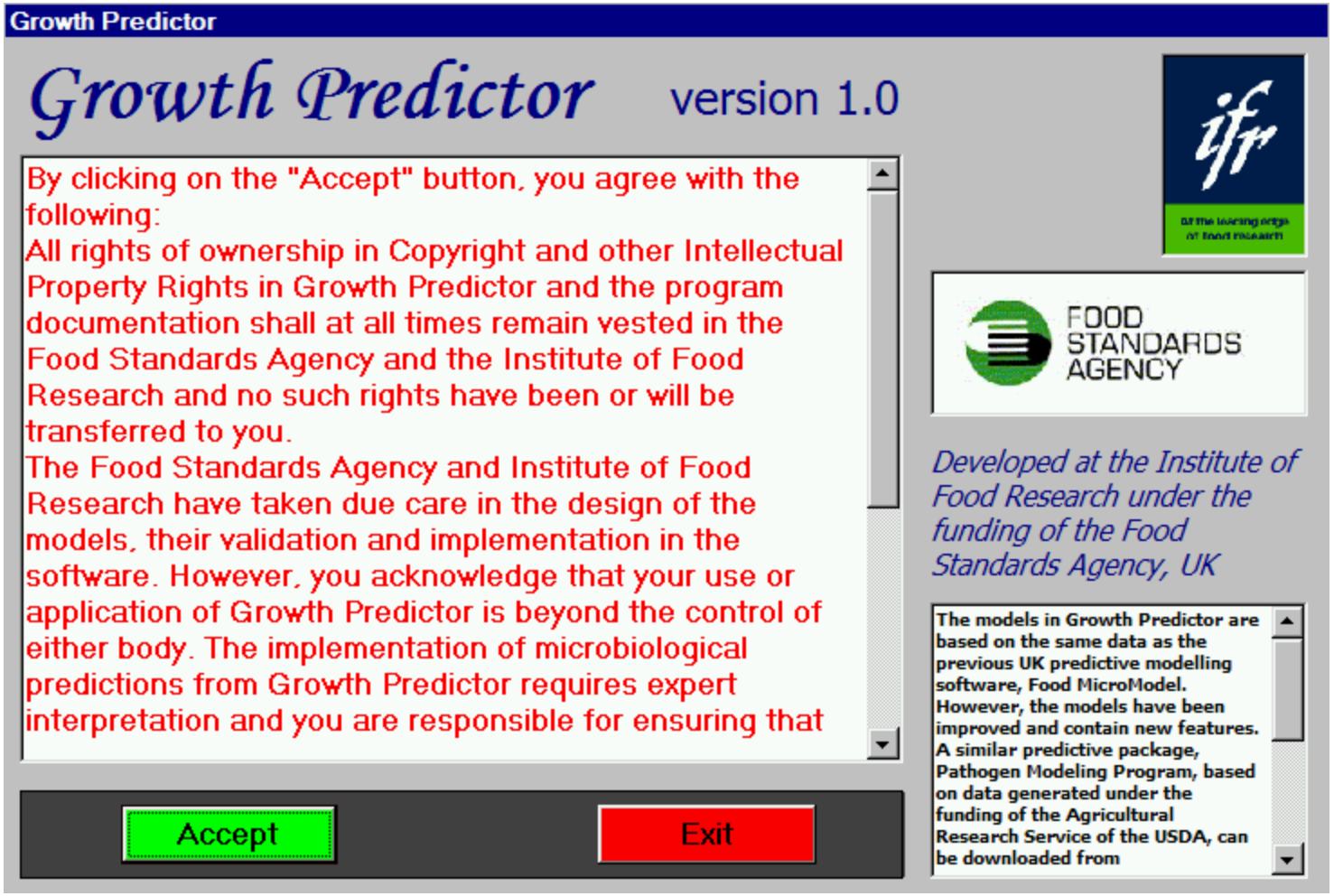
# Access to ComBase Predictor



# ComBase Predictor

Growth model | Thermal inactivation model | Non thermal survival model

**Temperature input:** Static | Changing temperature

**Water activity:** NaCl | Aw

**Observation duration:** Time (h) 23.00

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) |
|---|---|---|---|---|---|---|---|
| 3 | 0.001836 | Help | 20 | 7 | 0.5 | 0.44 | 0.69 |

*Aeromonas hydrophila*

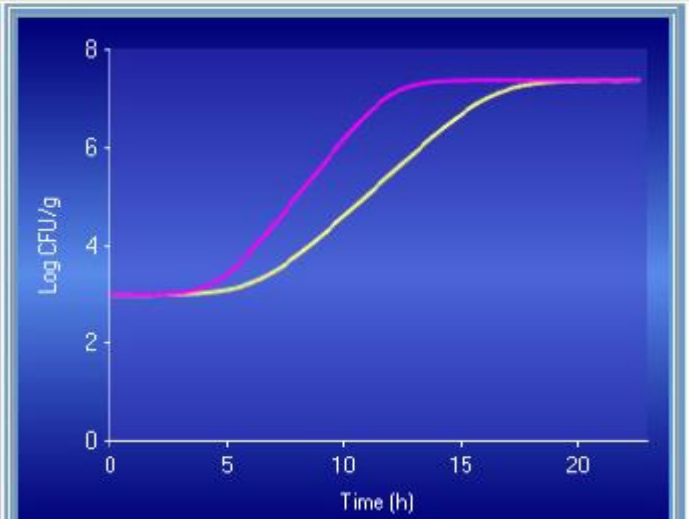
| Initial level <=7 | Phys.state [0-1] | | T (°C) [2-37] | pH [4.6-7.5] | NaCl (%) [0.0-4.5] | Max.rate (log.conc/h) | Dbl.time (h) |
|---|---|---|---|---|---|---|---|
| 3 | 0.001836 | Help | 25 | 7 | 0.5 | 0.60 | 0.50 |

remove last row

Predict

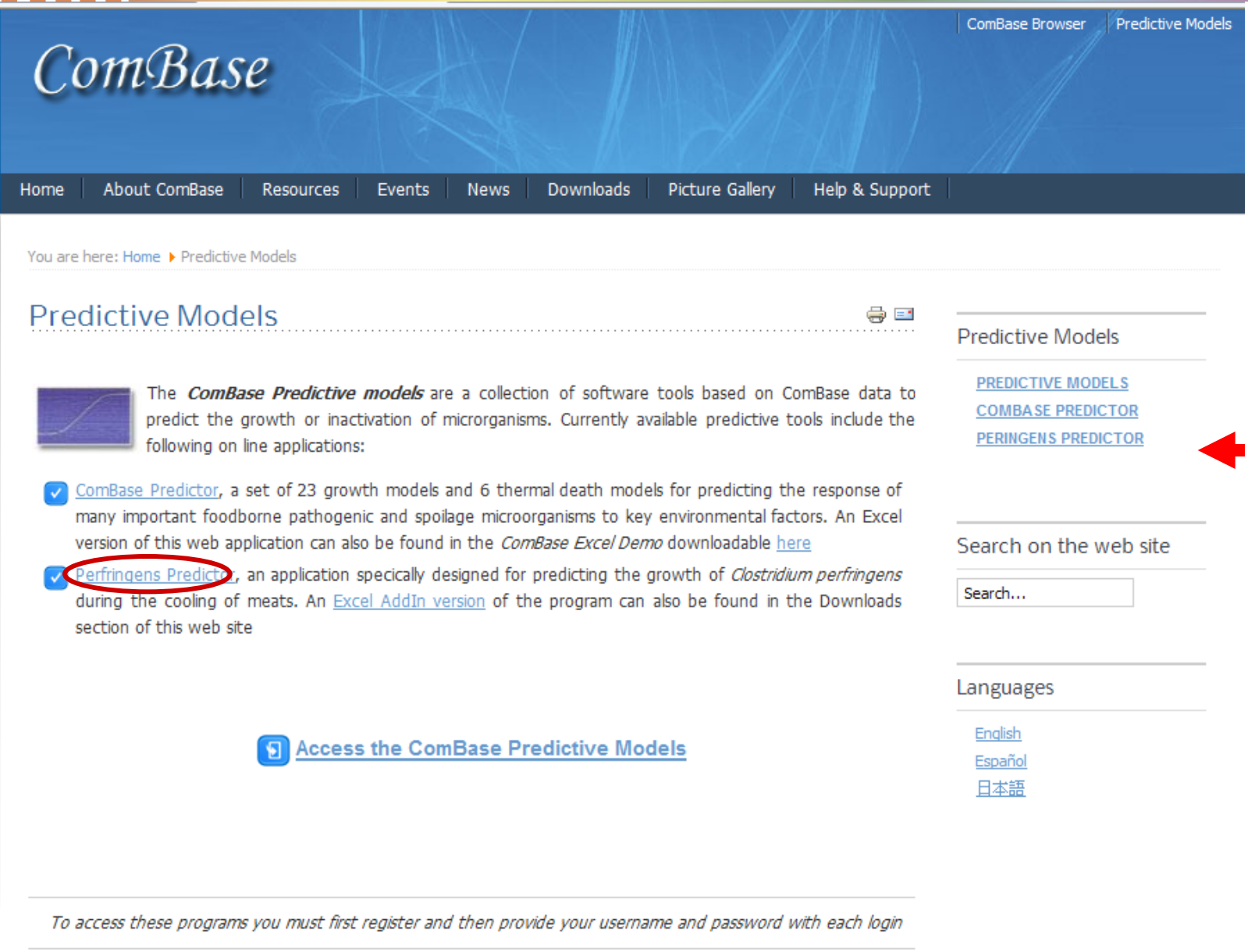
**Predictions**

```
time(h)  conc.(Log10 cells/g)
   0.00 3.00     3.00
   0.00 3.00     3.00
   0.46 3.00     3.00
   0.92 3.00     3.00
   1.38 3.00     3.00
   1.84 3.00     3.01
   2.30 3.01     3.02
   2.76 3.01     3.03
   3.22 3.02     3.06
   3.68 3.03     3.11
```

