Modelling in foods: Kinetics and Tools

IAFP Webinar

Organized by:

Microbial Modeling and Risk Analysis PDG

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Webinar Housekeeping

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Audio is being transmitted over the computer so please have your speakers 'on' and volume turned up in order to hear. A telephone connection is not available.

Questions should be submitted to the presenters during the presentation via the Q & A section at the right of the screen.

It is important to note that all opinions and statements are those of the individual making the presentation and not necessarily the opinion or view of IAFP.

This webinar is being recorded and will be available for access by IAFP members at within one week.

Facilitated Discussion

- Moderator
    - Marcel Zwietering
    - Wageningen University
    - marcel.zwietering@wur.nl

- Questions should be submitted via the Text Chat section at the bottom of the screen.

Modelling in foods: Kinetics and Tools

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Food Protection®

Contact information for presenters

- Lihan Huang, Ph.D., CFS
- USDA Agricultural Research Service
  - lihan.huang@ars.usda.gov
- Antonio Valero, PhD
- University of Cordoba (SPAIN)
  - avalero@uco.es

- At the end: Keep your browsers open to complete the survey

Dr. Lihan Huang

Research Leader of the Residue Chemistry and Predictive Microbiology Research Unit at the Eastern Regional Research Center (ERRC) of the USDA.

Dr. Huang has earned a Ph.D. Dregree in Food Science and Technology and is currently the Research Leader of the Residue Chemistry and Predictive Microbiology Research Unit at ERRC.

Prior to joining ERRC, Dr. Huang worked in the Research and Development Department of Campbell Soup Company and conducted research on thermal processing of low-acid foods in semi-rigid containers and aseptic processing of foods containing solid particulate.

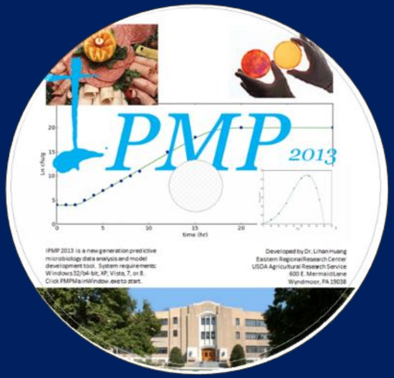
He is the developer of the USDA Integrated Pathogen Modeling Program (IPMP-2013) and a new product called IPMP-Global Fit. He also serves as a Lead Scientist of a project.

Dr. Huang is a member of the International Association for Food Protection

USDA Integrated Pathogen Modeling Program

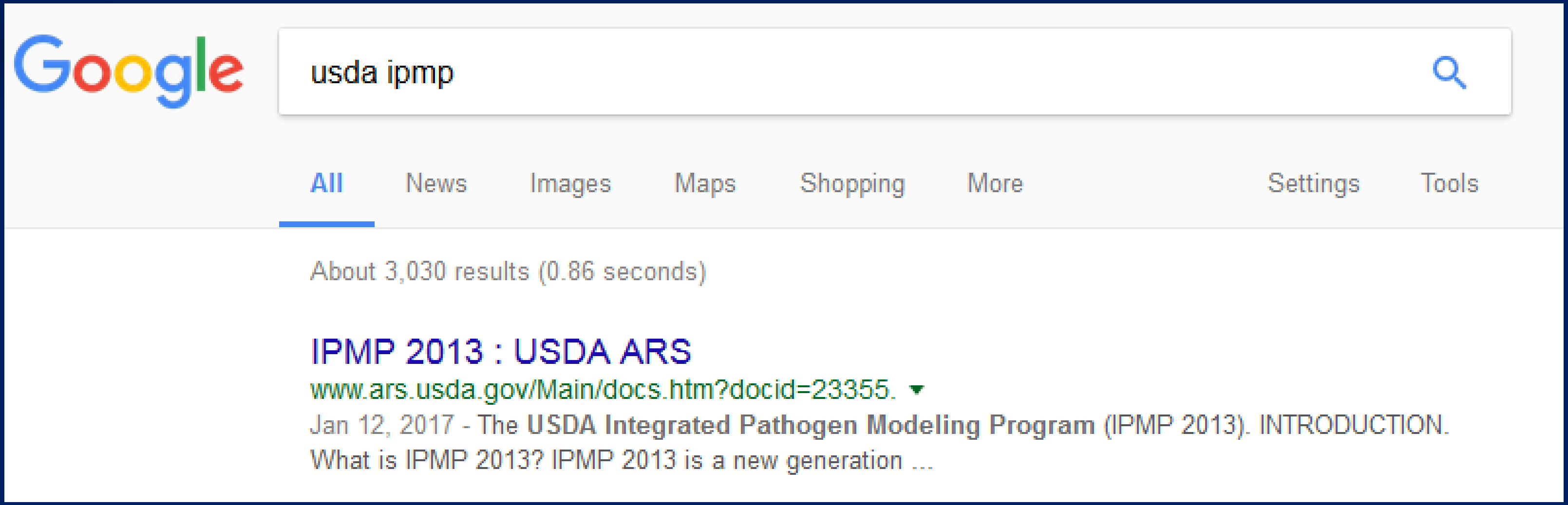
A platform for easy and accurate data analysis in predictive modeling

Lihan Huang, Ph.D.
Research Leader
Residue Chemistry and Predictive Microbiology Research Unit
Eastern Regional Research Center
USDA Agricultural Research Service
Wyndmoor, PA



USDA Integrated Pathogen Modeling Program (IPMP)

What is it? Google it.



About 3,030 results (0.86 seconds)

IPMP 2013 : USDA ARS
www.ars.usda.gov/Main/docs.htm?docid=23355.
Jan 12, 2017 - The **USDA Integrated Pathogen Modeling Program** (IPMP 2013). INTRODUCTION. What is IPMP 2013? IPMP 2013 is a new generation ...

A suite of data analysis tools that contains 20+ most frequently used models

- Intelligent, interactive data analysis and model development
- Very easy-to-use graphical-user interfaces to guide every step
- Standardized data analysis and interpretation

Website to download

- IPMP is located in a secured USDA website
- https://www.ars.usda.gov/northeast-area/wyndmoor-pa/eastern-regional-research-center/docs/ipmp-2013/
- A tutorial
- Download Instructions
- Compiled software (zipped file)
  - Windows 32 or 64 bit, Vista to Windows 10

Primary and secondary models

- Primary model (time)
  - Isothermal curves (growth and survival)
  - Growth rate and lag time
  - D value
- Secondary model (temperature)
  - Effect of temperature on growth rate and lag time
  - Effect of temperature on D values (z value)

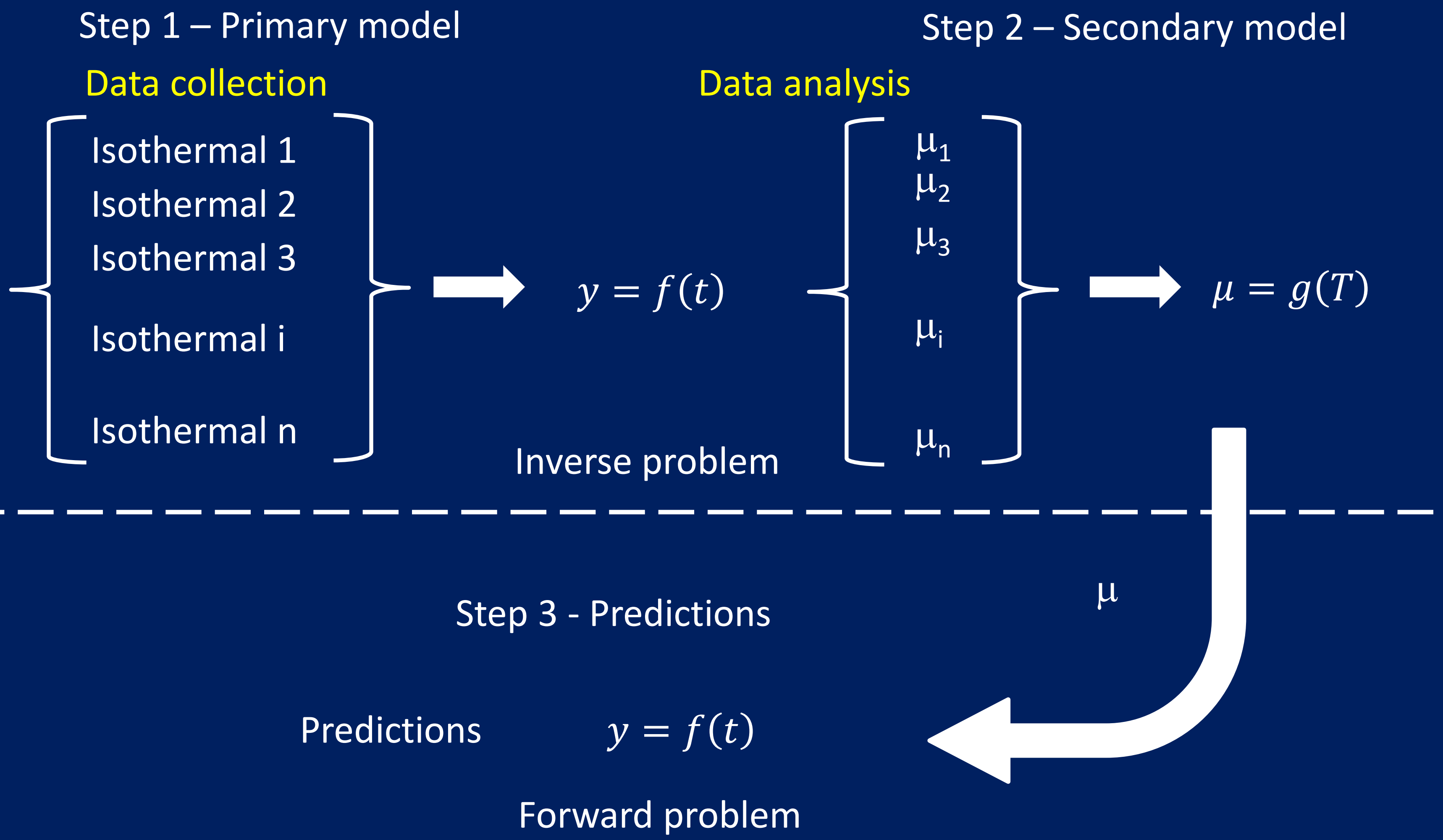
Predictive Microbiology as An Inverse Problem

- $y = f(x, a, b)$
- x is the independent variable
- y is the dependent variable
- a and b are coefficients
- We know x and y, but do not know a and b
- We will find a way to identify a and b from x and y
- This is an inverse problem

Predictive Microbiology as A Forward Problem

- $y = f(x, a, b)$
- x is the independent variable
- y is the dependent variable
- a and b are coefficients
- We know a and b
- We want to know how y changes with x
- This is a forward problem

The Traditional Approach:
a 3-step process



Step 1 – Primary model

Data collection

Isothermal 1

Isothermal 2

Isothermal 3

Isothermal i

Isothermal n

$y = f(t)$

Inverse problem

Step 2 – Secondary model

Data analysis

μ_1

μ_2

μ_3

μ_i

μ_n

$\mu = g(T)$

μ

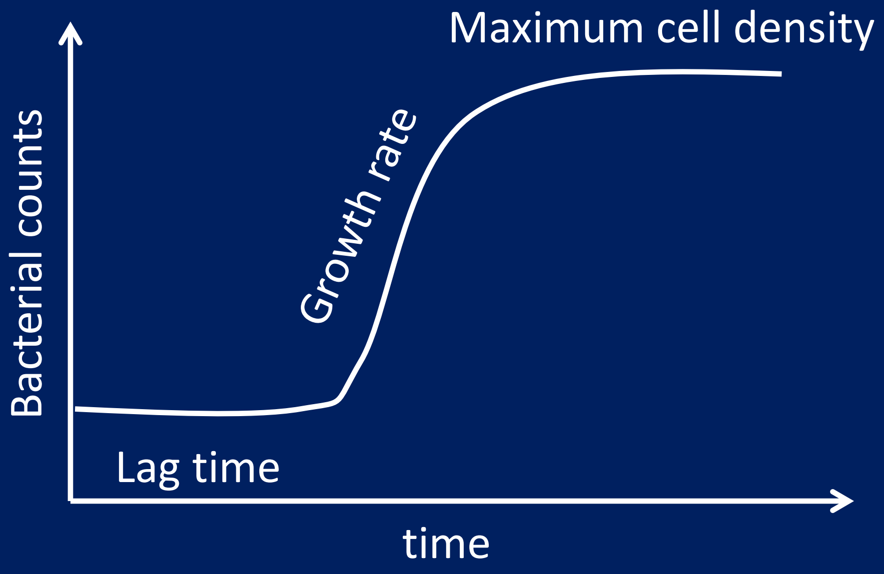
Step 3 - Predictions

Predictions $y = f(t)$

Forward problem

Primary Models for Growth

Isothermal growth curves



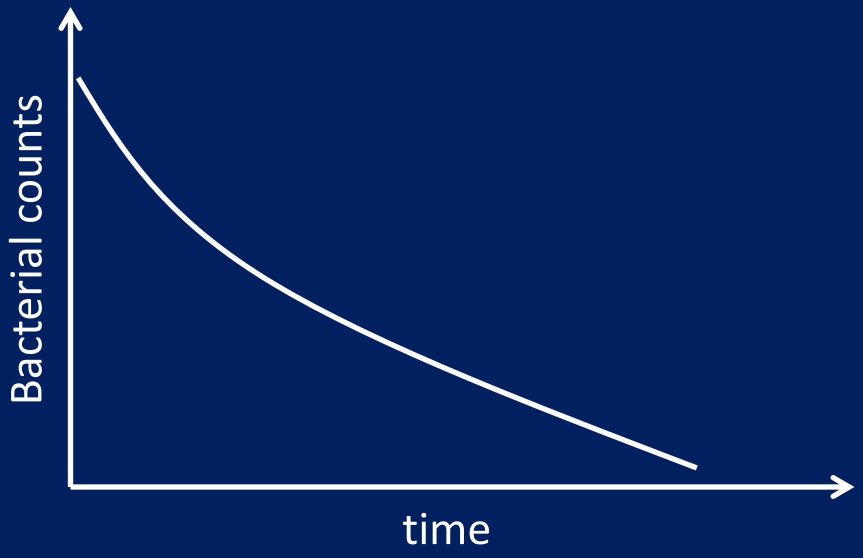
- Gompertz model
- Baranyi model
- Huang model
- Buchanan 3-phase (trilinear) model

We are interested in answering 3 questions from a growth curve

1. How long is the lag phase?
2. How fast can a microorganism grow?
3. What is the maximum cell density?

Primary Models for Survival (Inactivation)

- Linear model
- Weibull model
- Gompertz model



We are interested in answering 1 question from a survival curve

How fast does a microorganism die off?

Secondary Models

- What is the relationship between rate and temperature?
- What are the minimum, optimum, and maximum growth temperatures?

Techniques for Data Analysis

- Linear regression
- Nonlinear regression
- Typical inverse problems

Commercial and Free Data Analysis and Statistical/Math Tools

Providing software solutions sir

THE POWER OF 9

Mathematica 9 adds 400+ new features, including the new Wolfram Predictive Interface, social network analysis, enterprise CDF deployment, and more »

IBM Software > Business Analytics > SPSS >

SPSS software

Predictive analytics software and solutions

Statistical Discovery.™ From SAS.

Products & Services > MATLAB

MATLAB

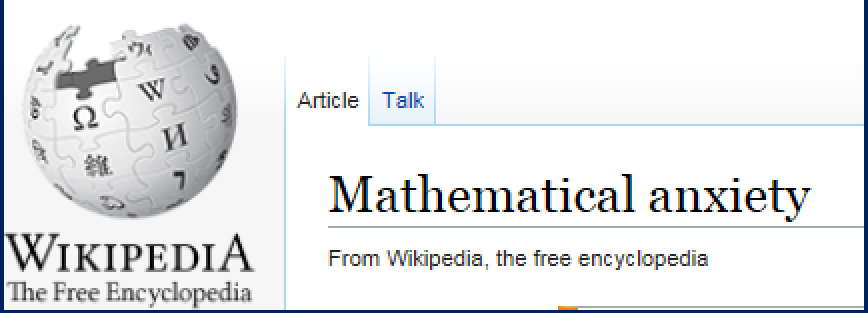
The Language of Technical Computing

Commercial Data Analysis and Statistical/Math Tools

- Very powerful
- Product-specific programming
- Not so user-friendly
- Training and learning
- Most are very expensive
- Difficult to learn and use

Some mysteries of predictive modeling

- Math is too hard
- I don’t know which model to choose
- I don’t know which model is better
- I don’t have a program to do it
- I don’t know how to program



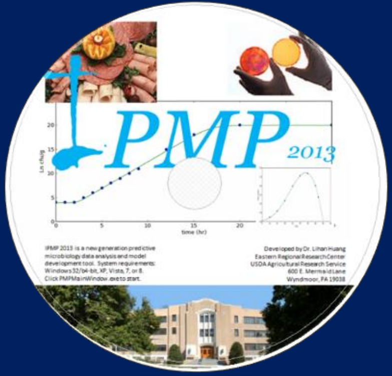
Mathematical anxiety

From Wikipedia, the free encyclopedia

Specific to Nonlinear Regression

- Initial guess values
- Improper initial guess values may not help in finding solutions (convergence)
- Graphical visualization helps finding suitable initial guess values

USDA - IPMP



IPMP 2013 is a new generation predictive
microbiology data analysis and model
development tool. System requirements:
Windows 32/64-bit, XP, Vista, 7, or 8.
Click PMPMainWindow.exe to start.