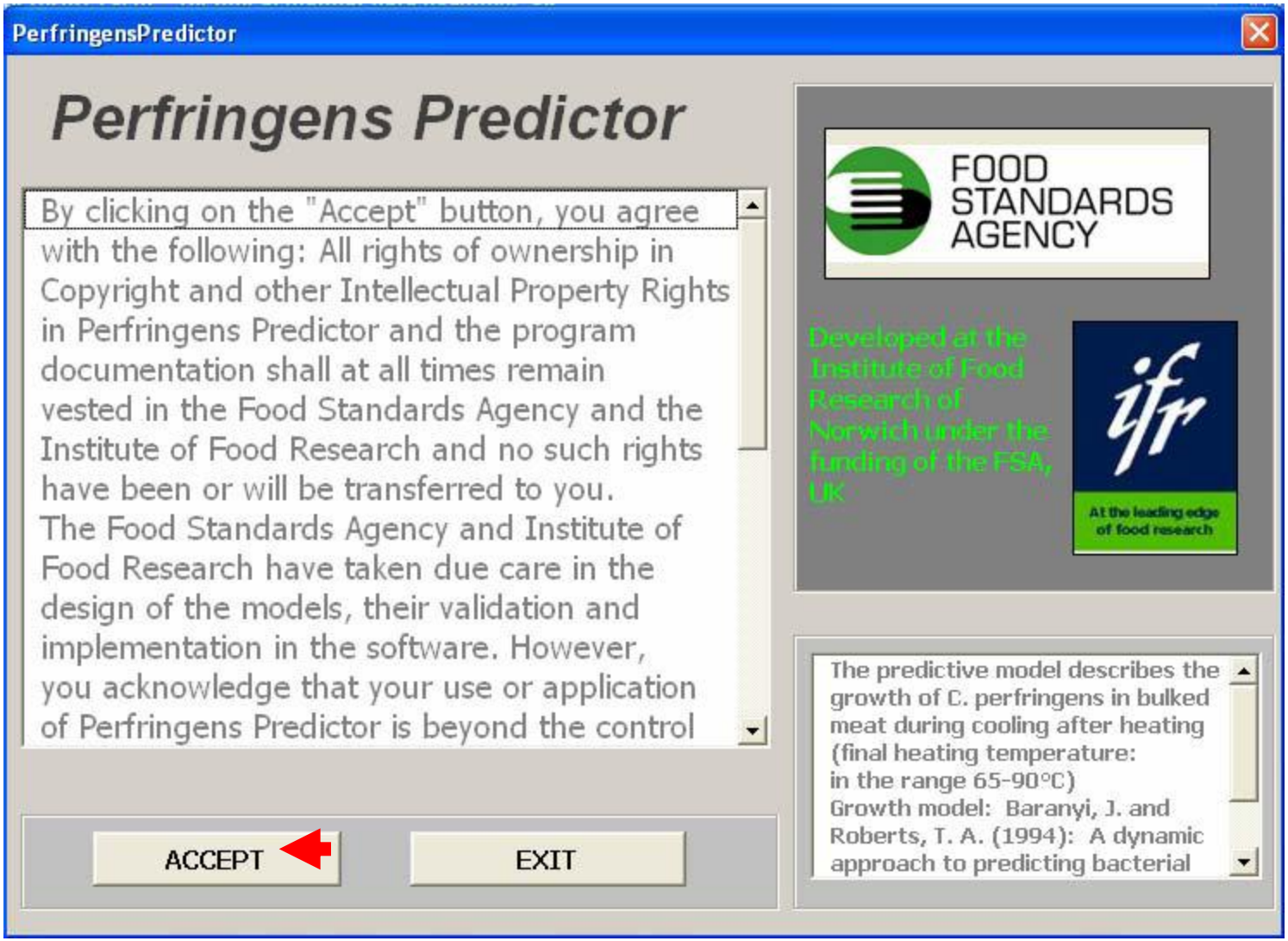


# Third application

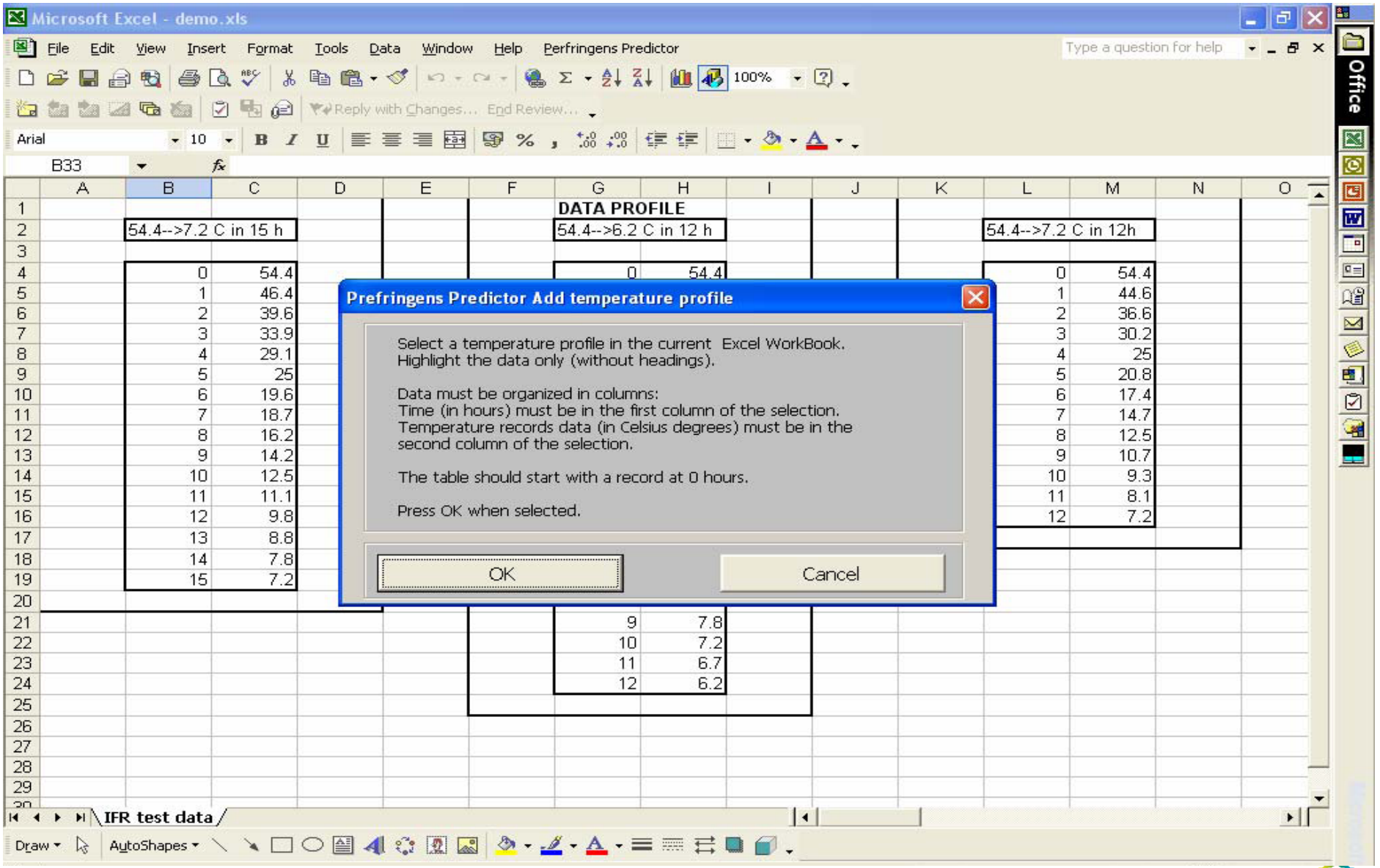
# Access to Perfringens Predictor



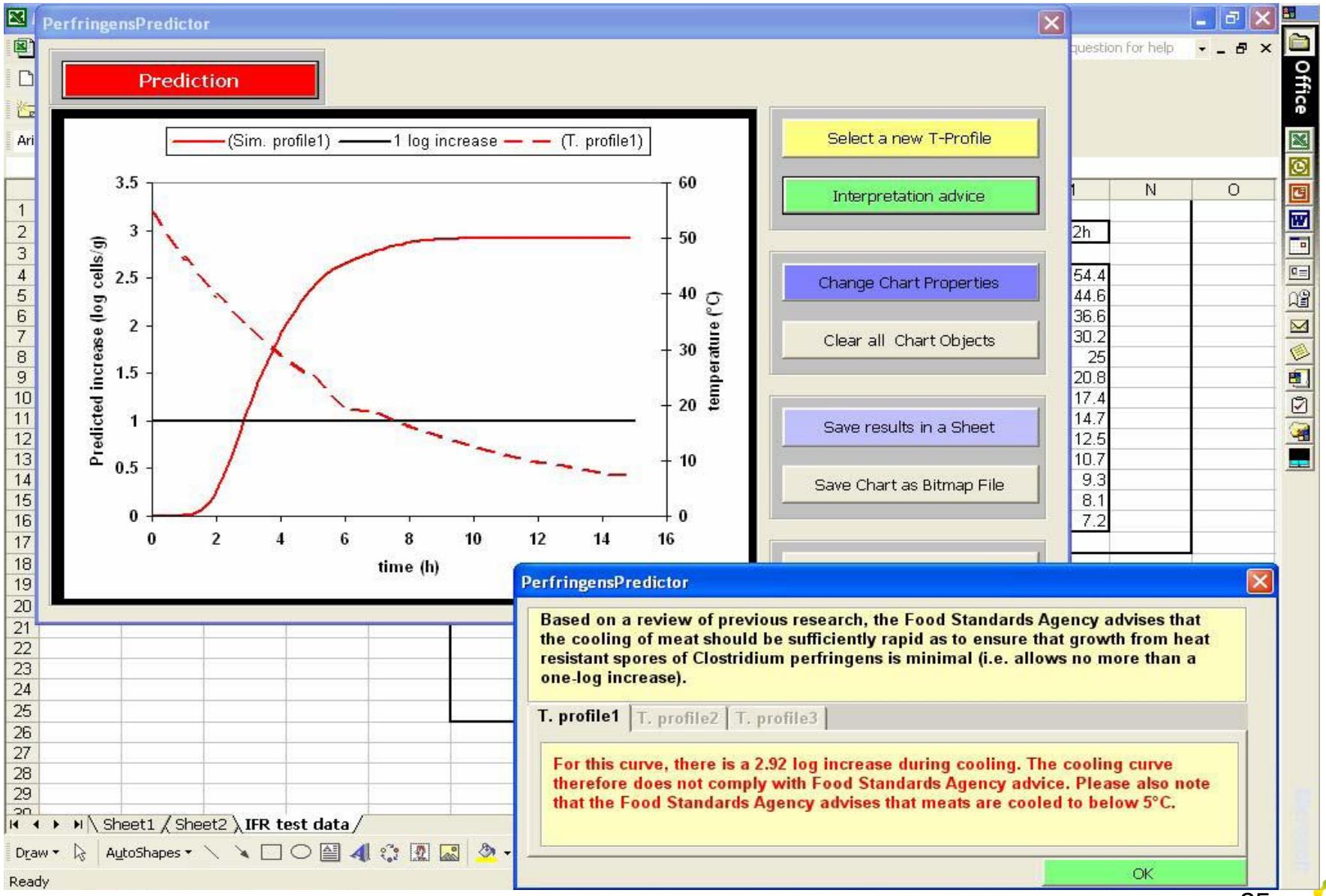
# Access to Perfringens Predictor



# Use of Perfringens Predictor from Excel file

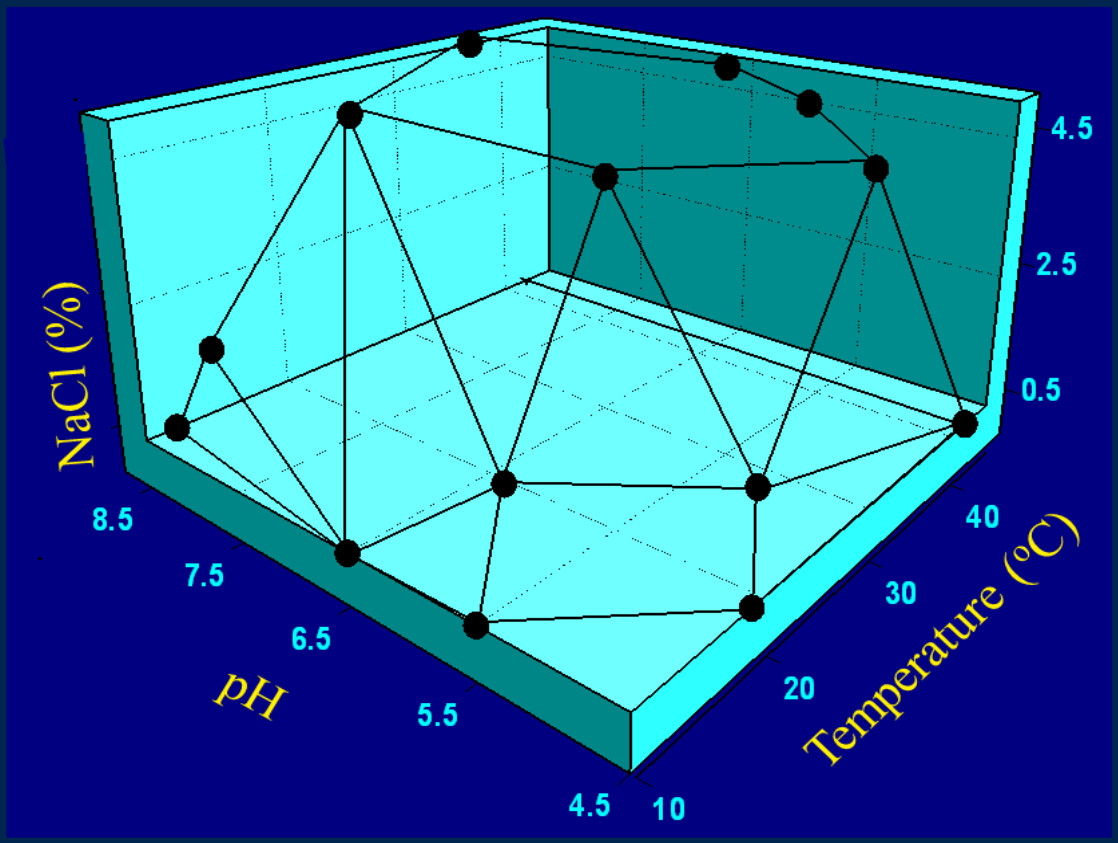


# Use of Perfringens Predictor



# Fourth application

# 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

# 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 :

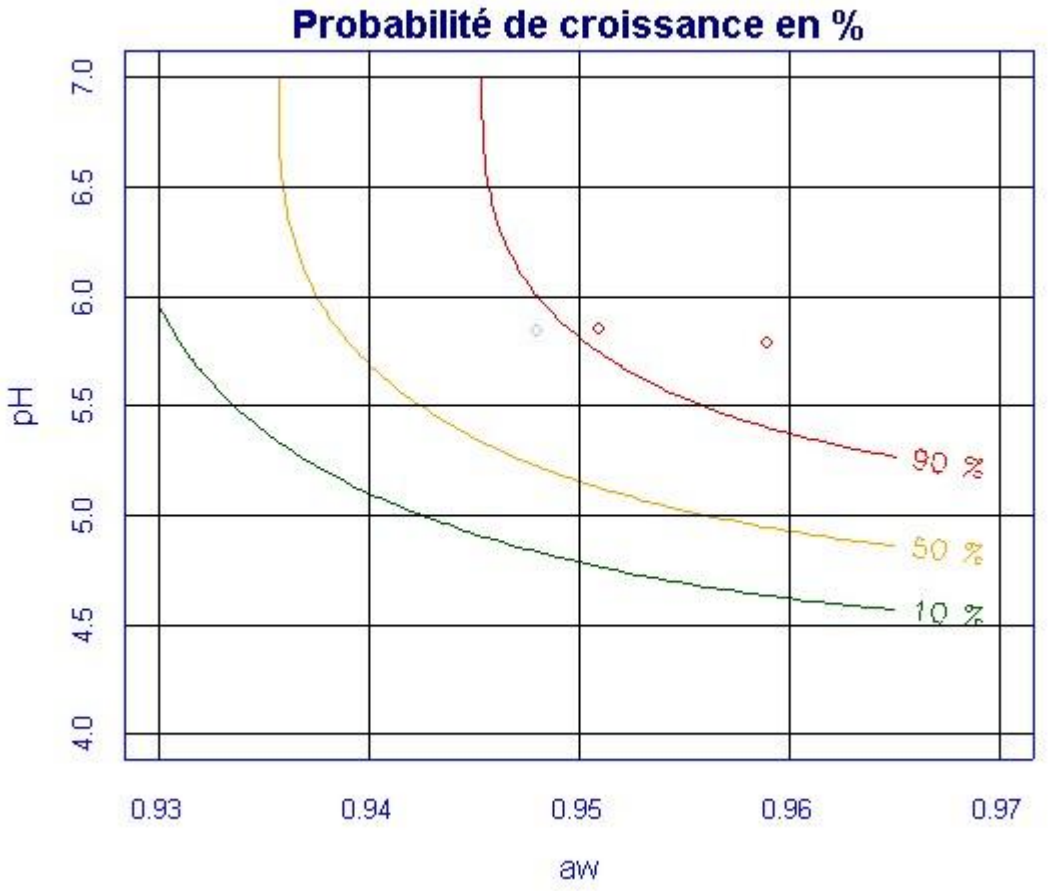
**2 applications**

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

# First application

**Sym'Previus : growth interface**

# Sym'Previus shows "growth bounderies" according to 2 factors




***L. monocytogenes***
**T = 8° C**

# Sym'Previus : probabilistic module

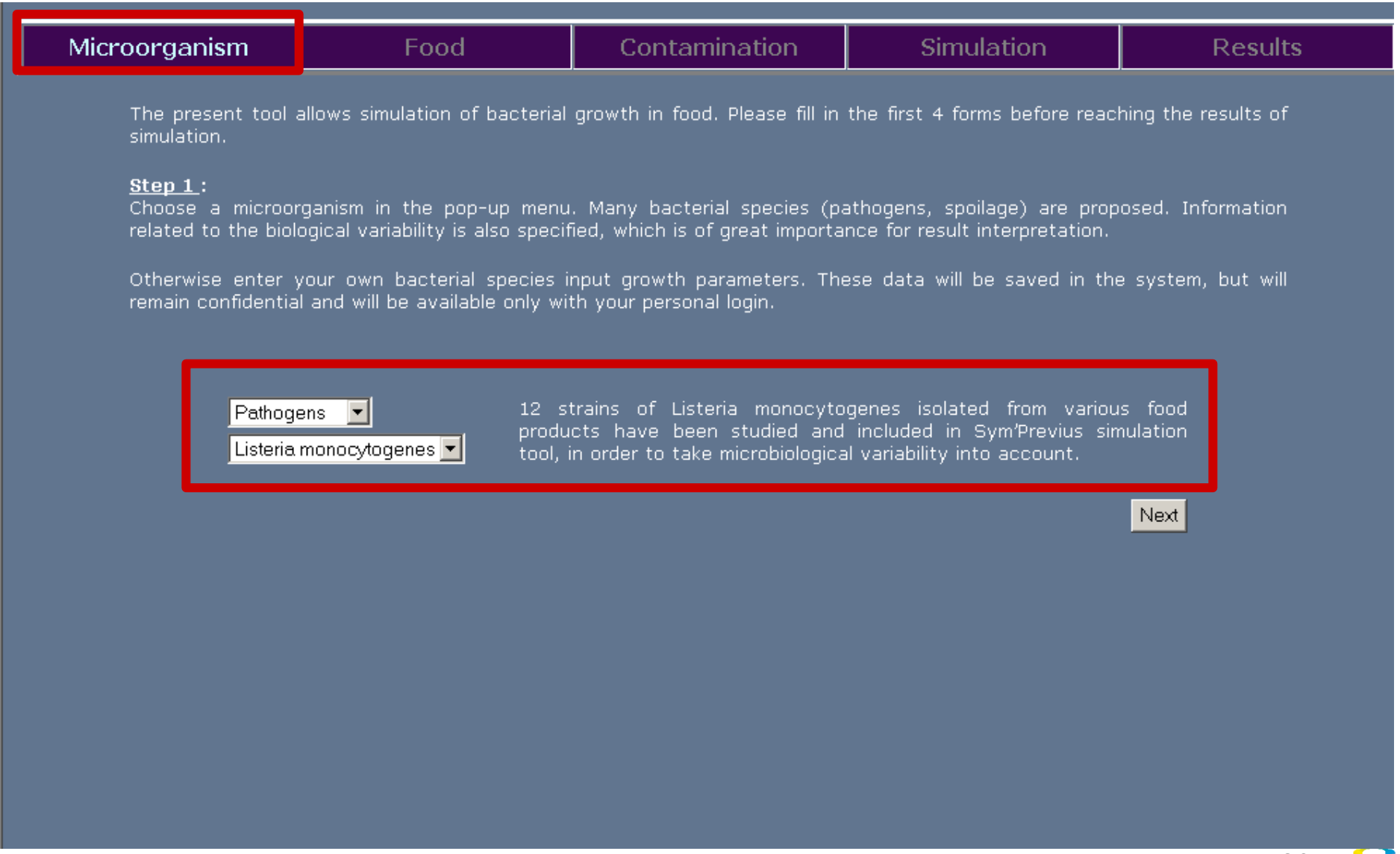
# Probabilistic software

❖ Growth simulation of a bacteria in a food taking into account variabilities related to :