Developed by Dr. Lihan Huang
Eastern Regional Research Center
USDA Agricultural Research Service
600 E. Mermaid Lane
Wyndmoor, PA 19038

- Based on a modern object-oriented computing language
- Advanced scientific computing libraries
- Modern graphical-user interface
- 20+ mathematical models
- Accuracy identical or equivalent to SAS and R

IPMP User Interface

Exit

Menu bar

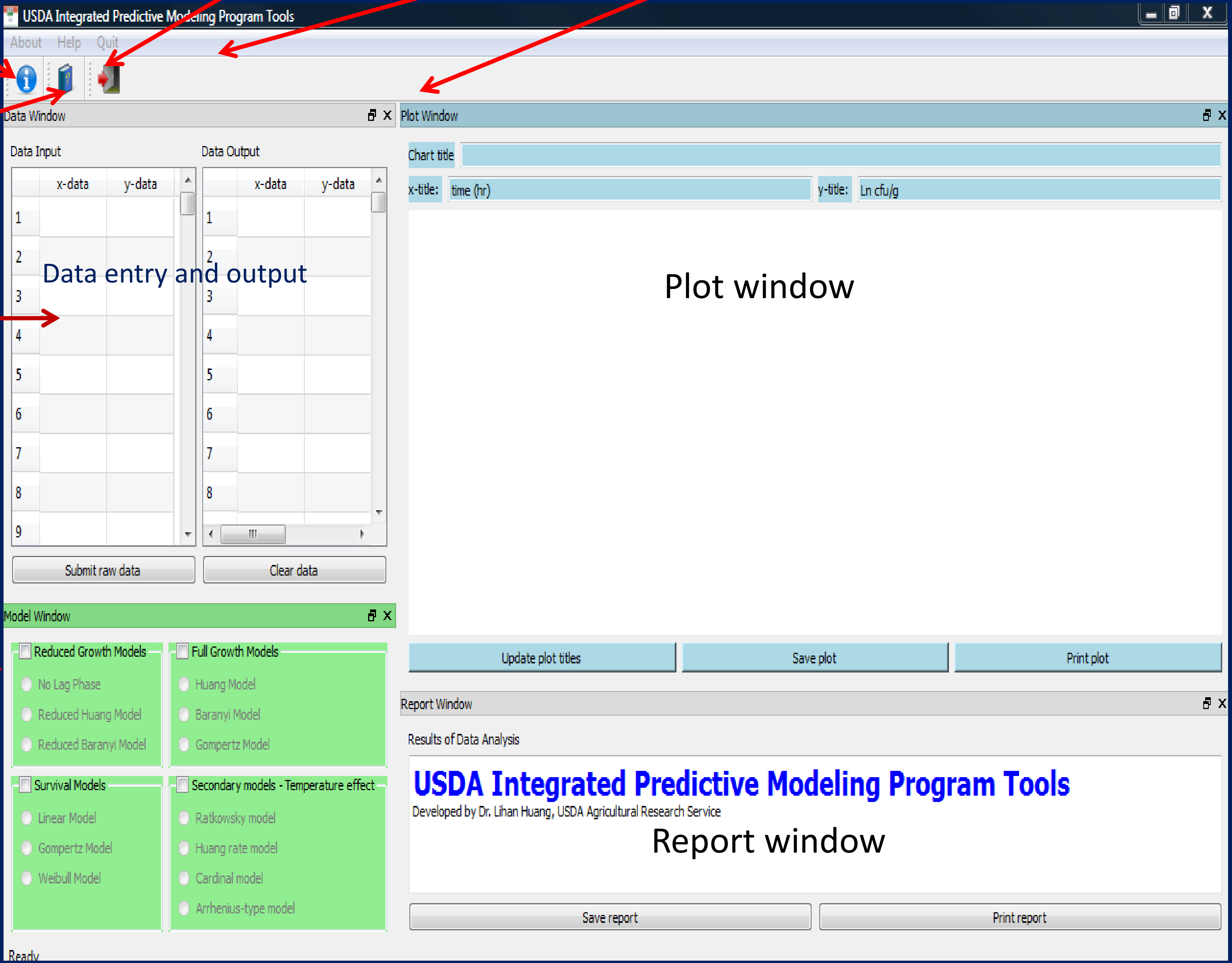
Tool bar

About IPMP

Help

Data window

Model window



USDA Integrated Predictive Modeling Program Tools

Chart title:

x-title: time (hr)

y-title: Ln cfu/g

Results of Data Analysis

USDA Integrated Predictive Modeling Program Tools

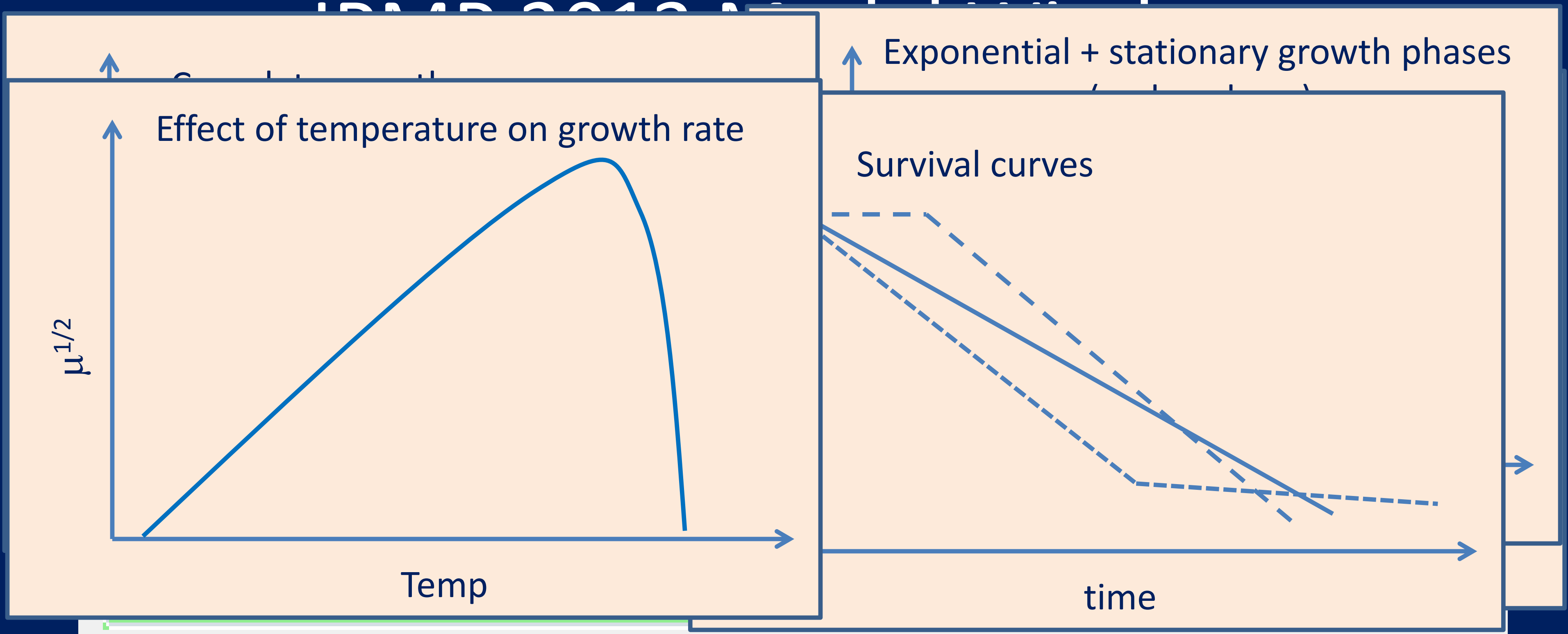
Developed by Dr. Lihan Huang, USDA Agricultural Research Service

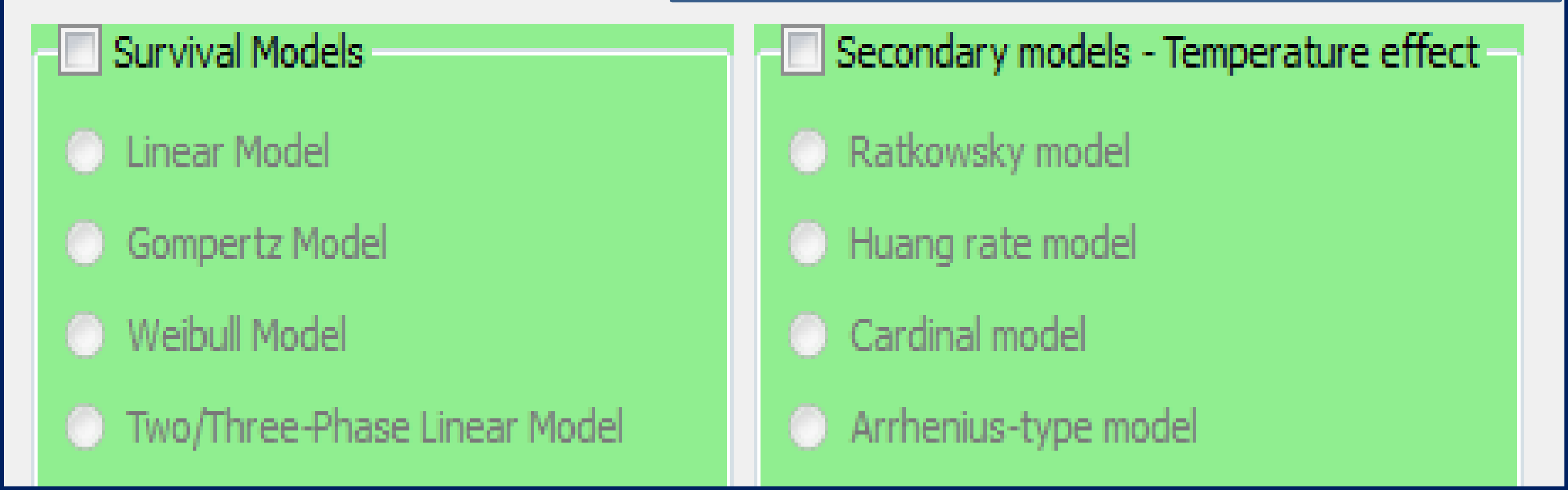
Ready

Data entry and output

Plot window

Report window





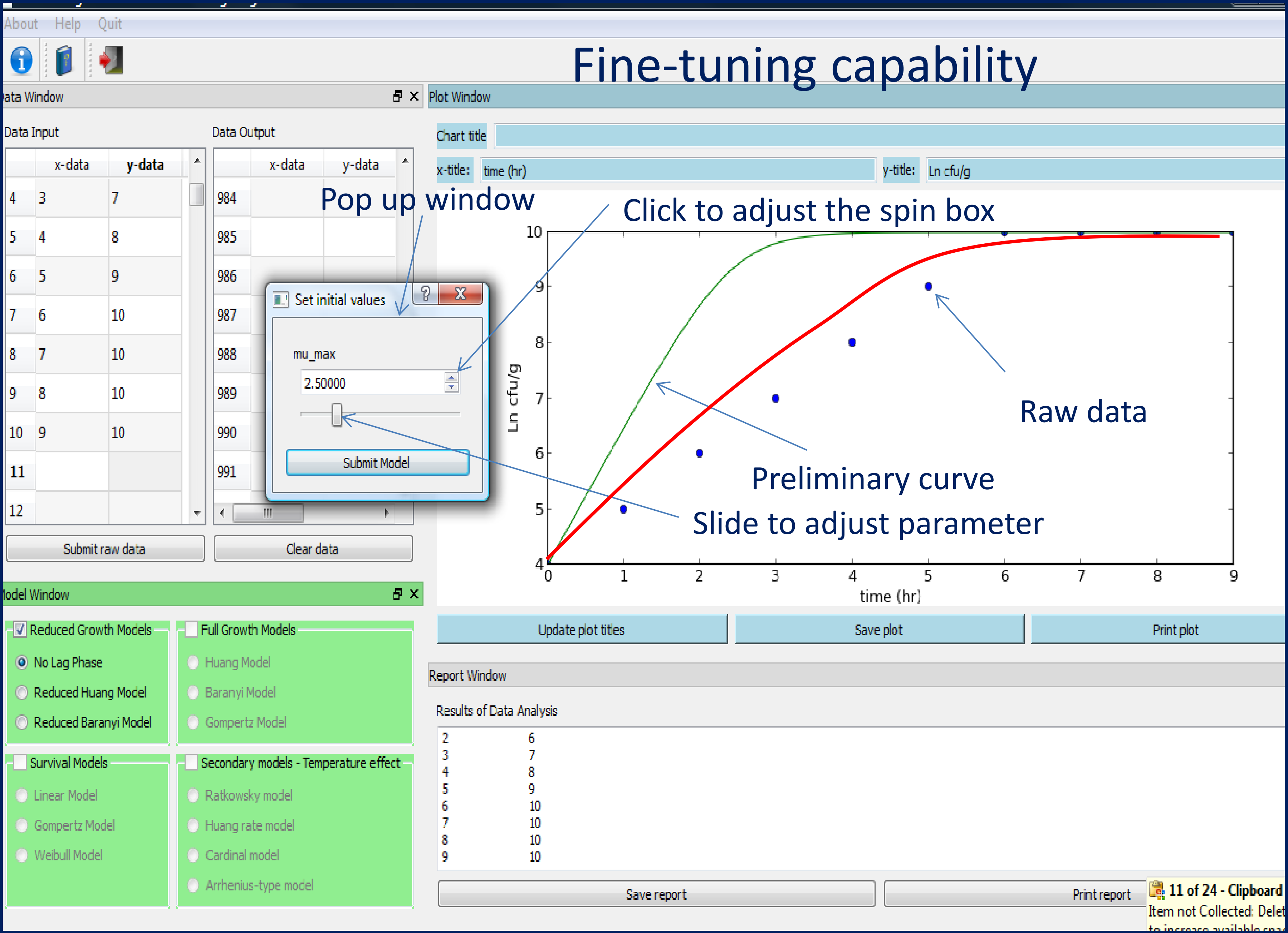
☐ Survival Models

- ○ Linear Model
- ○ Gompertz Model
- ○ Weibull Model
- ○ Two/Three-Phase Linear Model

☐ Secondary models - Temperature effect

- ○ Ratkowsky model
- ○ Huang rate model
- ○ Cardinal model
- ○ Arrhenius-type model

IPMP 2013 Data Analysis



Fine-tuning capability

Pop up window

Click to adjust the spin box

Raw data

Preliminary curve

Slide to adjust parameter

Data Input

	x-data	y-data
4	3	7
5	4	8
6	5	9
7	6	10
8	7	10
9	8	10
10	9	10
11		
12		

Data Output

	x-data	y-data
984		
985		
986		
987		
988		
989		
990		
991		

Chart title

x-title: time (hr)

y-title: Ln cfu/g

mu_max: 2.50000

☑ Reduced Growth Models
- ● No Lag Phase
- ○ Reduced Huang Model
- ○ Reduced Baranyi Model

☐ Full Growth Models
- ○ Huang Model
- ○ Baranyi Model
- ○ Gompertz Model

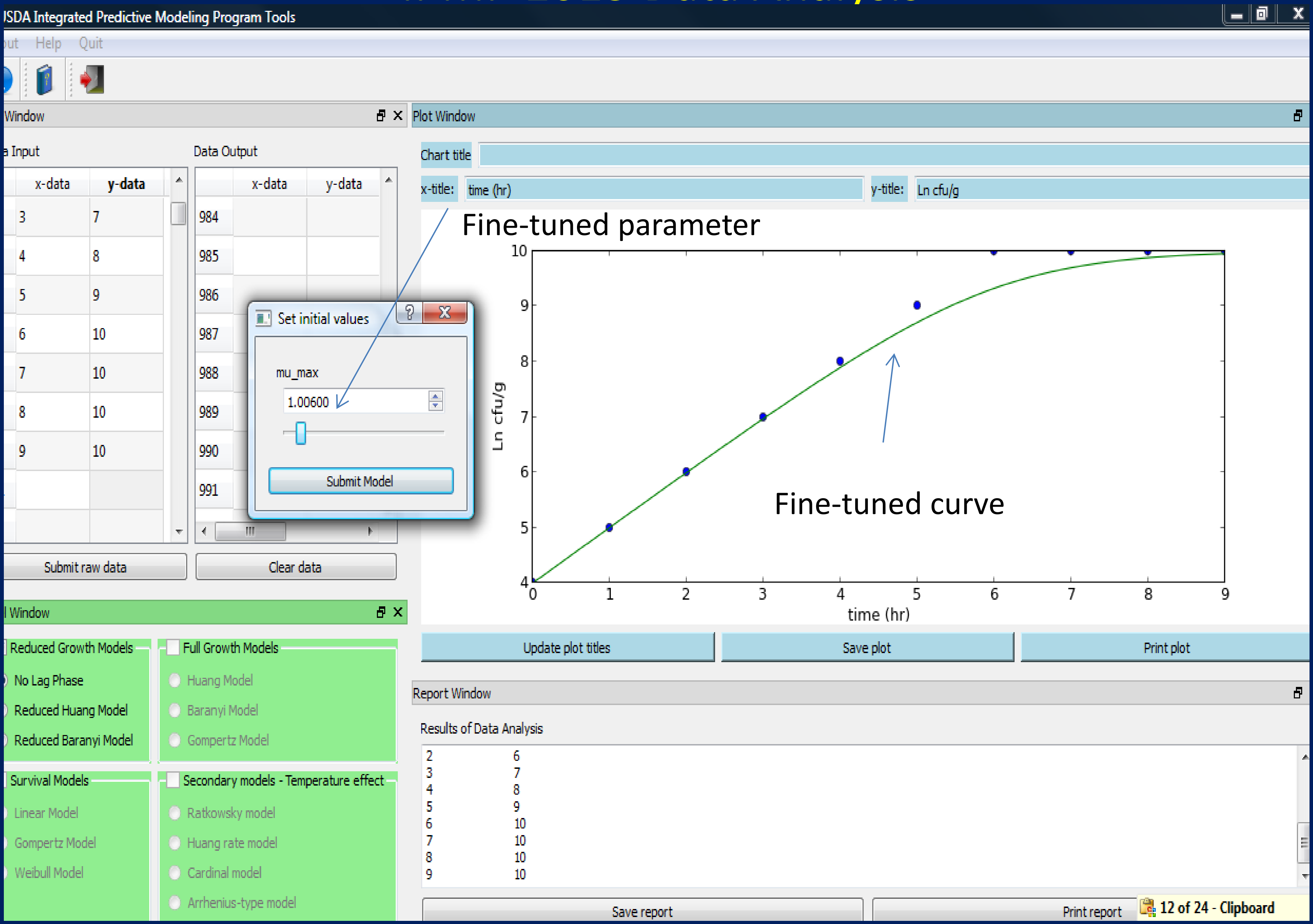
☐ Survival Models
- ○ Linear Model
- ○ Gompertz Model
- ○ Weibull Model

☐ Secondary models - Temperature effect
- ○ Ratkowsky model
- ○ Huang rate model
- ○ Cardinal model
- ○ Arrhenius-type model

Results of Data Analysis

```
2    6
3    7
4    8
5    9
6    10
7    10
8    10
9    10
```

IPMP 2013 Data Analysis



Fine-tuned parameter

Fine-tuned curve

x-data	y-data
3	7
4	8
5	9
6	10
7	10
8	10
9	10

	x-data	y-data
984		
985		
986		
987		
988		
989		
990		
991		

Set initial values

mu_max

1.00600

Submit Model

Chart title:

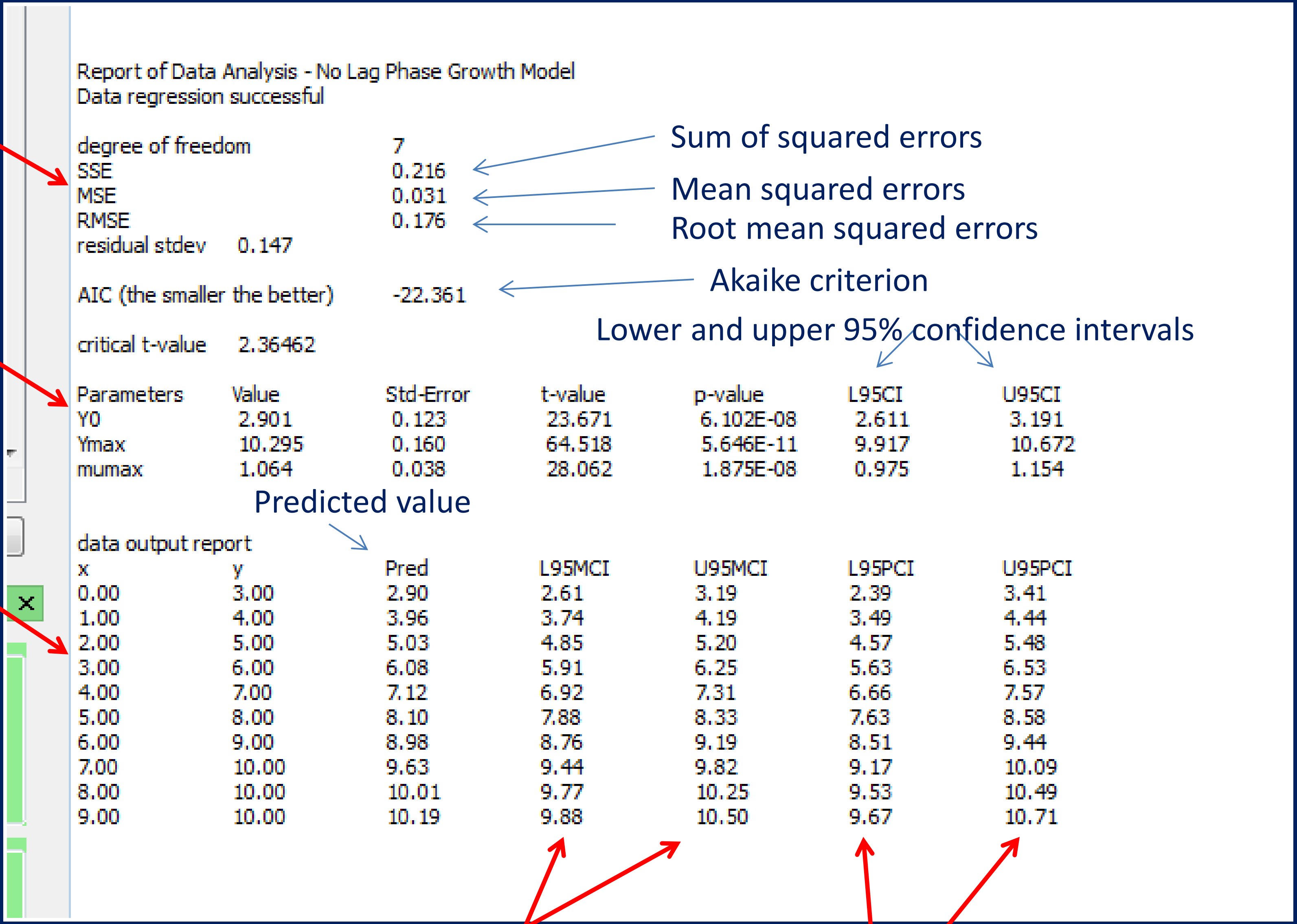
x-title: time (hr)

y-title: Ln cfu/g

Results of Data Analysis

```
2    6
3    7
4    8
5    9
6    10
7    10
8    10
9    10
```

Report Generation



```
Report of Data Analysis - No Lag Phase Growth Model
Data regression successful

degree of freedom              7
SSE                            0.216
MSE                            0.031
RMSE                           0.176
residual stdev      0.147

AIC (the smaller the better)   -22.361

critical t-value    2.36462

Parameters      Value       Std-Error   t-value     p-value     L95CI       U95CI
Y0              2.901       0.123       23.671      6.102E-08   2.611       3.191
Ymax            10.295      0.160       64.518      5.646E-11   9.917       10.672
mumax           1.064       0.038       28.062      1.875E-08   0.975       1.154

data output report
x               y           Pred        L95MCI      U95MCI      L95PCI      U95PCI
0.00            3.00        2.90        2.61        3.19        2.39        3.41
1.00            4.00        3.96        3.74        4.19        3.49        4.44
2.00            5.00        5.03        4.85        5.20        4.57        5.48
3.00            6.00        6.08        5.91        6.25        5.63        6.53
4.00            7.00        7.12        6.92        7.31        6.66        7.57
5.00            8.00        8.10        7.88        8.33        7.63        8.58
6.00            9.00        8.98        8.76        9.19        8.51        9.44
7.00            10.00       9.63        9.44        9.82        9.17        10.09
8.00            10.00       10.01       9.77        10.25       9.53        10.49
9.00            10.00       10.19       9.88        10.50       9.67        10.71
```

Error analysis

Sum of squared errors

Mean squared errors

Root mean squared errors

Akaike criterion

Parameters

Lower and upper 95% confidence intervals

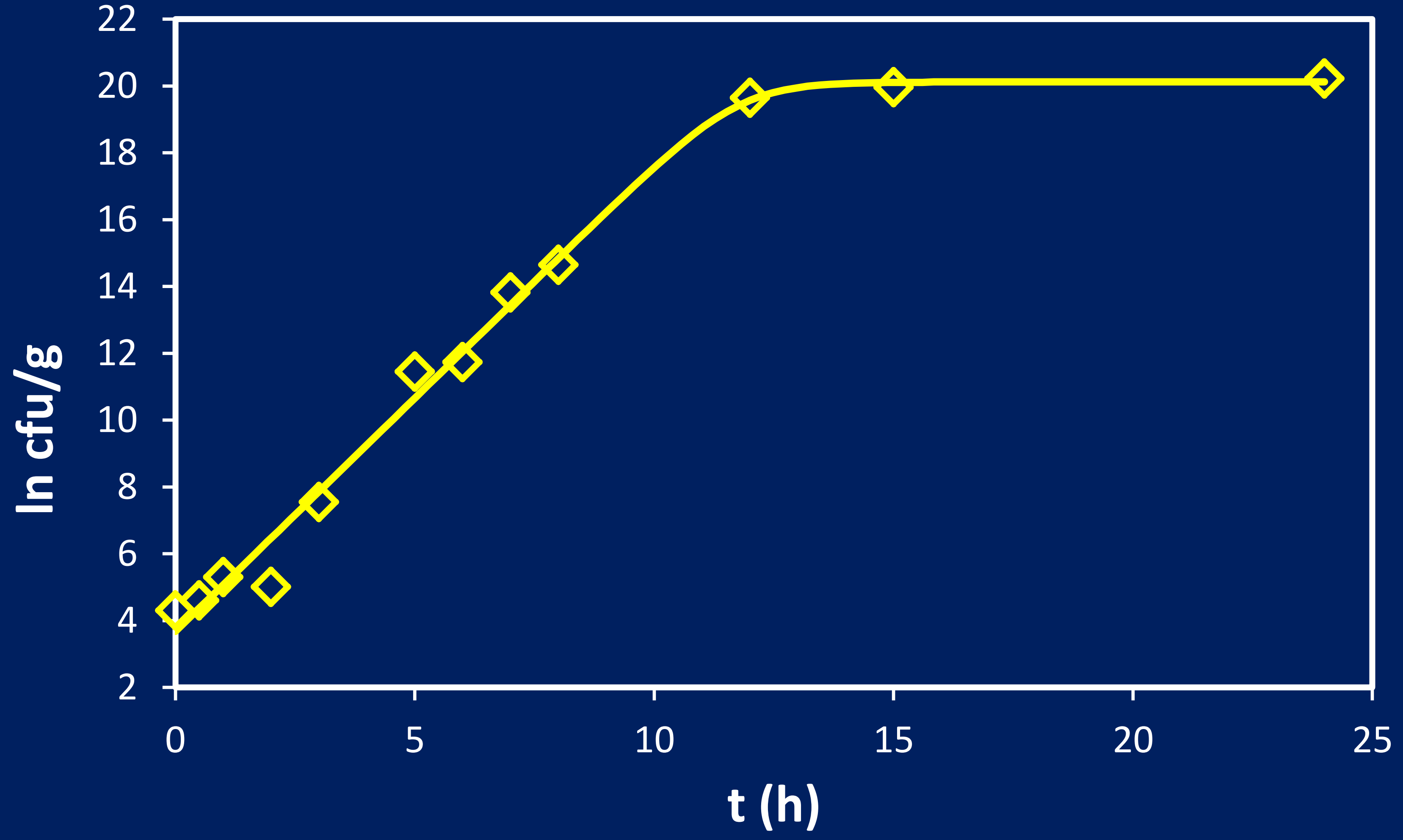
Predicted value

Raw data

Lower and upper 95% confidence intervals for the expected value (mean)

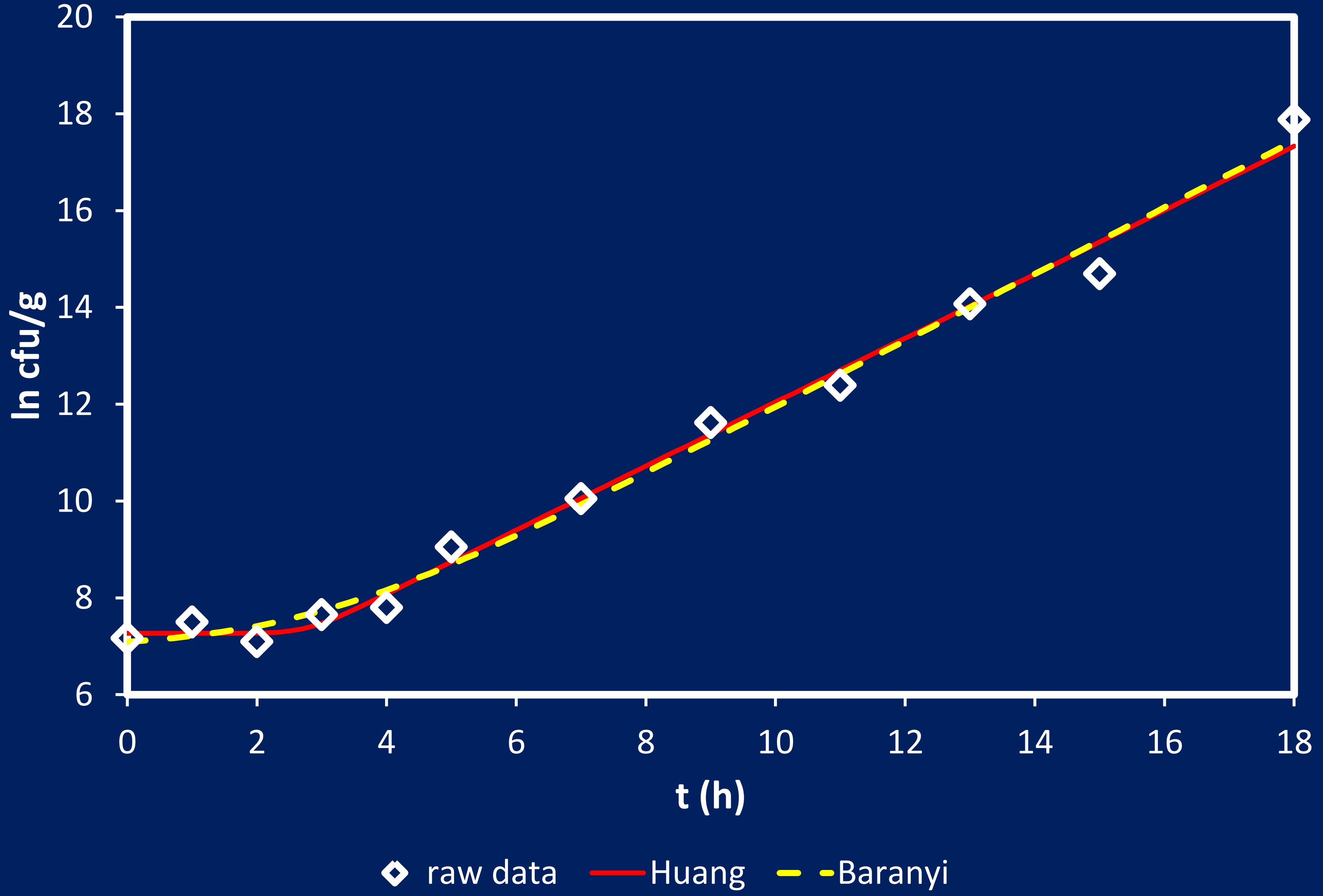
Lower and upper 95% confidence intervals for individual prediction

Exponential growth and stationary phase



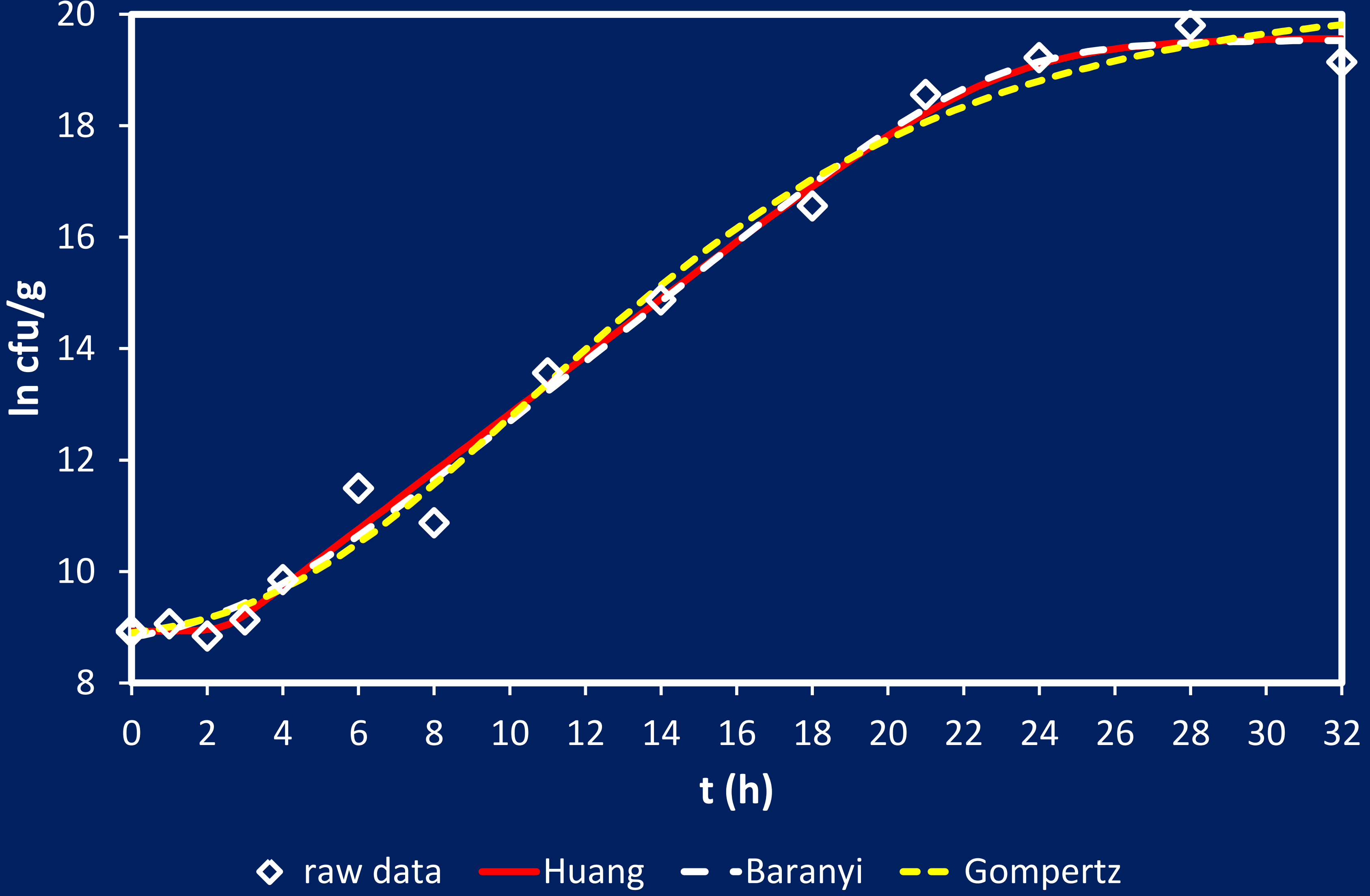
Cronobacter sakazakii in reconstituted infant formula