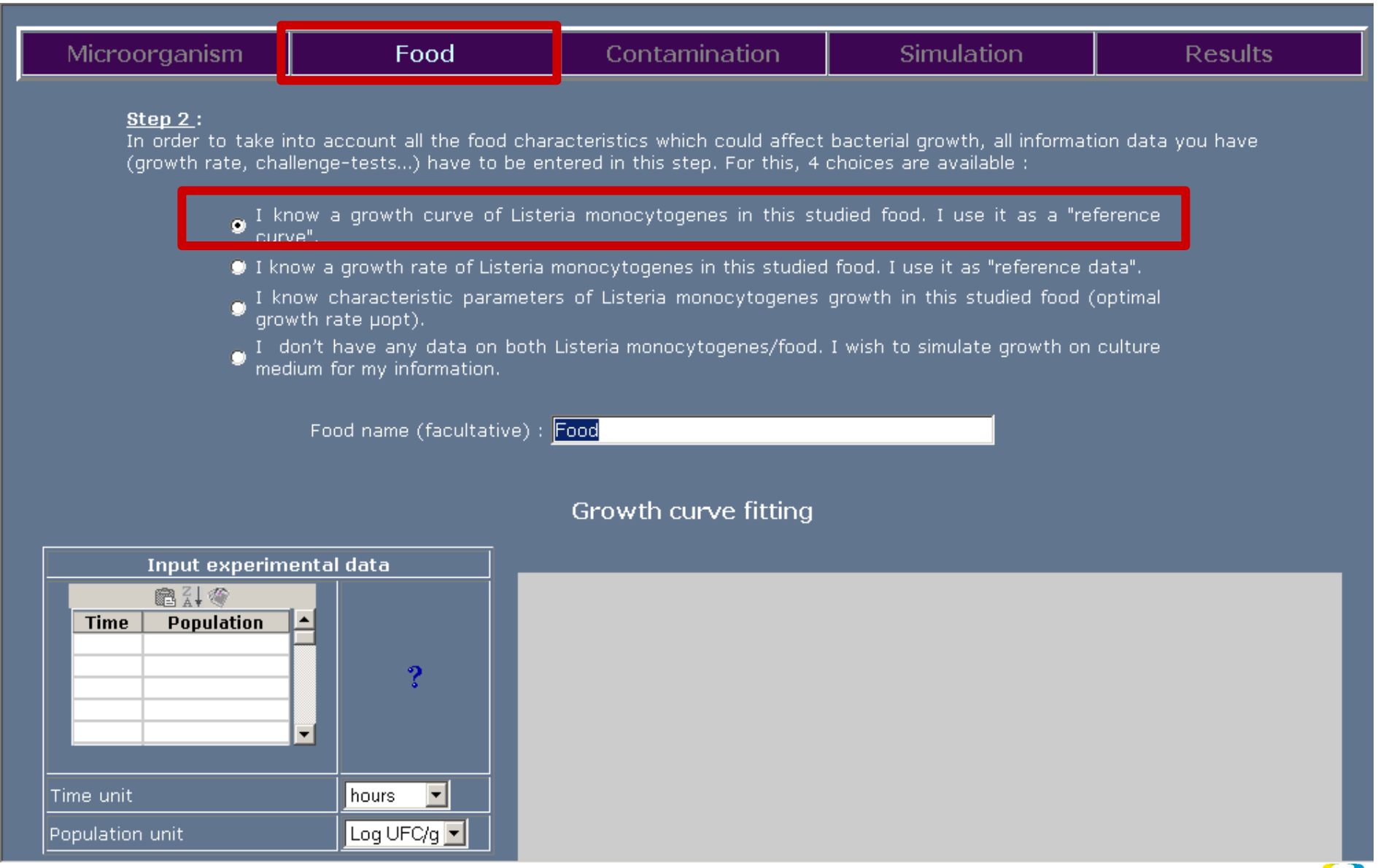
- strains
- food
- initial contaminations.

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

# How to use the probabilistic software?



# Use of probabilistic software



# 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: hours

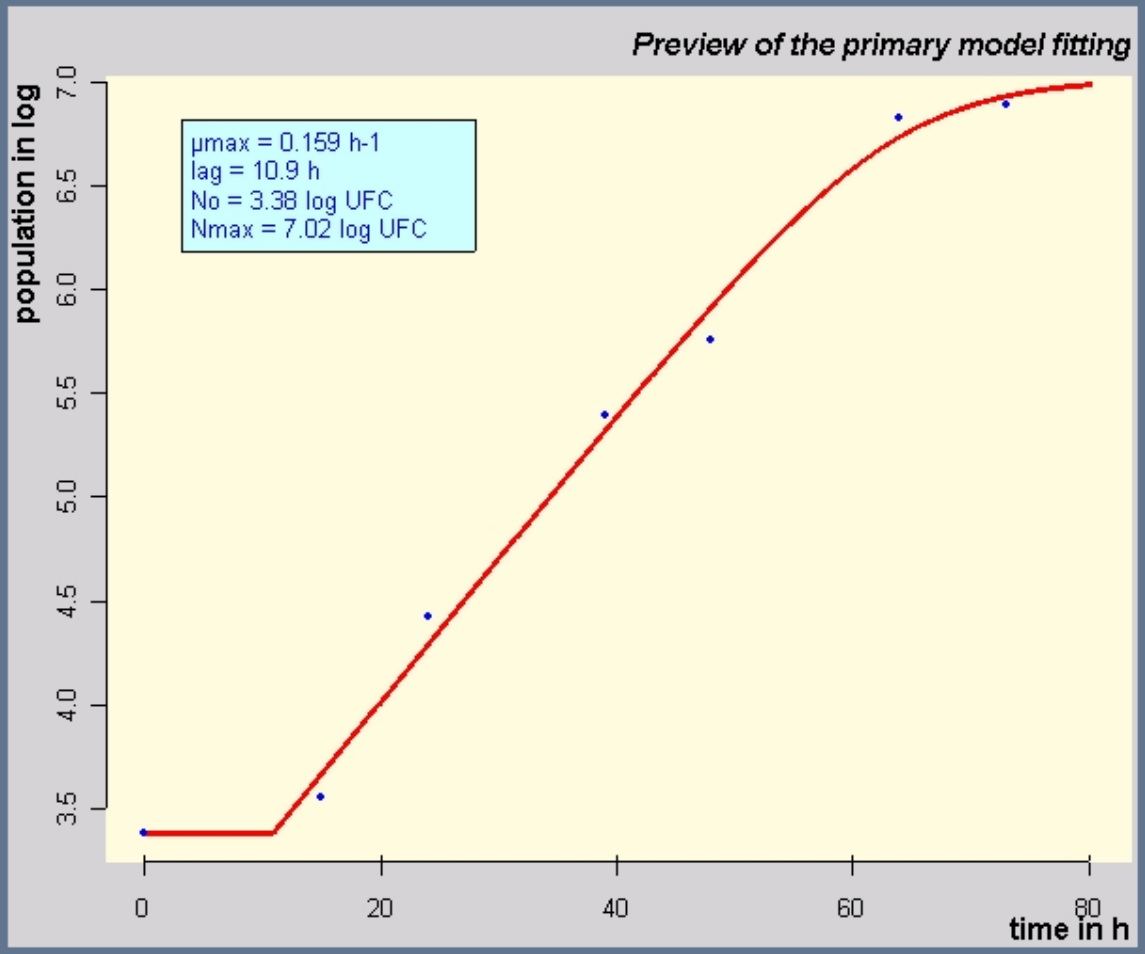
Population unit: Log UFC/g

**Initial Values for fitting (facultative) :**

| | |
|---|---|
| Initial contamination (log CFU/g) | |
| Maximal contamination (log CFU/g) | |
| Lag time (h) | |
| growth rate (/h) | |