Lag phase and exponential growth



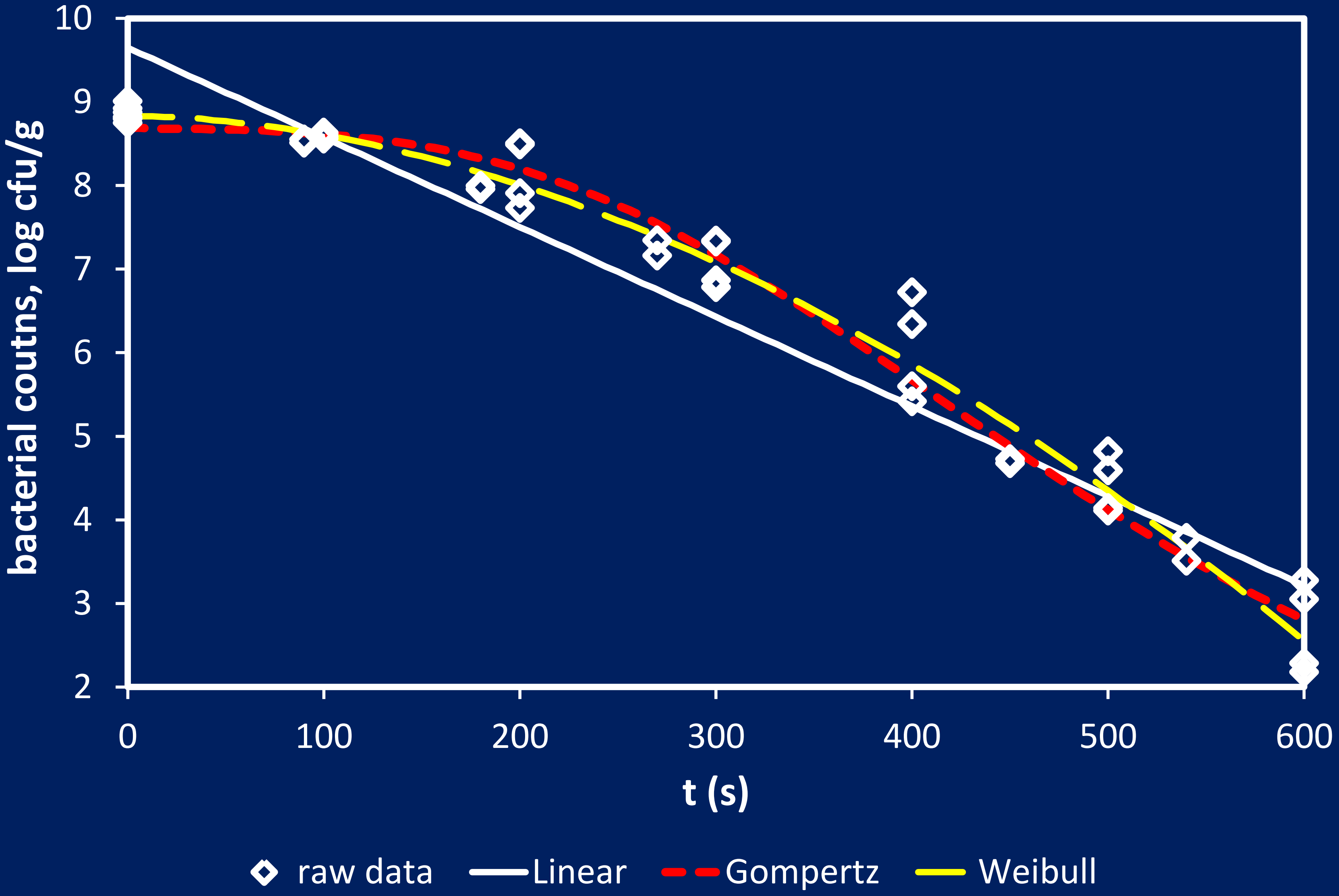
Listeria monocytogenes in beef frankfurters

Lag phase, exponential growth, and stationary phase



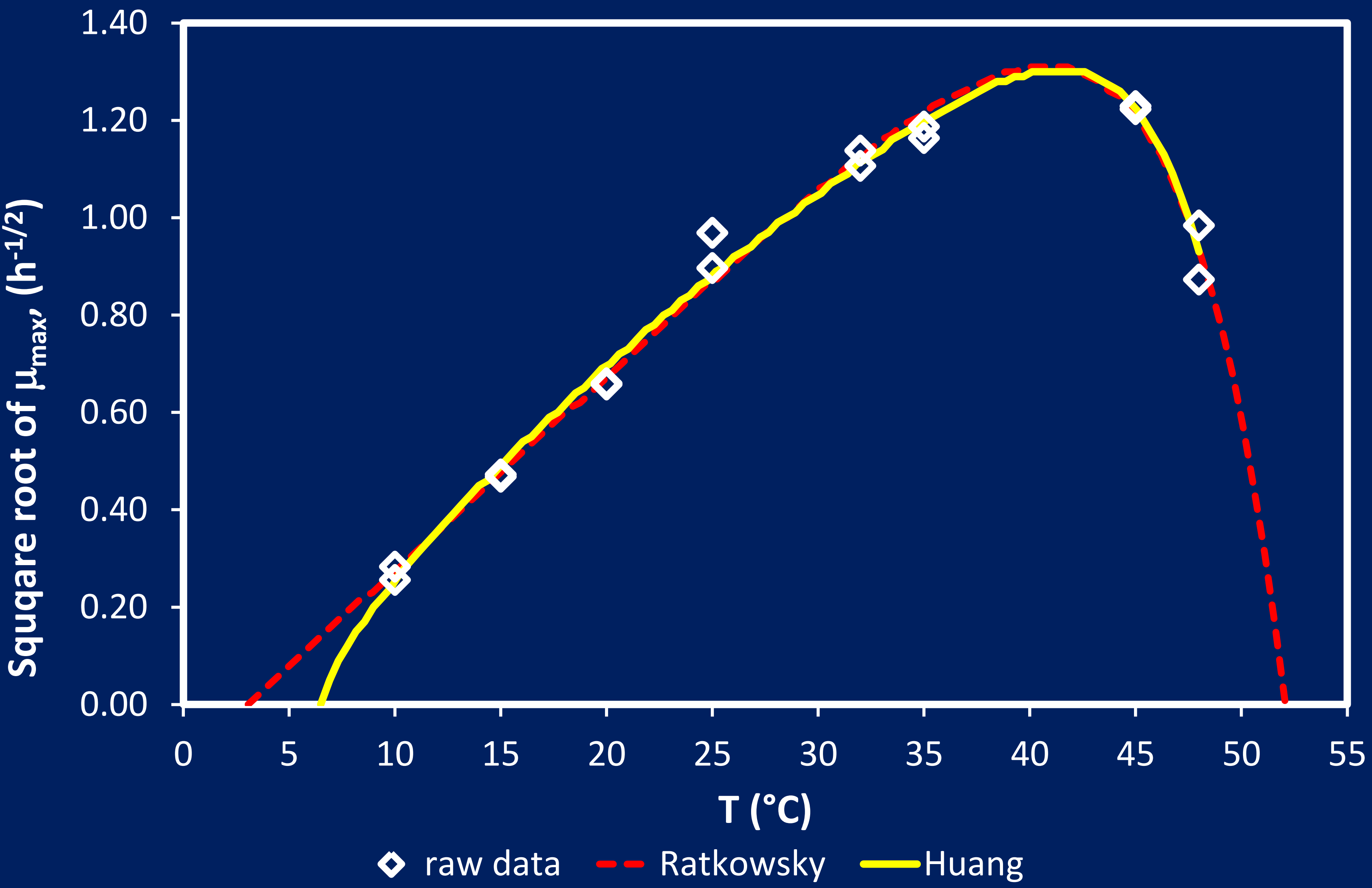
E. coli O157:H7 in beef

Survival curves



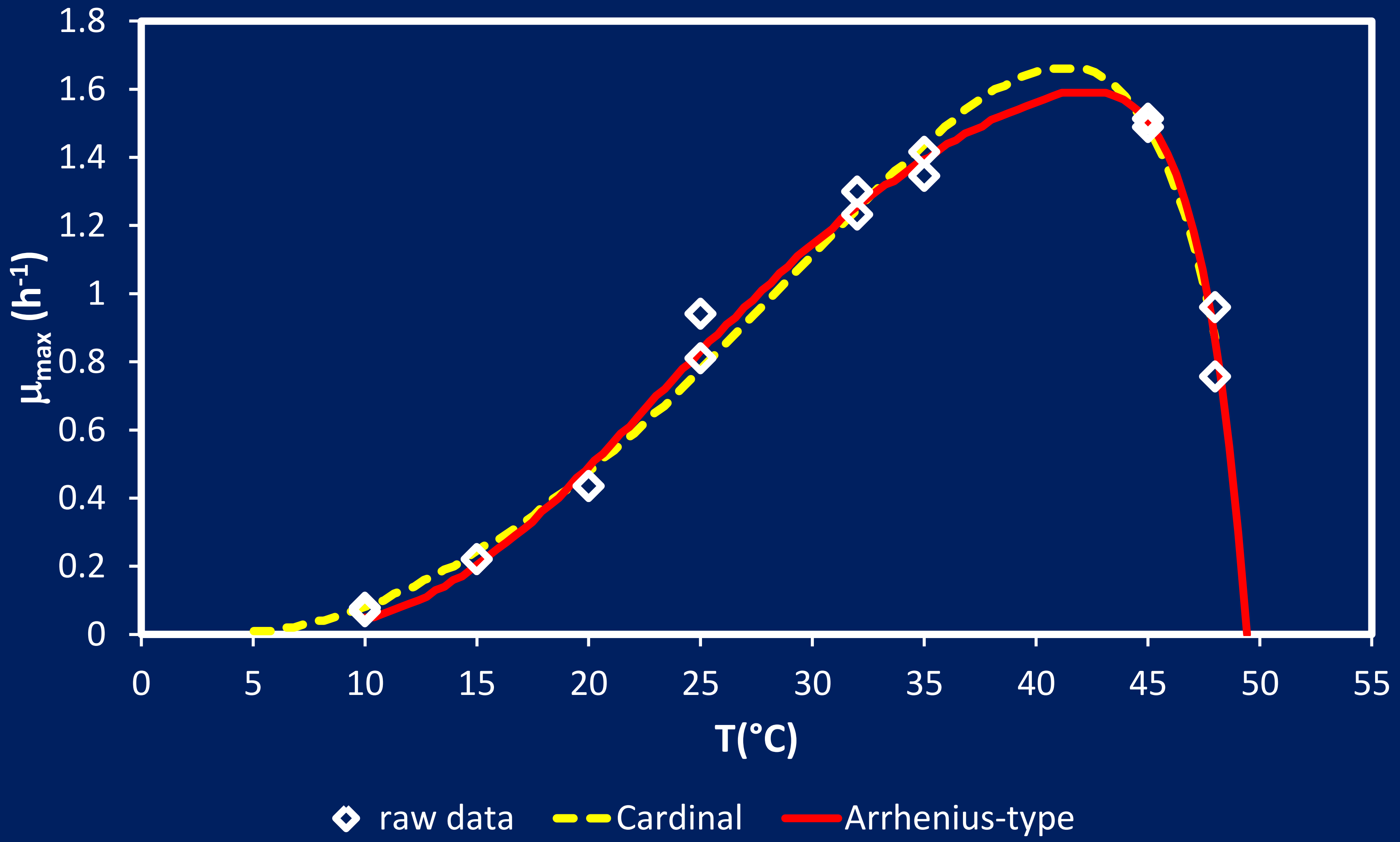
L. monocytogenes in ground beef

Temperature effect – Square-root Models



Cronobacter sakazakii in reconstituted infant formula

Cardinal model/Arrhenius-type model



Cronobacter sakazakii in reconstituted infant formula

Performance of IPMP

Comparison with Standard Statistical Packages

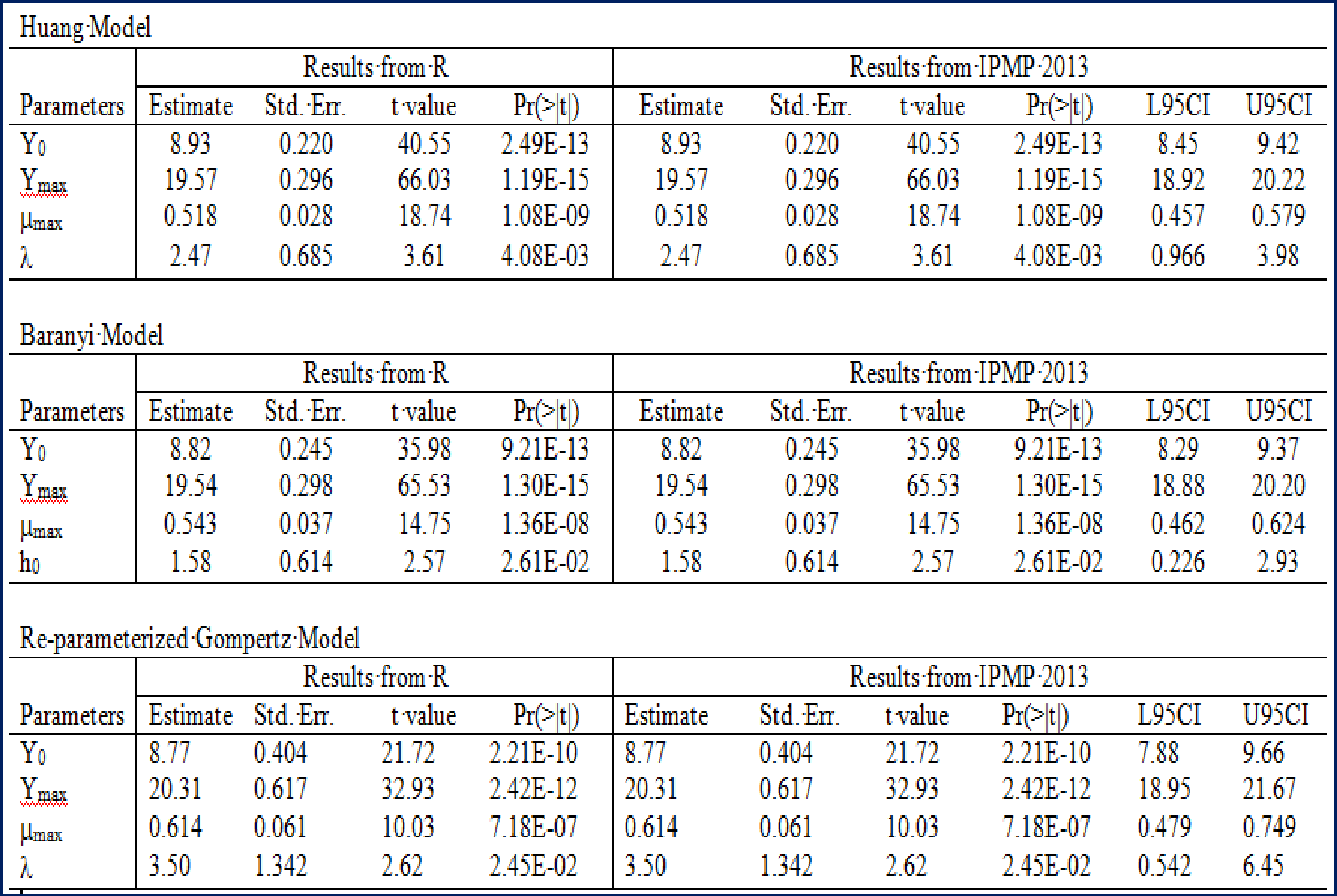
sas

THE
POWER
TO KNOW.

Providing software solutions since 1976

R

Comparison with Standard Statistical Packages



Huang Model

	Results from R				Results from IPMP 2013					
Parameters	Estimate	Std. Err.	t value	Pr(>|t|)	Estimate	Std. Err.	t value	Pr(>|t|)	L95CI	U95CI
Y_0	8.93	0.220	40.55	2.49E-13	8.93	0.220	40.55	2.49E-13	8.45	9.42
Y_{max}	19.57	0.296	66.03	1.19E-15	19.57	0.296	66.03	1.19E-15	18.92	20.22
μ_{max}	0.518	0.028	18.74	1.08E-09	0.518	0.028	18.74	1.08E-09	0.457	0.579
λ	2.47	0.685	3.61	4.08E-03	2.47	0.685	3.61	4.08E-03	0.966	3.98

Baranyi Model

	Results from R				Results from IPMP 2013					
Parameters	Estimate	Std. Err.	t value	Pr(>|t|)	Estimate	Std. Err.	t value	Pr(>|t|)	L95CI	U95CI
Y_0	8.82	0.245	35.98	9.21E-13	8.82	0.245	35.98	9.21E-13	8.29	9.37
Y_{max}	19.54	0.298	65.53	1.30E-15	19.54	0.298	65.53	1.30E-15	18.88	20.20
μ_{max}	0.543	0.037	14.75	1.36E-08	0.543	0.037	14.75	1.36E-08	0.462	0.624
h_0	1.58	0.614	2.57	2.61E-02	1.58	0.614	2.57	2.61E-02	0.226	2.93

Re-parameterized Gompertz Model

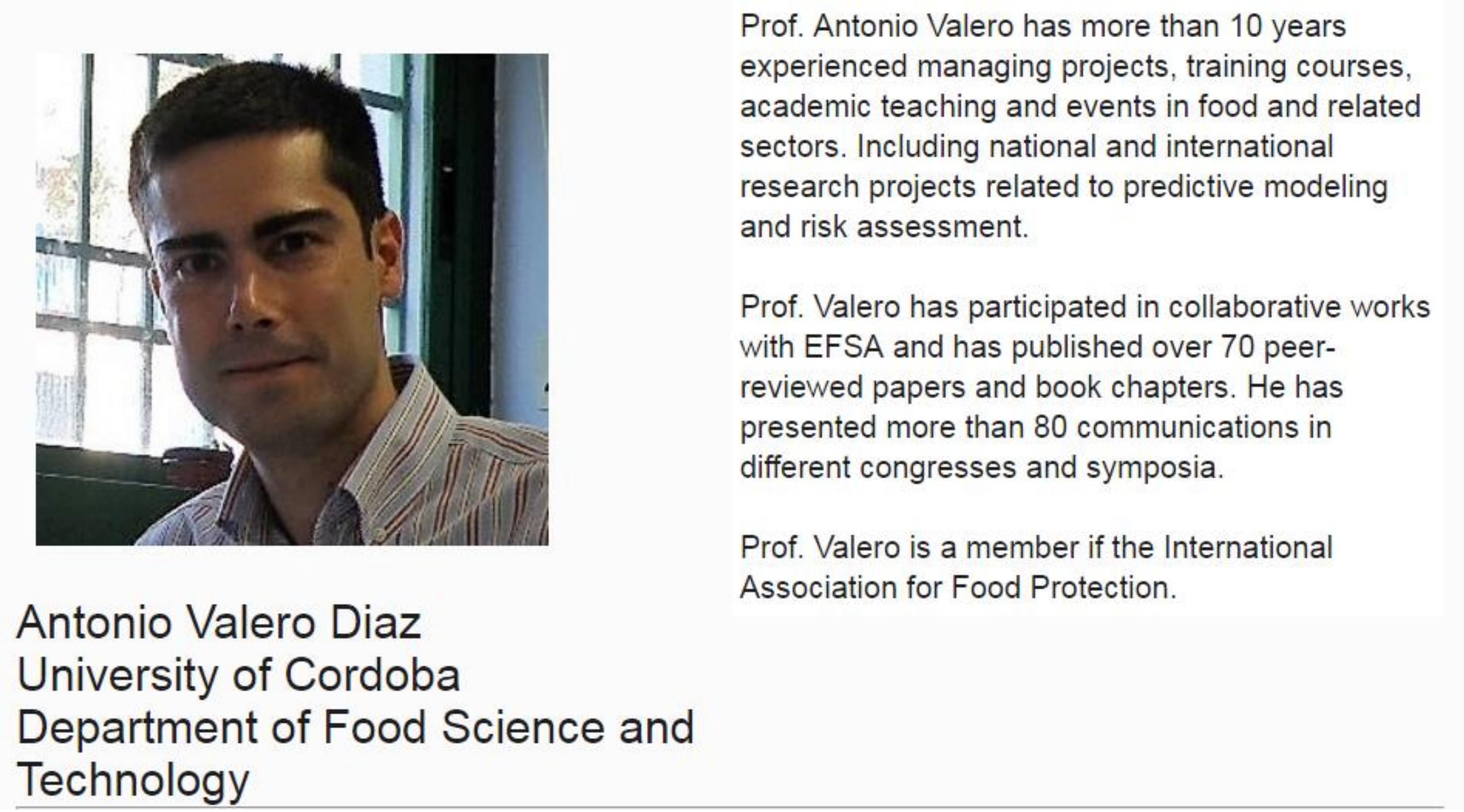
	Results from R				Results from IPMP 2013					
Parameters	Estimate	Std. Err.	t value	Pr(>|t|)	Estimate	Std. Err.	t value	Pr(>|t|)	L95CI	U95CI
Y_0	8.77	0.404	21.72	2.21E-10	8.77	0.404	21.72	2.21E-10	7.88	9.66
Y_{max}	20.31	0.617	32.93	2.42E-12	20.31	0.617	32.93	2.42E-12	18.95	21.67
μ_{max}	0.614	0.061	10.03	7.18E-07	0.614	0.061	10.03	7.18E-07	0.479	0.749
λ	3.50	1.342	2.62	2.45E-02	3.50	1.342	2.62	2.45E-02	0.542	6.45

IPMP for Data Analysis

- Simple data entry
- Choose models that suit your data
- Use graphical interfaces to adjust parameters for faster (almost guaranteed) convergence
- All data analysis and calculation are done behind the scene
- Fast and accurate
- Compare different models for the same set of data
- IPMP has significantly lowered the bar for those who want to work on predictive modeling

Thank you!

Lihan.Huang@ars.usda.gov

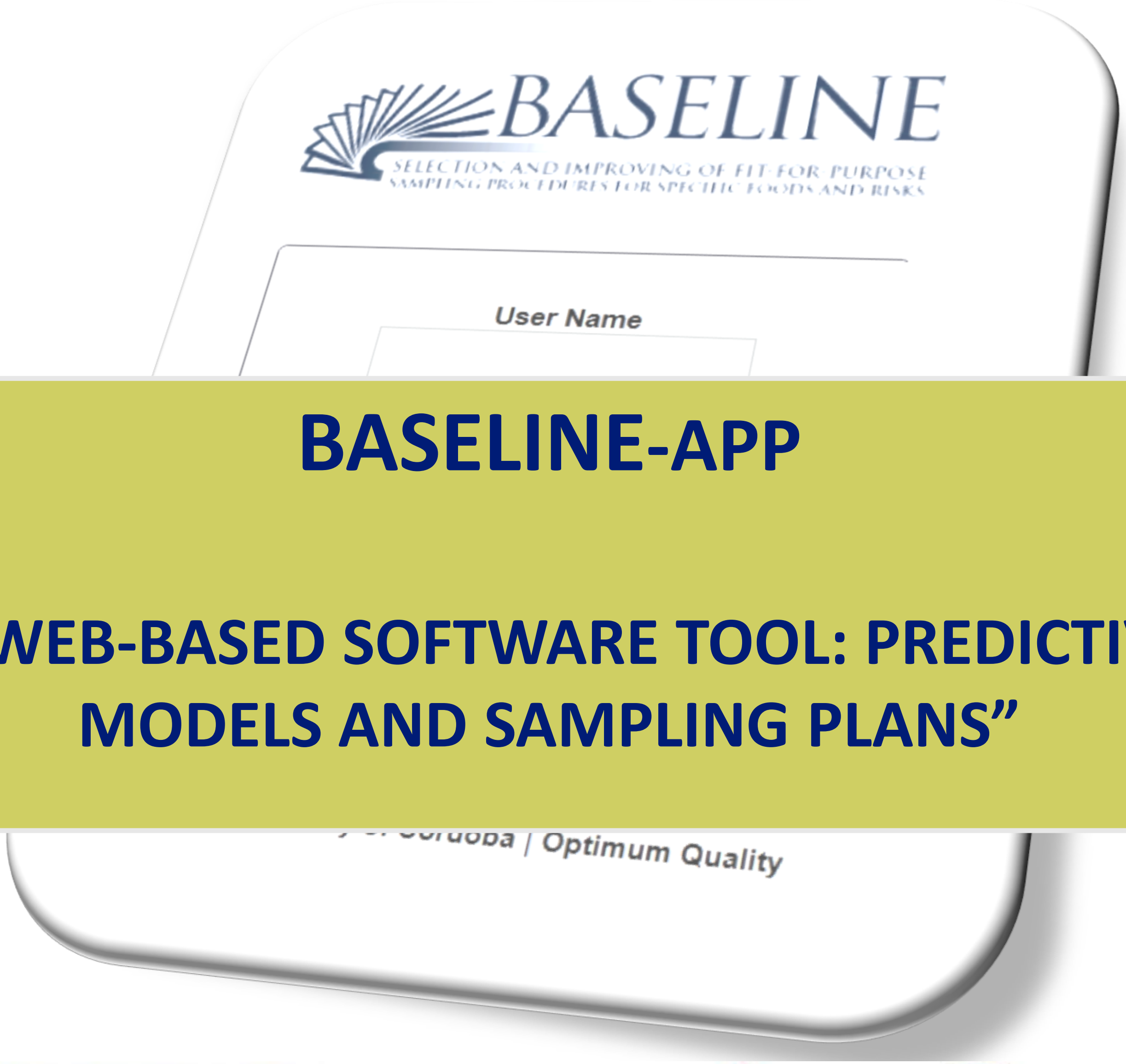


Antonio Valero Diaz
University of Cordoba
Department of Food Science and Technology

Prof. Antonio Valero has more than 10 years experienced managing projects, training courses, academic teaching and events in food and related sectors. Including national and international research projects related to predictive modeling and risk assessment.

Prof. Valero has participated in collaborative works with EFSA and has published over 70 peer-reviewed papers and book chapters. He has presented more than 80 communications in different congresses and symposia.

Prof. Valero is a member if the International Association for Food Protection.



BASELINE

SELECTION AND IMPROVING OF FIT-FOR-PURPOSE SAMPLING PROCEDURES FOR SPECIFIC FOODS AND RISKS

User Name

Cordoba | Optimum Quality

BASELINE-APP

"A WEB-BASED SOFTWARE TOOL: PREDICTIVE MODELS AND SAMPLING PLANS"

Contents

- Software features:
  - Literature review and models development

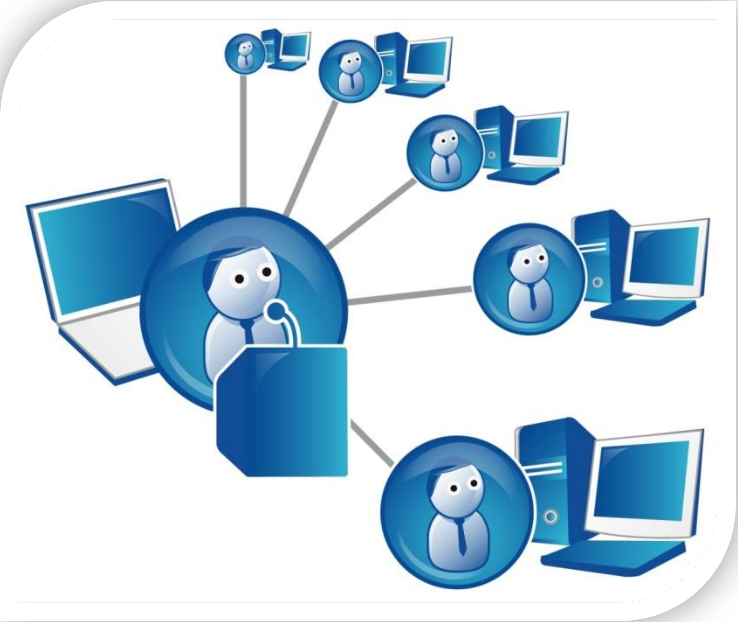
- Predictive models:
  - Growth /inactivation
  - Models validation

- Optimization of sampling plans:
  - Attributes / concentration-based
  - Specific sampling plans

- Derivation of Microbiological Criteria
  - Case studies

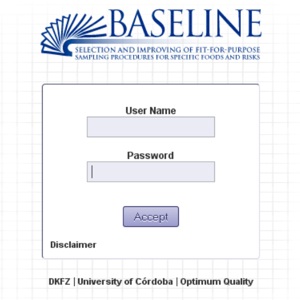
- Conclusions

- Questions



Software features

- **Free access online platform**
- **Graphical user-interface:**
  - **Tables**
  - **Graphs**
- **Flexibility: new models can be incorporated**
- **Comparison and Scenario Analysis studies**


BASELINE

SELECTION AND IMPROVING OF FIT-FOR-PURPOSE SAMPLING PROCEDURES FOR SPECIFIC FOODS AND RISKS

DKFZ | University of Córdoba | Optimum Quality

Free registration is available at www.baselineapp.com

Software features

The software tool allows:

1.Predict growth and inactivation of different microorganisms in different food matrices.

2.Design and apply Sampling plans in different food categories.

Models Module
75 predictive models implemented

\+

Sampling Plans Module

help user to design efficient statistical sampling plans

smallest number of samples necessary

while providing the largest confidence possible to detect a non-conforming lot

Literature review and models development

Model types:

Primary models:

Growth
Gompertz
Baranyi and Roberts (1994)
Three linear phase model

Inactivation
Lineal Model
Weibull

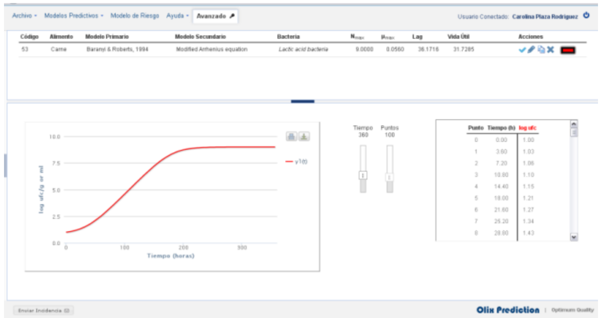
Secondary models
Ratkowsky type
Polynomial

$$\mathrm{Ln}(-\varphi_{max}) = a_0 + a_1(1/T) + a_2(1/pH) + a_3(1/b_w)$$

$$\ln(N(t)) = \ln(N_0) + \mu_{\max}A(t) - \ln\left[1 + \frac{e^{\mu_{\max}A(t)} - 1}{e^{(N_{\max}-N_0)}}\right]$$

$$\sqrt{\mu_{\max}} = b(T-T_{\min})\sqrt{a_w - a_{w\min}}\sqrt{1-10^{pH_{\min}-pH}}.$$

Integration of the mathematical models into easy to use software tools



Código	Alimento	Modelo Primario	Modelo Secundario	Bacteria	N_{max}	μ_{max}	Lag	Vida Útil	Acciones
53	Carne	Baranyi & Roberts, 1994	Modified Arrhenius equation	*Lactic acid bacteria*	9.0000	0.0560	36.1716	31.7285	✓ ✎ ✕

Punto	Tiempo (h)	log ufc
0	0.00	1.00
1	3.60	1.03
2	7.20	1.06
3	10.80	1.10
4	14.40	1.15
5	18.00	1.21
6	21.60	1.27
7	25.20	1.34
8	28.80	1.43

Literature review and models development

1. Identification of food matrices

Seafood

Plant products

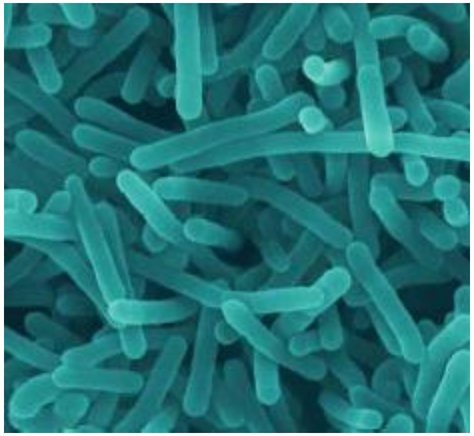
Egg / egg products

Milk / dairy products

Meat products

Literature review and models development

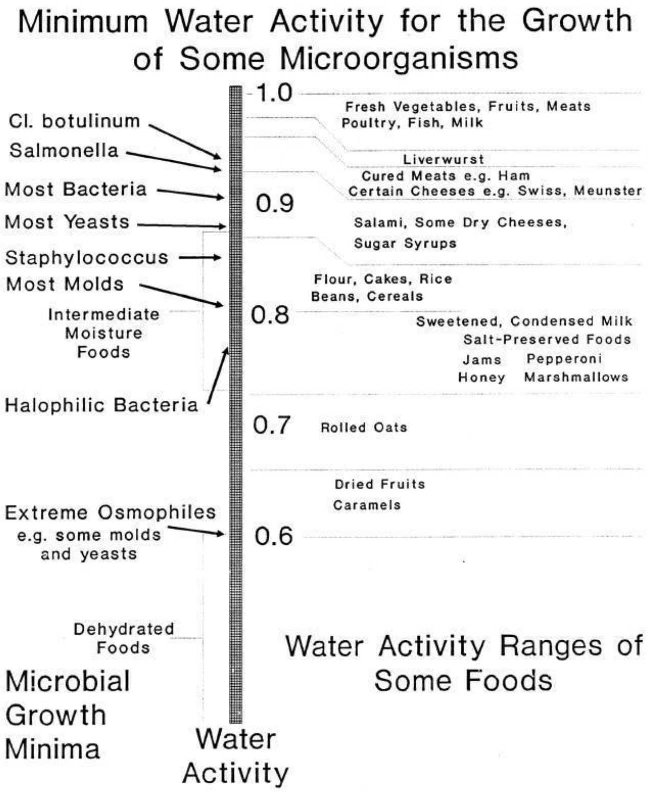
2. Identification of pathogens

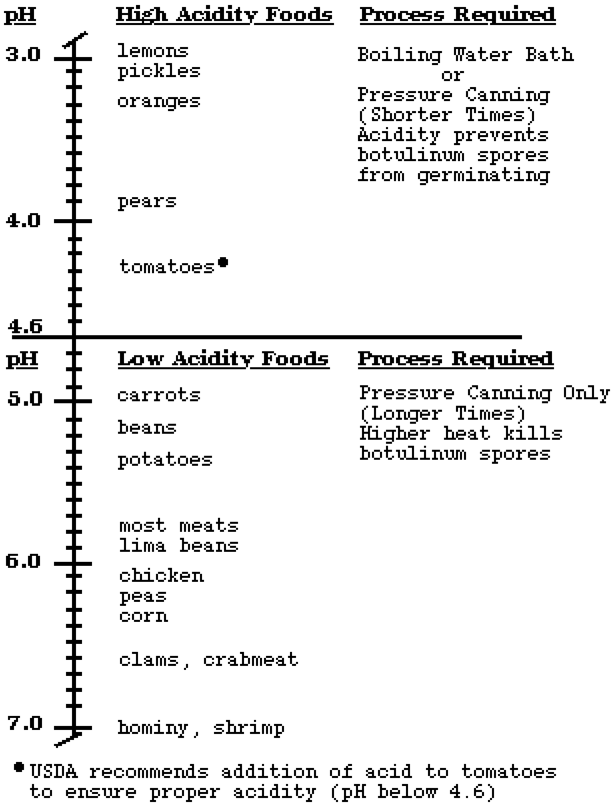


Vibrio parahaemolyticus
Listeria monocytogenes
VTEC
Campylobacter
Salmonella

Literature review and models development

3. Identification of specific environmental conditions





Literature review and models development

4. Literature review of available predictive models


International Journal of Food Microbiology 141 (2010) 137–150

Contents lists available at ScienceDirect

International Journal of Food Microbiology

journal homepage: www.elsevier.com/locate/ijfoodmicro

Predicting growth rates and growth boundary of *Listeria monocytogenes* — An international validation study with focus on processed and ready-to-eat meat and seafood

Ole Mejlholm [a], Annemarie Gunvig [b], Claus Borggaard [b], Jesper Blom-Hanssen [b], Lyndal Mellefont [c], Tom Ross [c], Francoise Leroi [d], Tony Else [e], Diana Visser [e], Paw Dalgaard [a,*]

[a] Seafood and Predictive Microbiology, Division of Seafood Research, National Food Institute (DTU Food), Technical University of Denmark, Søltofts Plads, Building 221, DK-2800, Kgs. Lyngby, Denmark
[b] Danish Meat Research Institute (DMRI), Roskilde, Denmark
[c] Tasmanian Institute of Agricultural Research (TIAR), University of Tasmania, Hobart, Tasmania, Australia
[d] Département des Sciences et Techniques Alimentaires Marines, Ifremer, Nantes, France
[e] PURAC biochem b.v., Gorinchem, The Netherlands


Available online at www.sciencedirect.com

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vative Food Science and Emerging Technologies 7 (2006) 152 – 159

Innovative
Food Science
&
Emerging
Technologies

www.elsevier.com/locate/ifset

dictive models of growth of microorganisms in salted
and cured meat products

atarzyna Kajak *, Danuta Kołożyn-Krajewska

University — SGGW, Faculty of Human Nutrition and Consumer Sciences, Warsaw, Poland

Received 11 August 2004; accepted 22 September 2005

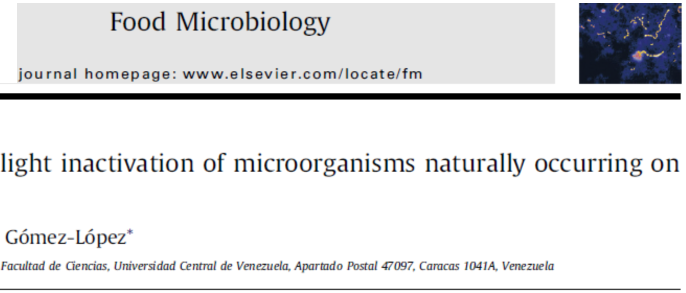

Extreme Heat Resistance of Food Borne Pathogens *Campylobacter jejuni, Escherichia coli,* and *Salmonella typhimurium* on Chicken Breast Fillet during Cooking

Aarieke E.I. de Jong,[1,2] Esther D. van Asselt,[1,3] Marcel H. Zwietering,[4] Maarten J. Nauta,[1,5] and Rob de Jonge[1]

[1] Laboratory for Zoonoses and Environmental Microbiology, National Institute for Public Health and the Environment (RIVM), 3720 BA Bilthoven, The Netherlands
[2] Division Consumer and Safety, New Food and Consumer Product Safety Authority (nVWA), 1018 BK Amsterdam, The Netherlands
[3] Rikilt, Institute of Food Safety, 6700 AE Wageningen, The Netherlands
[4] Laboratory of Food Microbiology, Wageningen University, 6700 EV Wageningen, The Netherlands
[5] National Food Institute, Technical University of Denmark, 1790 Copenhagen V, Denmark