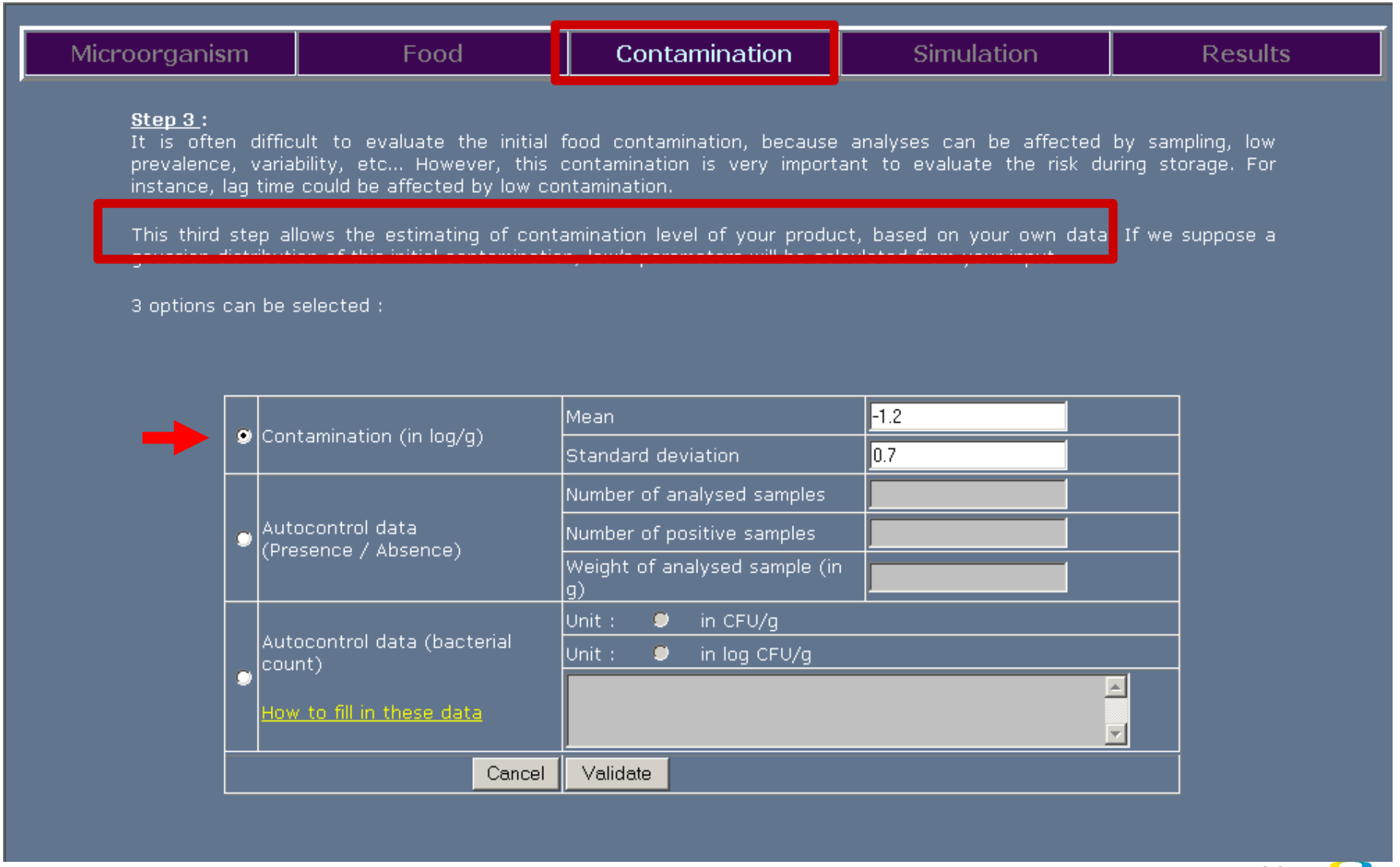
**Environmental conditions :**

| | | |
|---|---|---|
| Temperature | | 15 |
| pH | ☑ | 6 |
| Water activity | ☑ | 0.991 |
| Lactic acid | ☑ | 0 |
| Organic acids unit | | g/100g |