Correspondence should be addressed to Aarieke E.I. de Jong, aarieke.de.jong@vwa.nl

Received 9 August 2011; Accepted 21 October 2011


Food Microbiology

journal homepage: www.elsevier.com/locate/fm

eling the pulsed light inactivation of microorganisms naturally occurring on
table substrates

na Izquier, Vicente M. Gómez-López*

de Ciencia y Tecnología de Alimentos, Facultad de Ciencias, Universidad Central de Venezuela, Apartado Postal 47097, Caracas 1041A, Venezuela

Literature review and models development

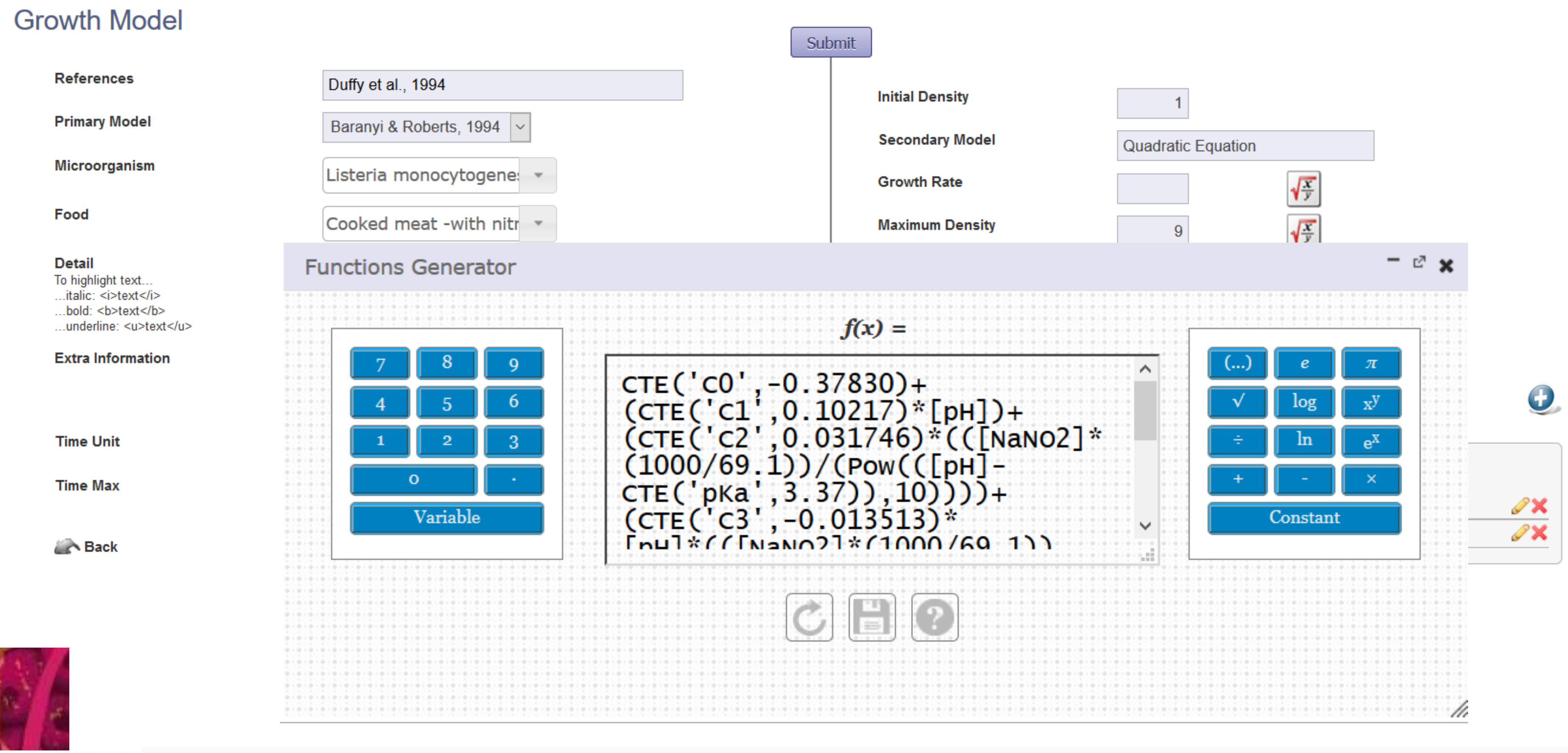
4. Literature review of available predictive models

Electronic library catalogues:
ScienceDirect
Wiley online library
Pubmed
Springer
Revicien
Academic google
Grey literature

More than 100 scientific references meeting the proposed requirements were analyzed.
Selection criteria were previously defined.

Literature review and models development

5. Implementation of selected predictive models in the software



Growth Model

References: Duffy et al., 1994

Primary Model: Baranyi & Roberts, 1994

Microorganism: Listeria monocytogene

Food: Cooked meat -with nitr

Detail

To highlight text...
...italic: <i>text</i>
...bold: text
...underline: <u>text</u>

Extra Information

Time Unit

Time Max

Initial Density: 1

Secondary Model: Quadratic Equation

Growth Rate:

Maximum Density: 9

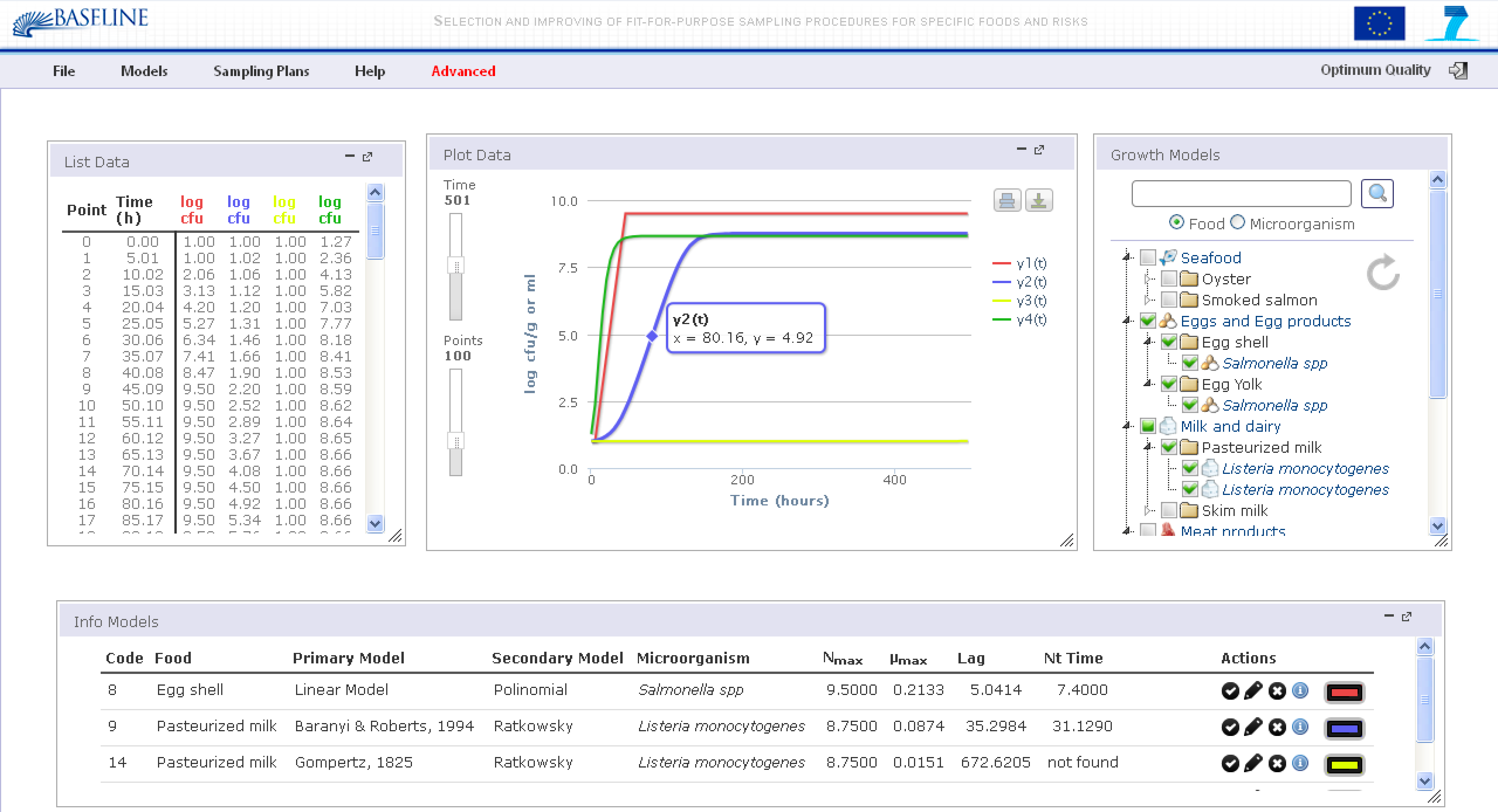
Functions Generator

f(x) =

```
CTE('c0',-0.37830)+
(CTE('c1',0.10217)*[pH])+
(CTE('c2',0.031746)*(([NaNO2]*
(1000/69.1))/(Pow(([pH]-
CTE('pKa',3.37)),10))))+
(CTE('c3',-0.013513)*
[pH]*(([NaNO2]*(1000/69.1))
```

Predictive models: growth/inactivation

6. Performance and visualization of predictive models



List Data

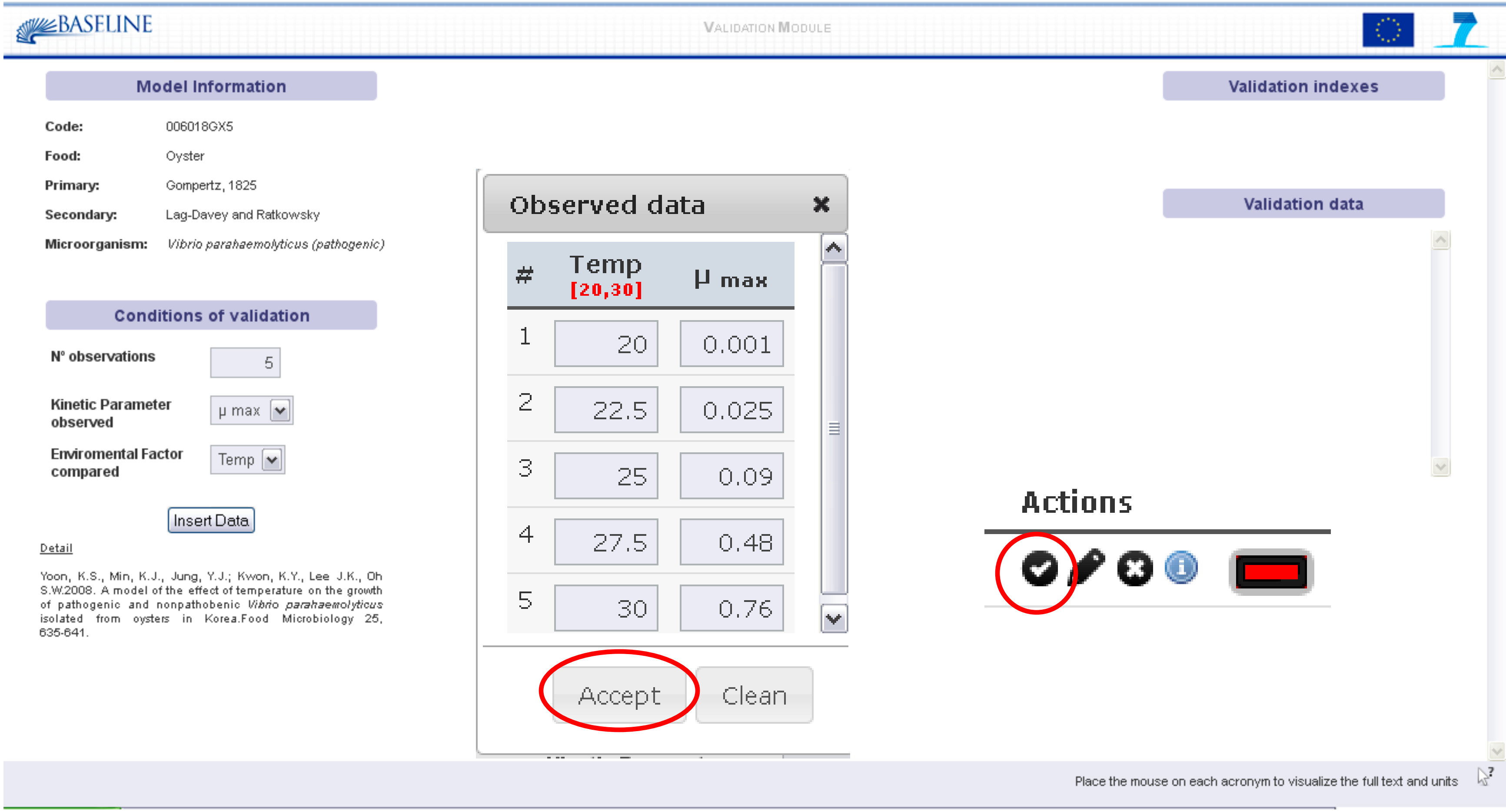
Point	Time (h)	log cfu	log cfu	log cfu	log cfu
0	0.00	1.00	1.00	1.00	1.27
1	5.01	1.00	1.02	1.00	2.36
2	10.02	2.06	1.06	1.00	4.13
3	15.03	3.13	1.12	1.00	5.82
4	20.04	4.20	1.20	1.00	7.03
5	25.05	5.27	1.31	1.00	7.77
6	30.06	6.34	1.46	1.00	8.18
7	35.07	7.41	1.66	1.00	8.41
8	40.08	8.47	1.90	1.00	8.53
9	45.09	9.50	2.20	1.00	8.59
10	50.10	9.50	2.52	1.00	8.62
11	55.11	9.50	2.89	1.00	8.64
12	60.12	9.50	3.27	1.00	8.65
13	65.13	9.50	3.67	1.00	8.66
14	70.14	9.50	4.08	1.00	8.66
15	75.15	9.50	4.50	1.00	8.66
16	80.16	9.50	4.92	1.00	8.66
17	85.17	9.50	5.34	1.00	8.66

● Food ○ Microorganism

- ☐ Seafood
  - ☐ Oyster
  - ☐ Smoked salmon
- ☑ Eggs and Egg products
  - ☑ Egg shell
    - ☑ *Salmonella spp*
  - ☑ Egg Yolk
    - ☑ *Salmonella spp*
- ☑ Milk and dairy
  - ☑ Pasteurized milk
    - ☑ *Listeria monocytogenes*
    - ☑ *Listeria monocytogenes*
  - ☐ Skim milk
- ☐ Meat products

Code	Food	Primary Model	Secondary Model	Microorganism	N_{max}	μ_{max}	Lag	Nt Time	Actions
8	Egg shell	Linear Model	Polinomial	*Salmonella spp*	9.5000	0.2133	5.0414	7.4000	🟥
9	Pasteurized milk	Baranyi & Roberts, 1994	Ratkowsky	*Listeria monocytogenes*	8.7500	0.0874	35.2984	31.1290	🟦
14	Pasteurized milk	Gompertz, 1825	Ratkowsky	*Listeria monocytogenes*	8.7500	0.0151	672.6205	not found	🟨

Models validation



Model Information

Code: 006018GX5
Food: Oyster
Primary: Gompertz, 1825
Secondary: Lag-Davey and Ratkowsky
Microorganism: *Vibrio parahaemolyticus (pathogenic)*

Conditions of validation

Nº observations: 5
Kinetic Parameter observed: μ max
Enviromental Factor compared: Temp

Detail

Yoon, K.S., Min, K.J., Jung, Y.J.; Kwon, K.Y., Lee J.K., Oh S.W.2008. A model of the effect of temperature on the growth of pathogenic and nonpathobenic *Vibrio parahaemolyticus* isolated from oysters in Korea.Food Microbiology 25, 635-641.

Observed data

#	Temp [20,30]	μ max
1	20	0.001
2	22.5	0.025
3	25	0.09
4	27.5	0.48
5	30	0.76

Validation indexes

Validation data

Actions

Place the mouse on each acronym to visualize the full text and units

Models validation

Model Information

Code: 006018GX5

Food: Oyster

Primary: Gompertz, 1825

Secondary: Lag-Davey and Ratkowsky

Microorganism: *Vibrio parahaemolyticus (pathogenic)*

Conditions of validation

Nº observations 5

Kinetic Parameter observed μ max

Enviromental Factor compared Temp

Edit Data

Detail

Yoon, K.S., Min, K.J., Jung, Y.J.; Kwon, K.Y., Lee J.K., Oh S.W.2008. A model of the effect of temperature on the growth of pathogenic and nonpathobenic *Vibrio parahaemolyticus* isolated from oysters in Korea.Food Microbiology 25, 635-641.

Validation indexes

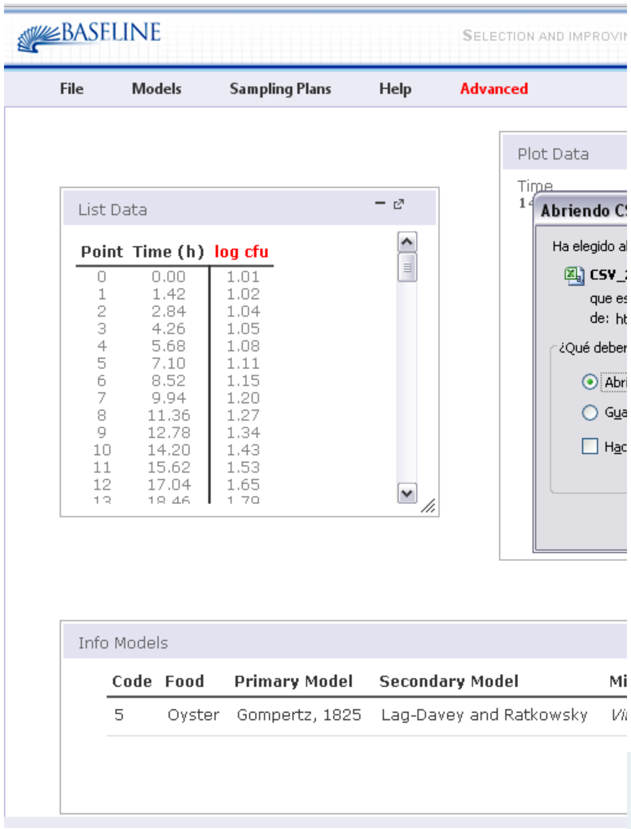
SEP = 25 %
RMSE = 0.03
Bf = 1.19
Af = 1.68

Validation data

Observ.	Predic.
0.001	0
0.025	0.03
0.09	0.16
0.48	0.37
0.76	0.68

Place the mouse on each acronym to visualize the full text and units

Data exportation



List Data

Point	Time (h)	log cfu
0	0.00	1.01
1	1.42	1.02
2	2.84	1.04
3	4.26	1.05
4	5.68	1.08
5	7.10	1.11
6	8.52	1.15
7	9.94	1.20
8	11.36	1.27
9	12.78	1.34
10	14.20	1.43
11	15.62	1.53
12	17.04	1.65

Info Models

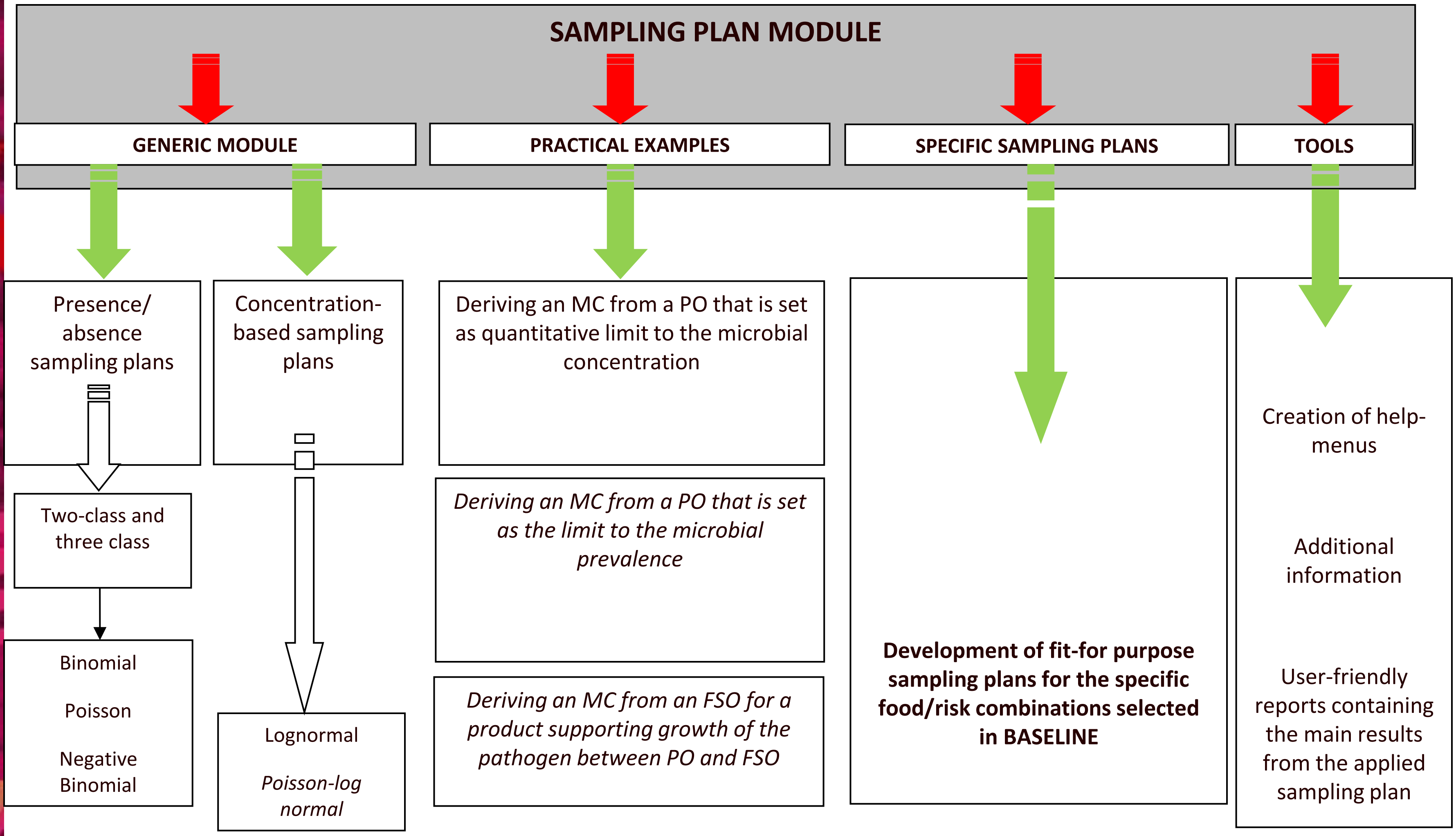
Code	Food	Primary Model	Secondary Model	Mi
5	Oyster	Gompertz, 1825	Lag-Davey and Ratkowsky	*Vi*

Growth Report

ID	Model	Food / Microorganism	N_{max} (log cfu/g)	μ_{max} (log cfu/h)	Lag (hours)
Model 1: 006018GX5	1st: Gompertz, 1825 2nd: Lag-Davey and Ratkowsky	Oyster *Vibrio parahaemolyticus* (pathogenic)	0.159	9	15.538

Conditions of prediction	
Time	133 hours
Model 1	
Initial Concentration	1 log cfu
Enviromental factors	• Temp: 25 °C

The predictive models and simulation algorithms used strictly corresponded to the references described in the software. The authors took precautions to use reliable information and decline all responsibility for errors or deficiencies in the database or software and manual accompanying it. Thus, the interpretation and correct use of the generated information lies with end-user. Sampling schemes generated in this software must be only used for scientific or personnel purposes. A validation is required for official implementation. In some cases expert interpretation by a food microbiologist may be required.



SAMPLING PLAN MODULE

GENERIC MODULE

Presence/ absence sampling plans

Two-class and three class

Binomial

Poisson

Negative Binomial

Concentration-based sampling plans

Lognormal

Poisson-log normal

PRACTICAL EXAMPLES

Deriving an MC from a PO that is set as quantitative limit to the microbial concentration

Deriving an MC from a PO that is set as the limit to the microbial prevalence

Deriving an MC from an FSO for a product supporting growth of the pathogen between PO and FSO

SPECIFIC SAMPLING PLANS

Development of fit-for purpose sampling plans for the specific food/risk combinations selected in BASELINE

TOOLS

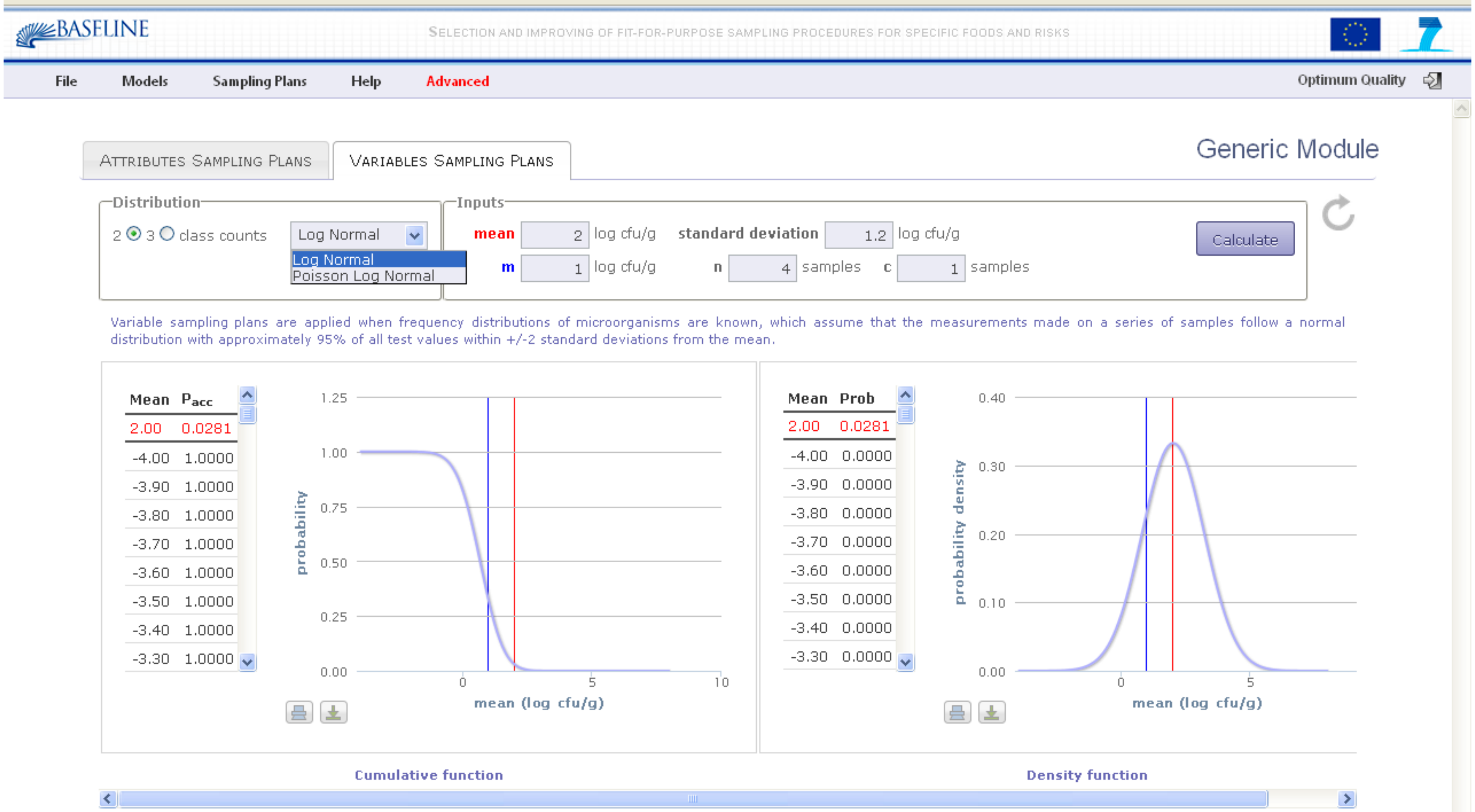
Creation of help-menus

Additional information

User-friendly reports containing the main results from the applied sampling plan

Optimization of sampling plans

- **Generic module:**
  - **Attributes: Binomial, Poisson, Negative Binomial, Trinomial distributions**
  - **Concentration-based: Log Normal, Poisson-log normal distributions**



Distribution

2 ● 3 ○ class counts — Log Normal

Log Normal
Poisson Log Normal

Inputs

mean 2 log cfu/g **standard deviation** 1.2 log cfu/g

m 1 log cfu/g **n** 4 samples **c** 1 samples

Variable sampling plans are applied when frequency distributions of microorganisms are known, which assume that the measurements made on a series of samples follow a normal distribution with approximately 95% of all test values within +/-2 standard deviations from the mean.

Mean	P_{acc}
2.00	0.0281
-4.00	1.0000
-3.90	1.0000
-3.80	1.0000
-3.70	1.0000
-3.60	1.0000
-3.50	1.0000
-3.40	1.0000
-3.30	1.0000

Mean	Prob
2.00	0.0281
-4.00	0.0000
-3.90	0.0000
-3.80	0.0000
-3.70	0.0000
-3.60	0.0000
-3.50	0.0000
-3.40	0.0000
-3.30	0.0000

Case studies

Derivation of Microbiological Criteria from established Performance Objectives

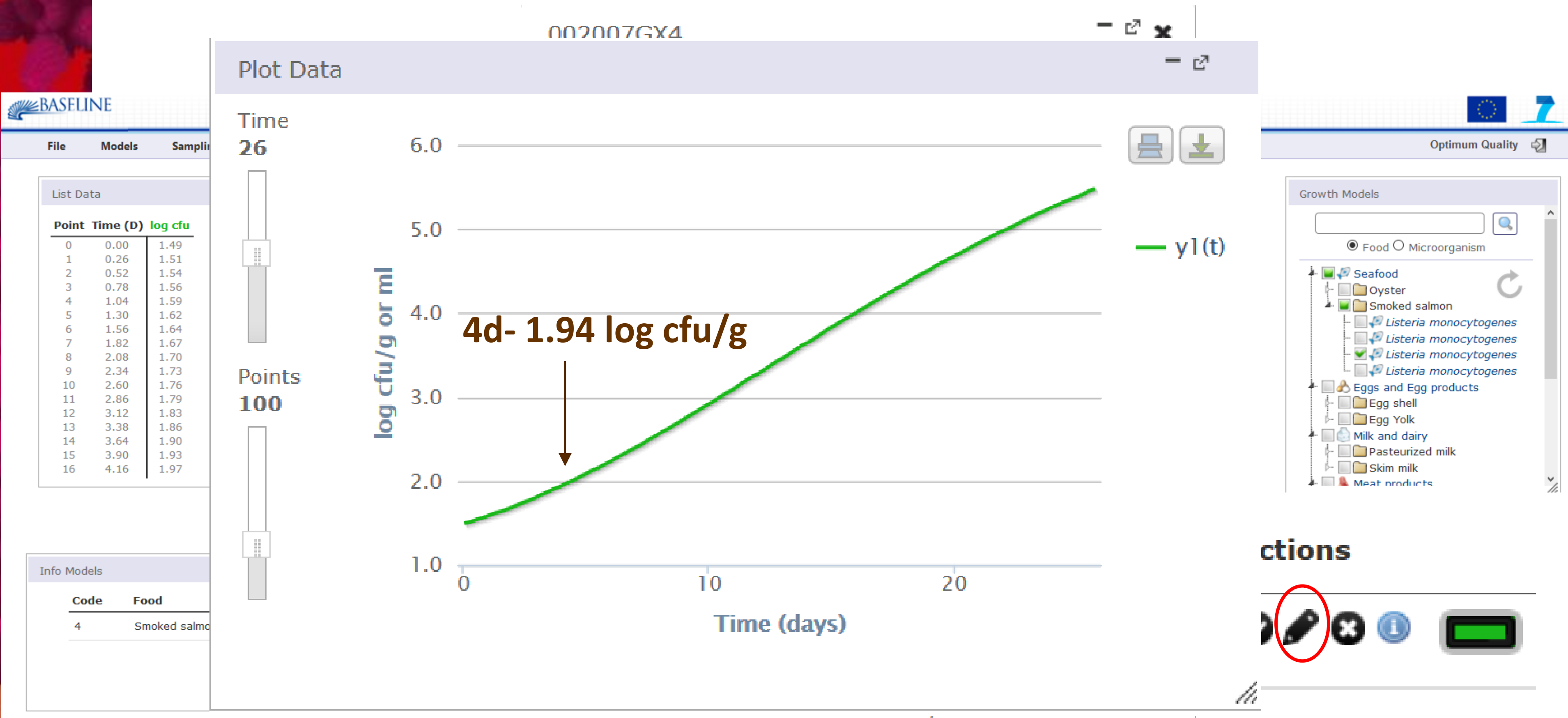
Case 1. Aplication of a PO / MC for concentration-based sampling plans

Smoked salmon contamination by *L. monocytogenes*.
Initial contamination of the product just after packaging: 1.5 log cfu/g
Storage conditions: 96 h at 4° C
Product formulation: 2ppm phenol + 3% salt

PO = P (log cfu/g >3) < 5 % of the samples comprising the lot

Which MC should be applied in order to comply with the selected PO?

Case studies



4d- 1.94 log cfu/g

List Data

Point	Time (D)	log cfu
0	0.00	1.49
1	0.26	1.51
2	0.52	1.54
3	0.78	1.56
4	1.04	1.59
5	1.30	1.62
6	1.56	1.64
7	1.82	1.67
8	2.08	1.70
9	2.34	1.73
10	2.60	1.76
11	2.86	1.79
12	3.12	1.83
13	3.38	1.86
14	3.64	1.90
15	3.90	1.93
16	4.16	1.97

Info Models

Code	Food
4	Smoked salmo

● Food ○ Microorganism

- ☑ Seafood
  - ☐ Oyster
  - ☑ Smoked salmon
    - ☐ *Listeria monocytogenes*
    - ☐ *Listeria monocytogenes*
    - ☑ *Listeria monocytogenes*
    - ☐ *Listeria monocytogenes*
- ☐ Eggs and Egg products
  - ☐ Egg shell
  - ☐ Egg Yolk
- ☐ Milk and dairy
  - ☐ Pasteurized milk
  - ☐ Skim milk
- ☐ Meat products

Journal of Food 106, 159-168.