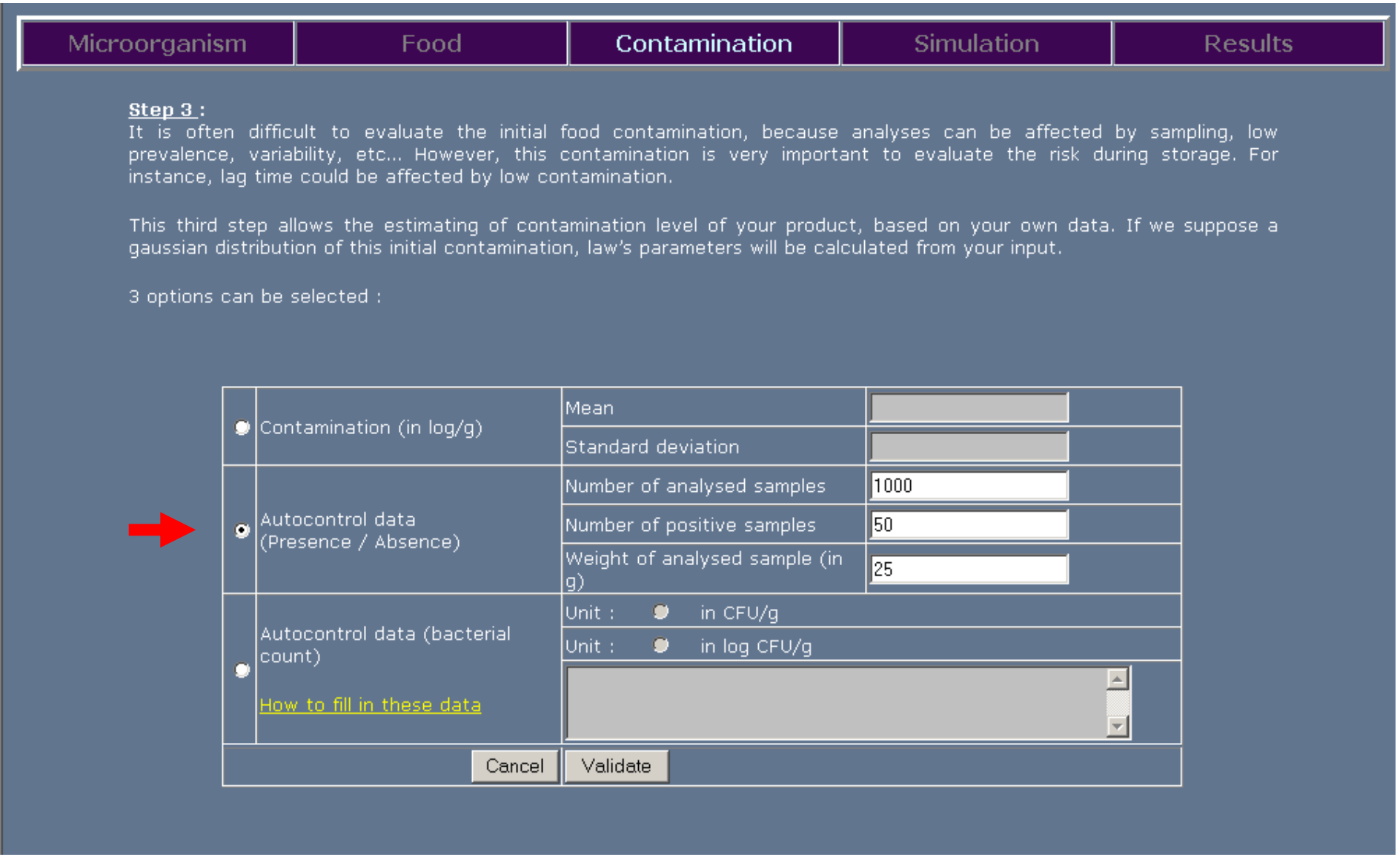



Cancel | Fit | Validate

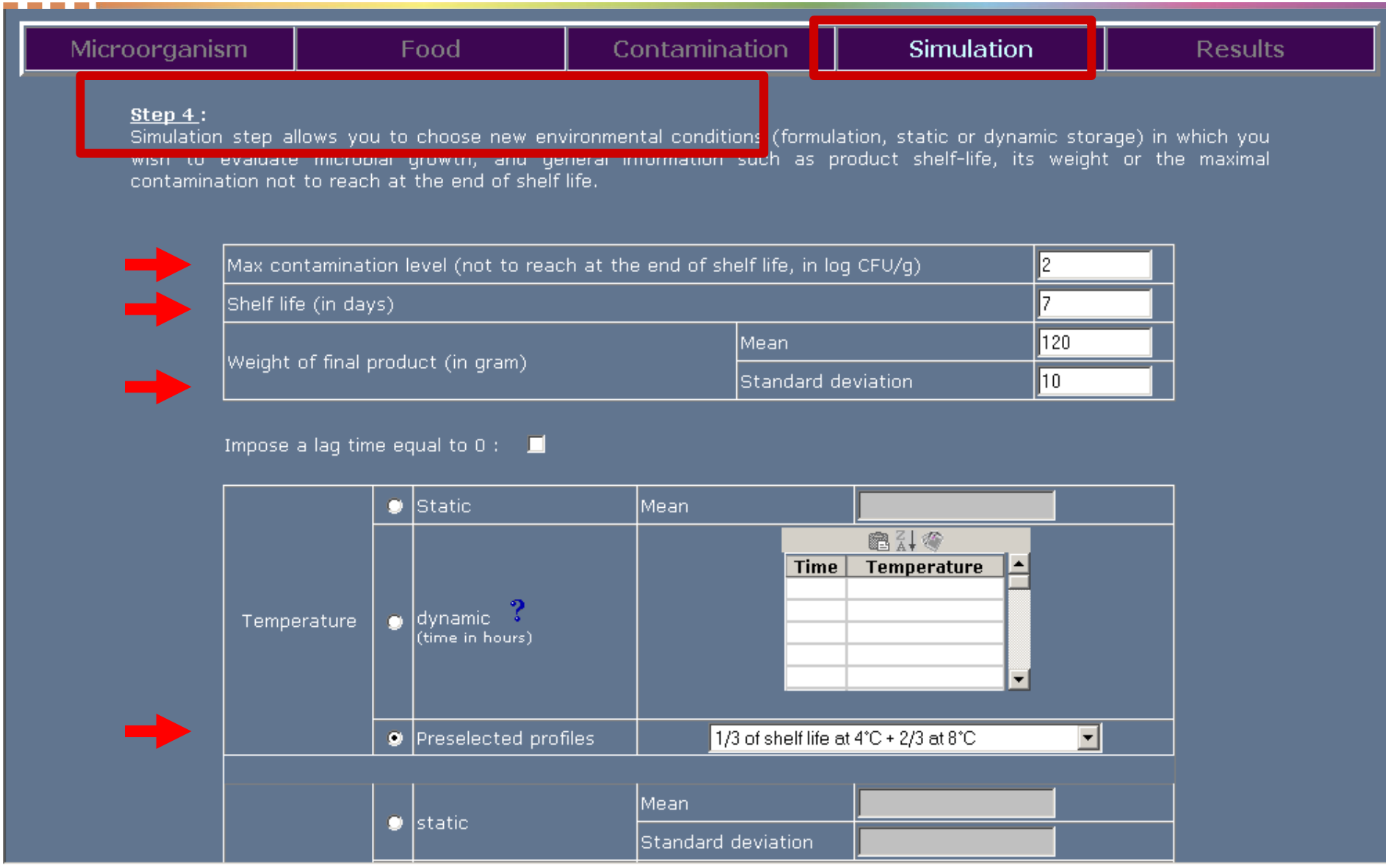
# Use of probabilistic software



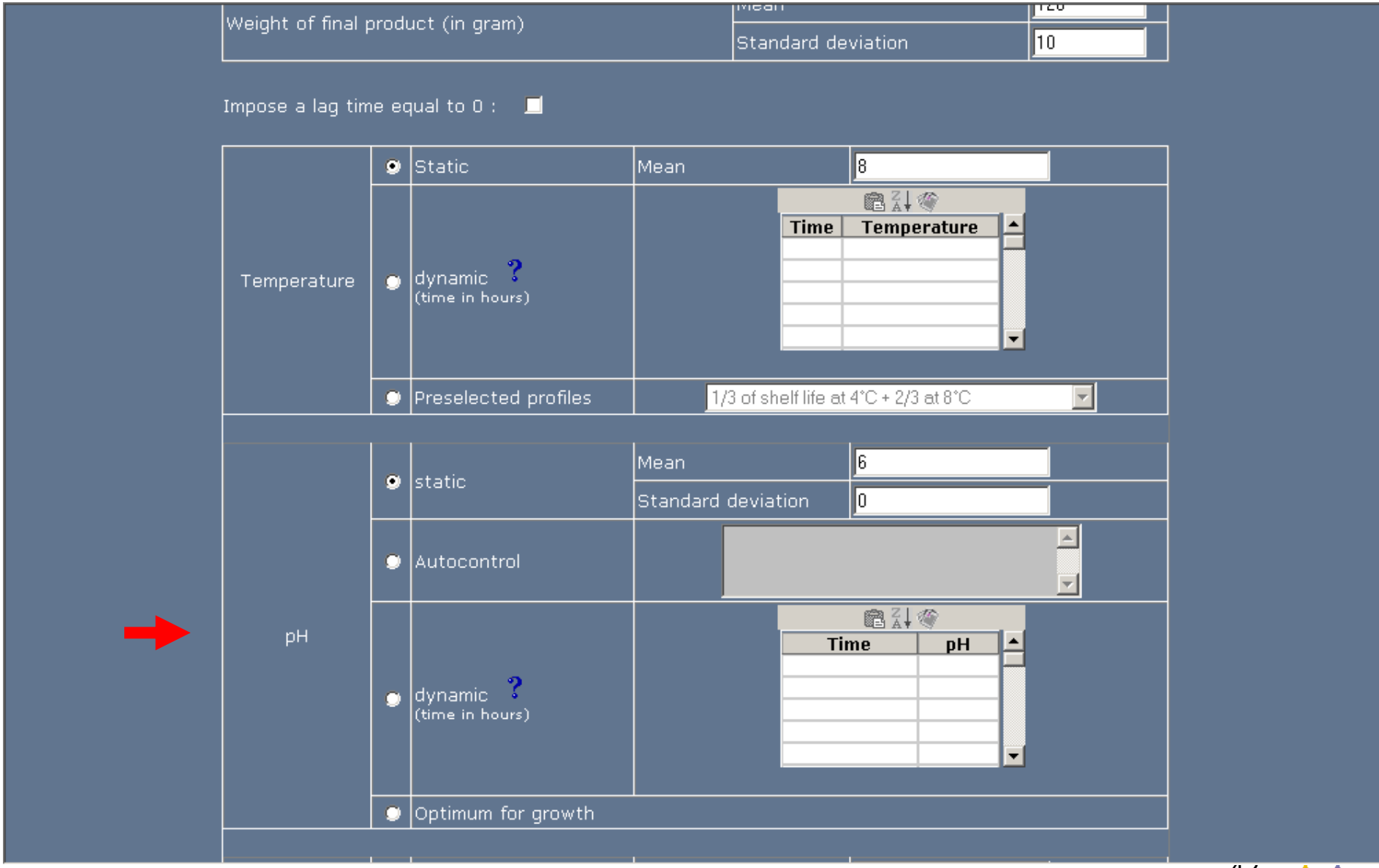
# Use of probabilistic software



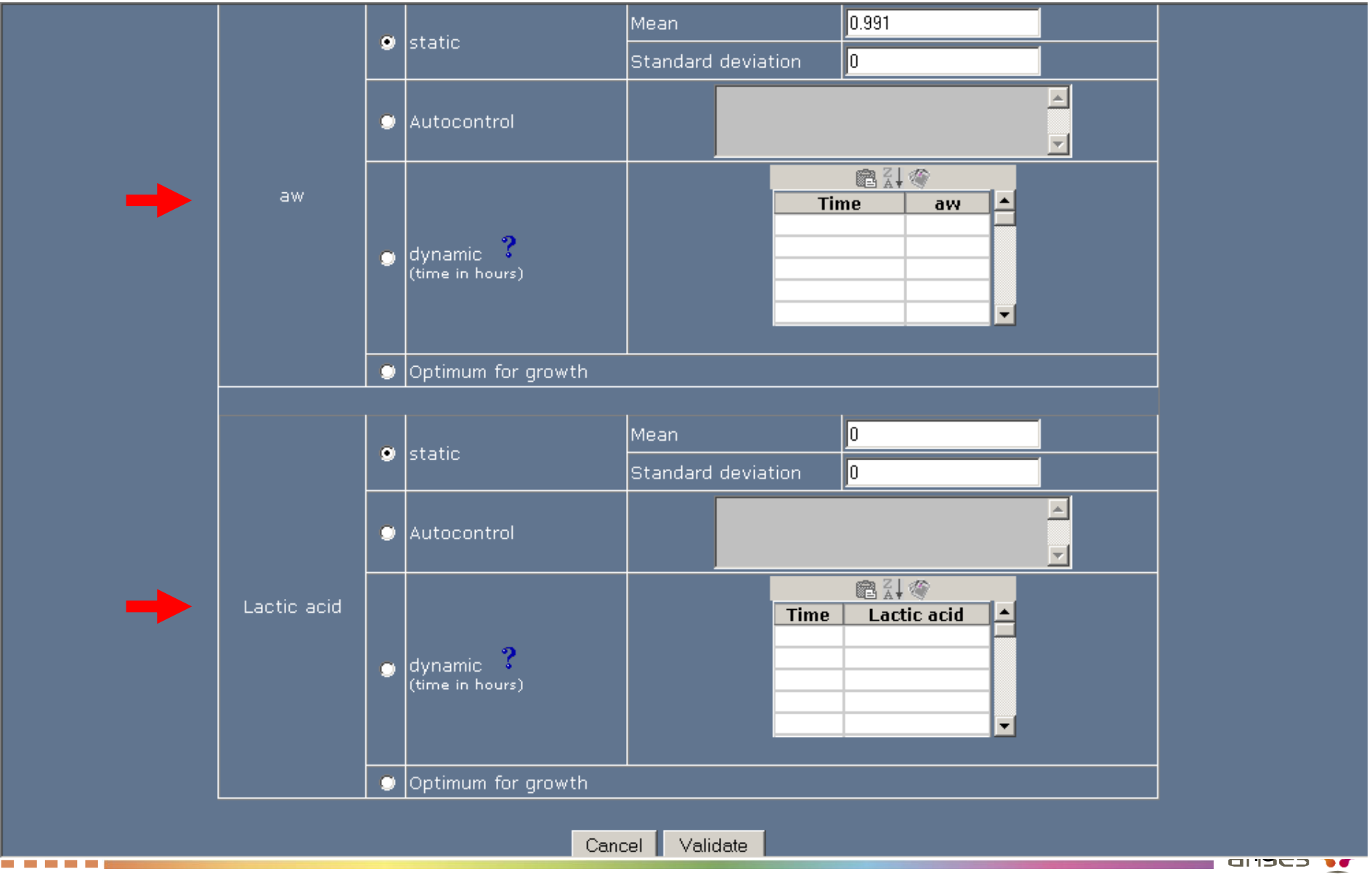
# Use of probabilistic software



# Use of probabilistic software



# Use of probabilistic software



# Result of one example

## Growth simulation of Listeria monocytogenes in Food

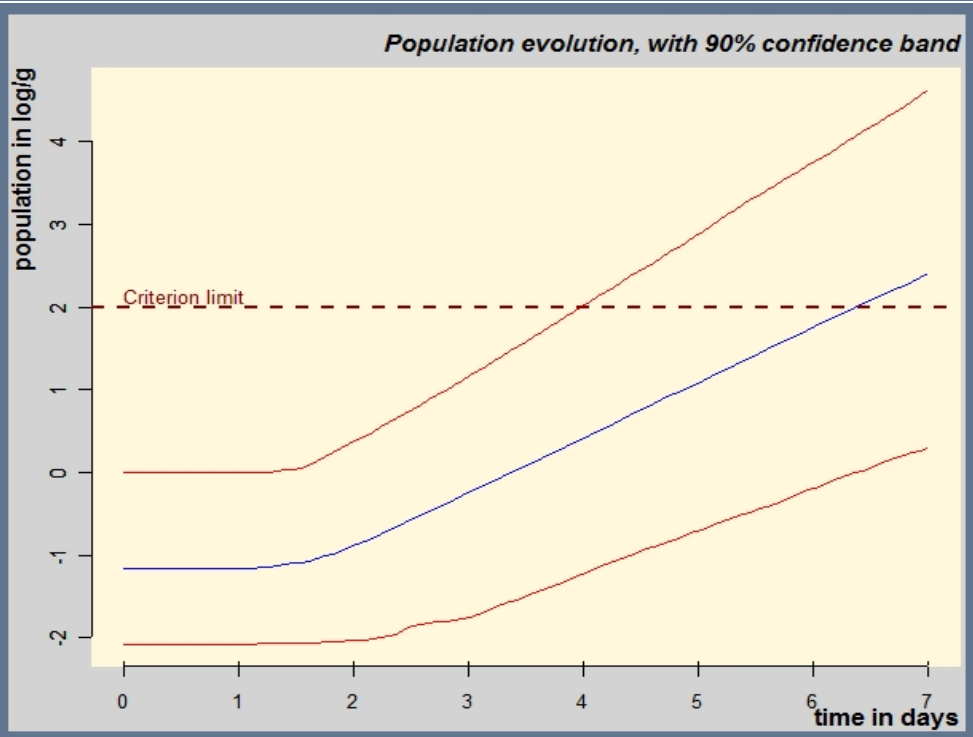
Probability than a food unit is contaminated is 95%. For these contaminated units, growth simulations are presented below :

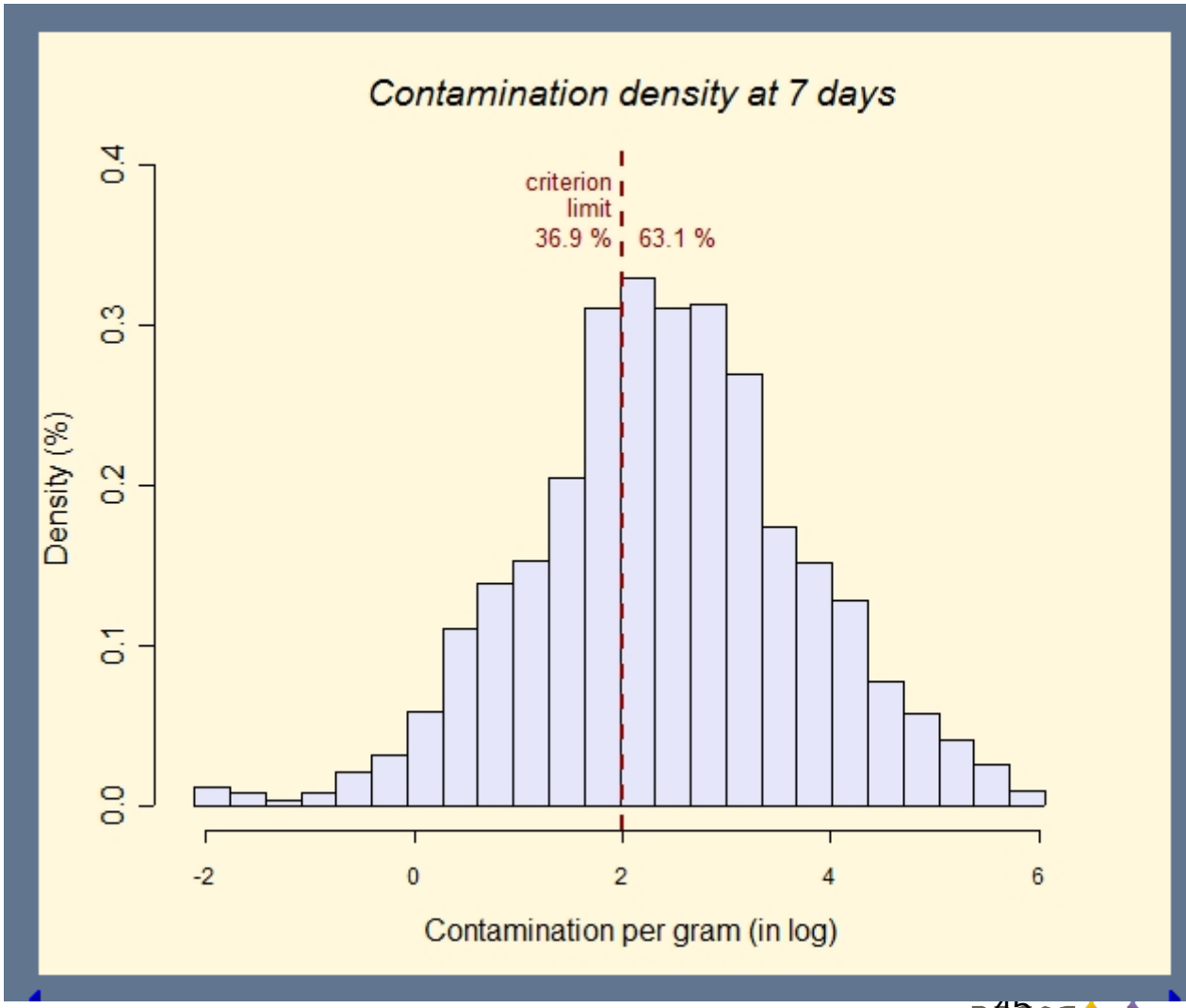
**Simulated parameters values**

| | 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
criterion limit
36.9 %
63.1 %
Density (%)
0.0
0.1
0.2
0.3
0.4
-2
0
2
4
6
Contamination per gram (in log)

# Conclusion related to probalistic approach

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

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

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