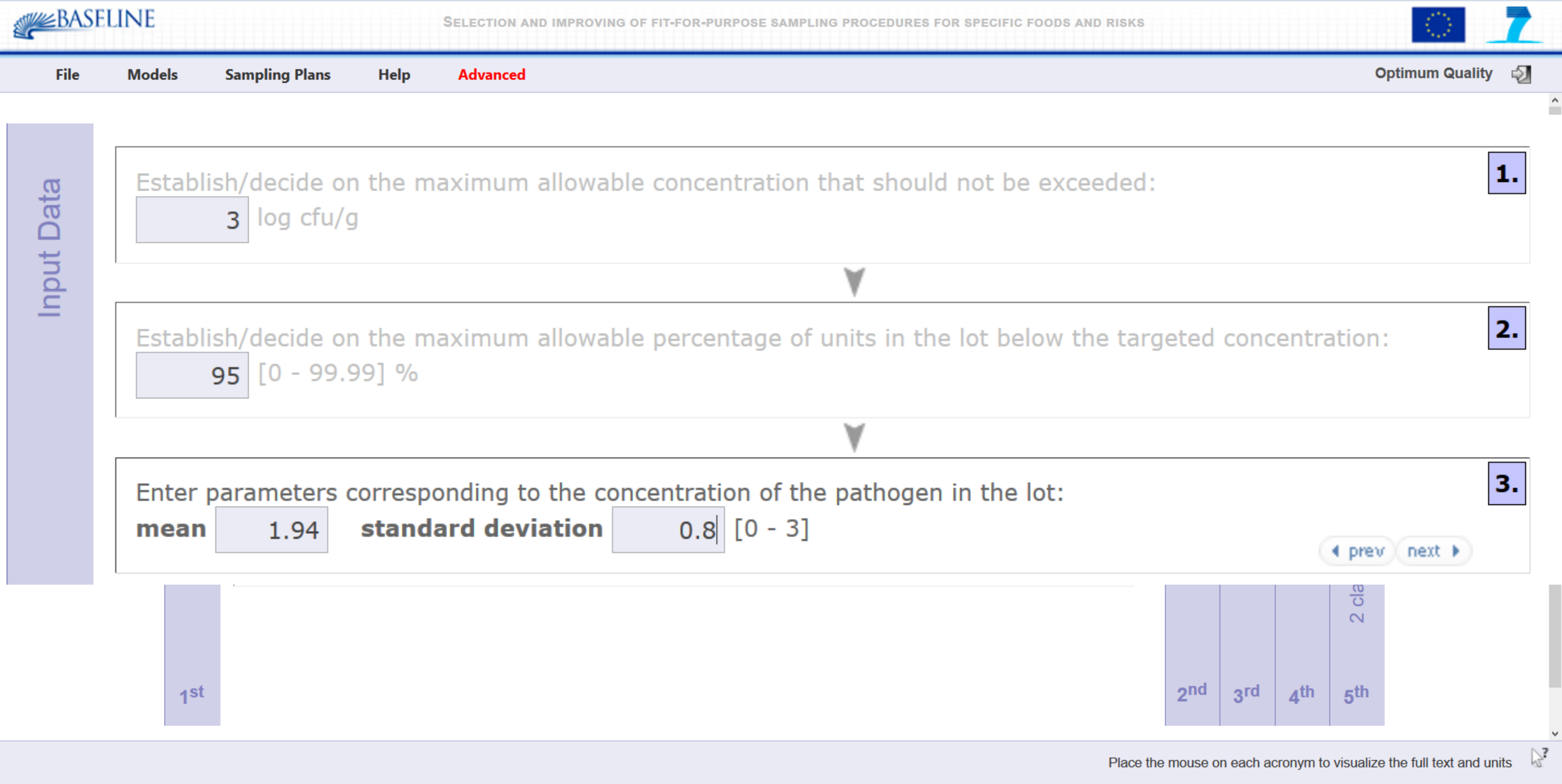
Case studies

L. monocytogenes is able to grow up to 1.94 log cfu/g at the end of storage
We consider a standard deviation of the lot = 0.8 log cfu/g (solid food contamination assumed)

Distribution of *L. monocytogenes* ~ lognormal (1.94, 0.8)

PO = P (log cfu/g >3) < 5 % of the samples comprising the lot

Case studies



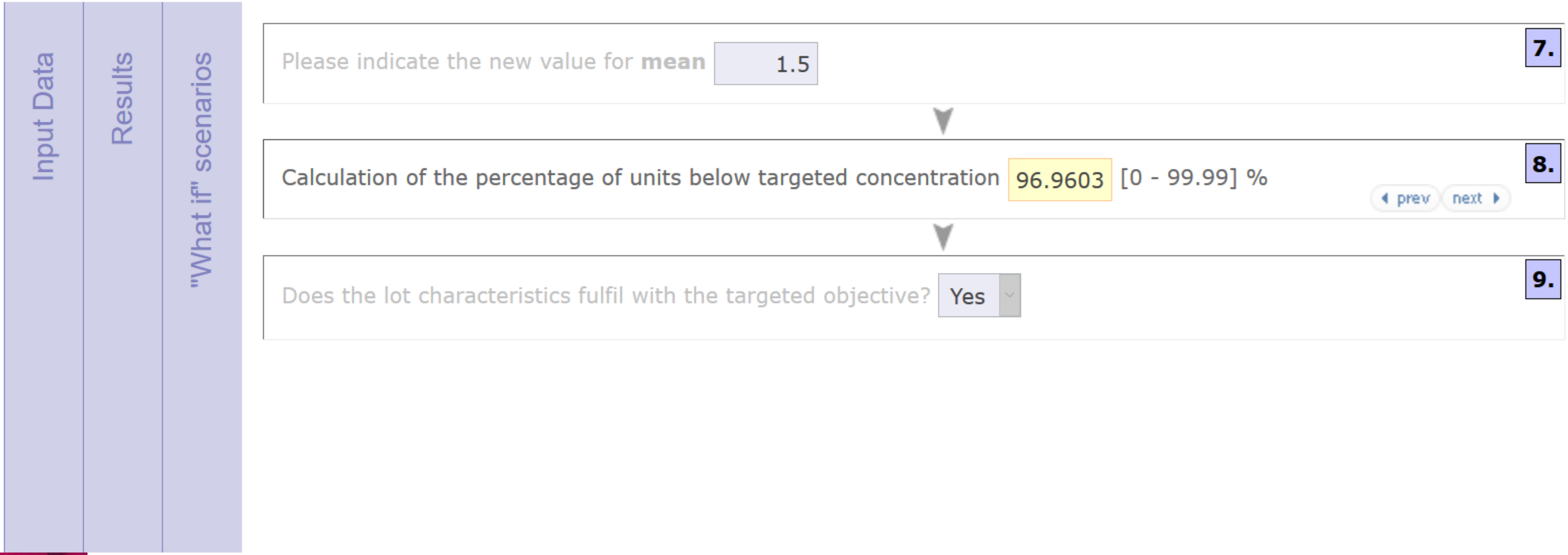
1. Establish/decide on the maximum allowable concentration that should not be exceeded: 3 log cfu/g

2. Establish/decide on the maximum allowable percentage of units in the lot below the targeted concentration: 95 [0 - 99.99] %

3. Enter parameters corresponding to the concentration of the pathogen in the lot: **mean** 1.94 **standard deviation** 0.8 [0 - 3]

Place the mouse on each acronym to visualize the full text and units

Case studies



7. Please indicate the new value for **mean** 1.5

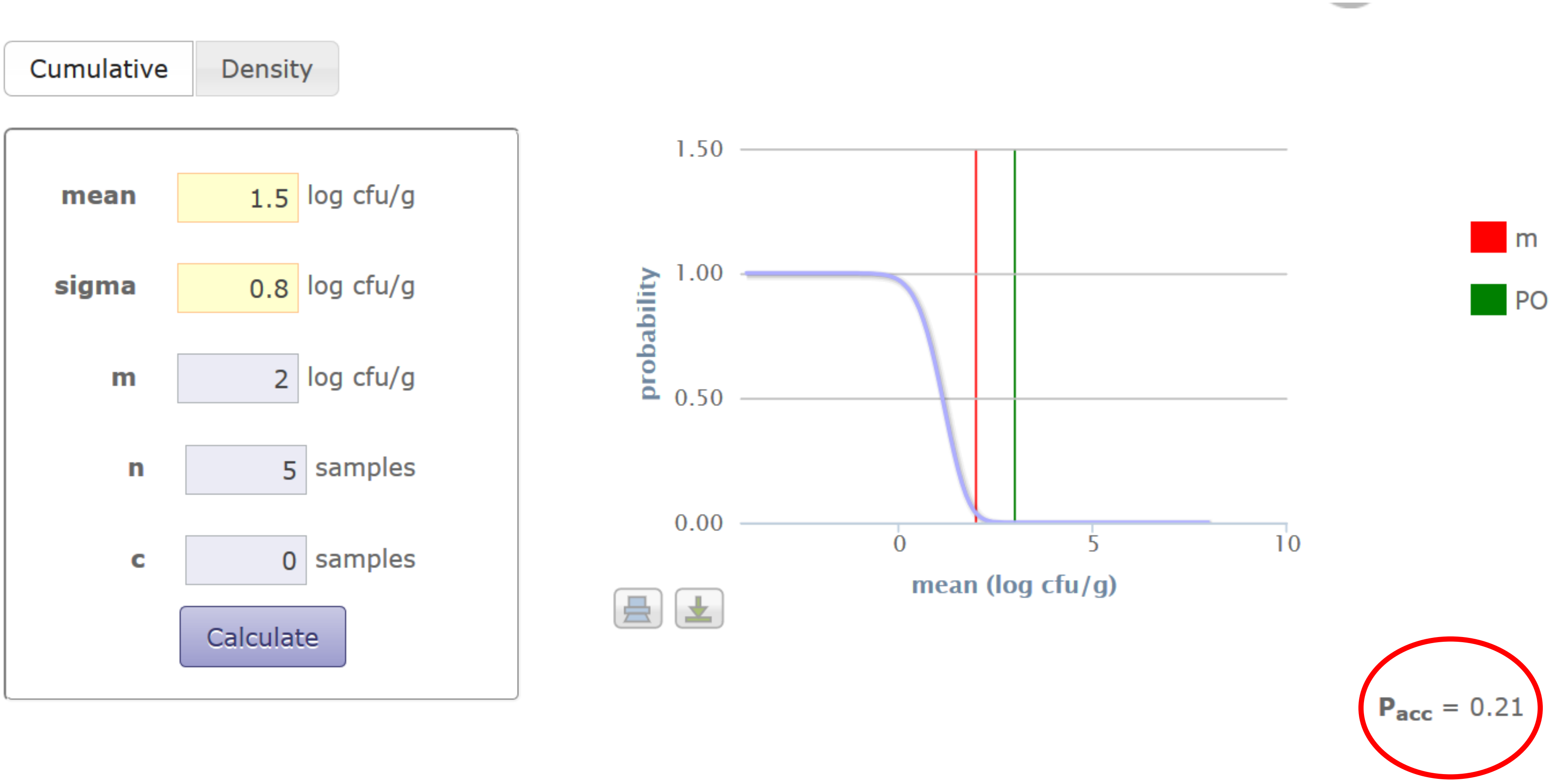
8. Calculation of the percentage of units below targeted concentration 96.9603 [0 - 99.99] %

9. Does the lot characteristics fulfil with the targeted objective? Yes

Case studies

2 class Sampling Plan (Variables)

5th



mean 1.5 log cfu/g

sigma 0.8 log cfu/g

m 2 log cfu/g

n 5 samples

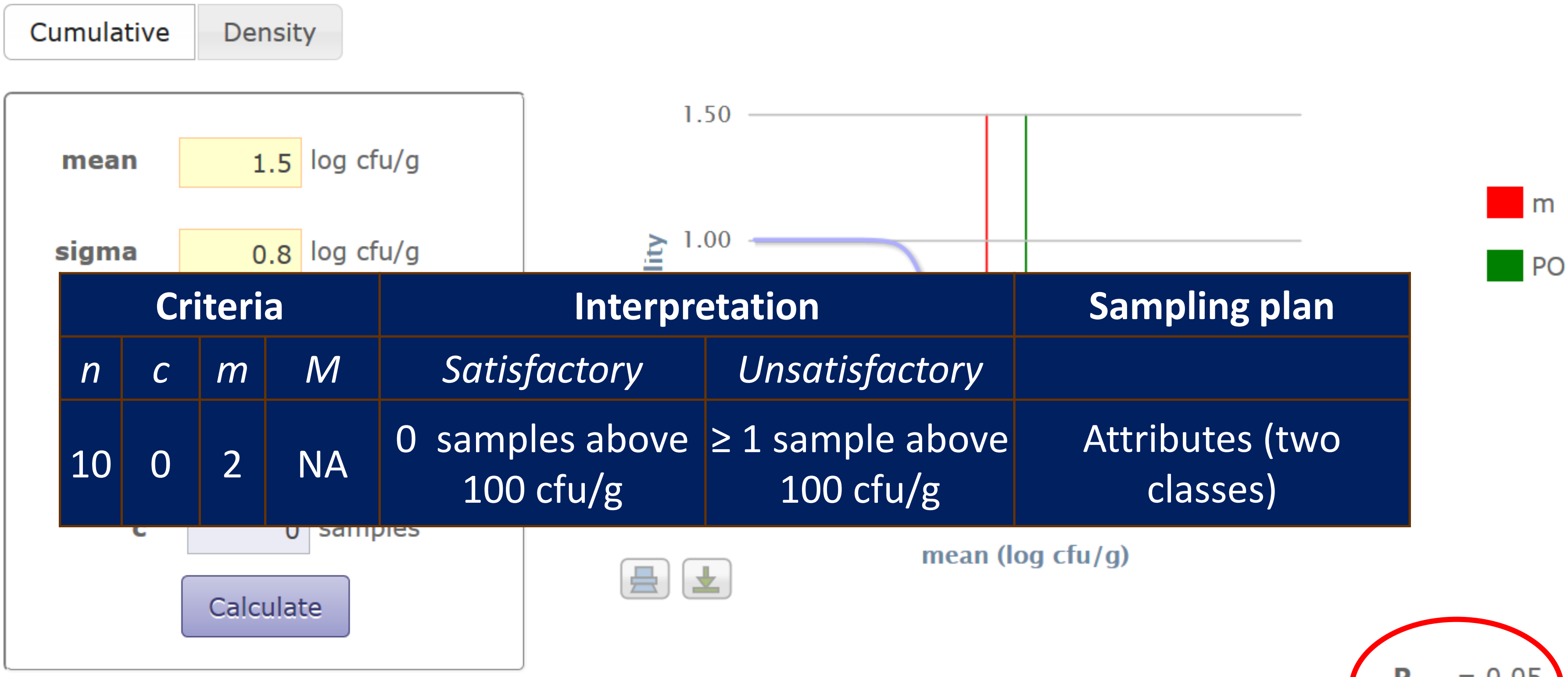
c 0 samples

P_{acc} = 0.21

Case studies

2 class Sampling Plan (Variables)

5th



mean 1.5 log cfu/g

sigma 0.8 log cfu/g

c 0 samples

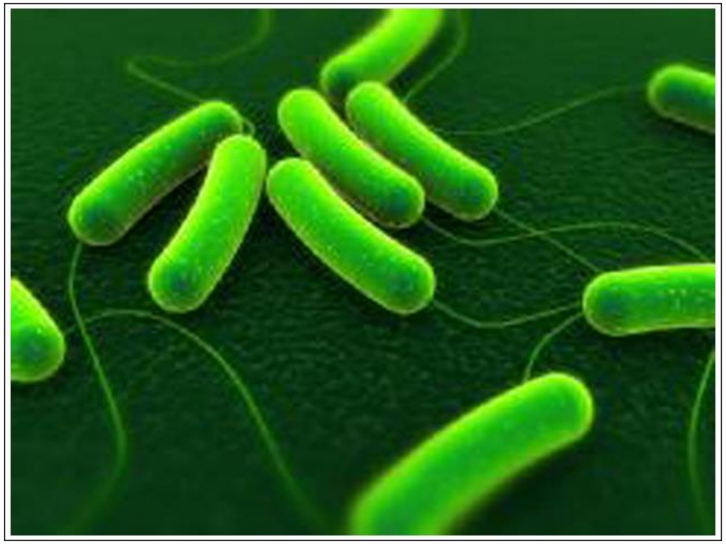
Criteria				Interpretation		Sampling plan
n	*c*	*m*	*M*	*Satisfactory*	*Unsatisfactory*	
10	0	2	NA	0 samples above 100 cfu/g	≥ 1 sample above 100 cfu/g	Attributes (two classes)

P_{acc} = 0.05

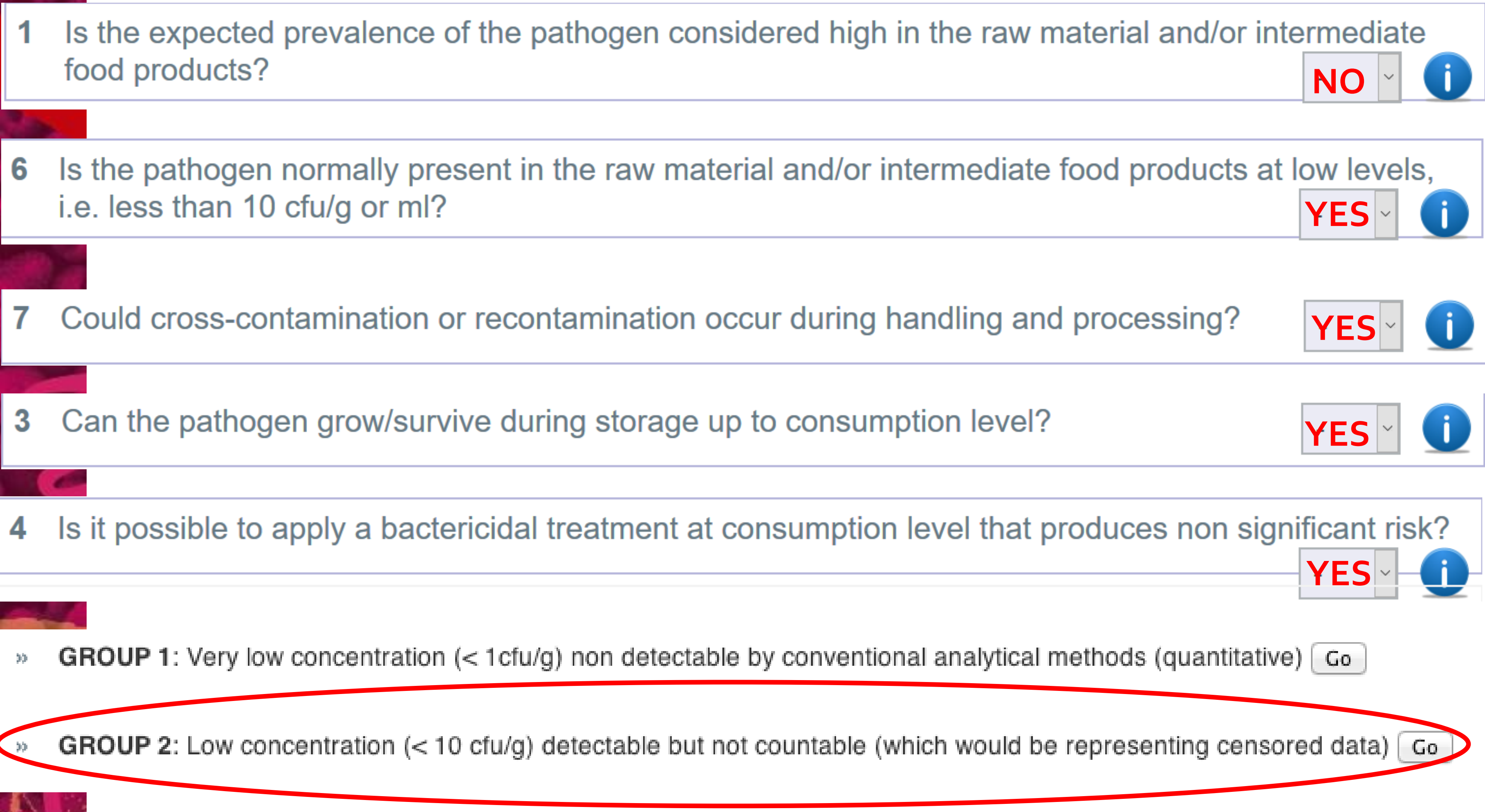
Derivation of Microbiological Criteria from established Performance Objectives

Case 2. Decision support tools for derivation of MC in foods.
Application to *Escherichia coli* O157:H7 in leafy greens

- Knowledge of expected prevalence /concentration in the studied food product
- Processing conditions
- Expected behaviour throughout the production chain
- Expected consumer handling and storage



Case studies



1 Is the expected prevalence of the pathogen considered high in the raw material and/or intermediate food products? NO

6 Is the pathogen normally present in the raw material and/or intermediate food products at low levels, i.e. less than 10 cfu/g or ml? YES

7 Could cross-contamination or recontamination occur during handling and processing? YES

3 Can the pathogen grow/survive during storage up to consumption level? YES

4 Is it possible to apply a bactericidal treatment at consumption level that produces non significant risk? YES

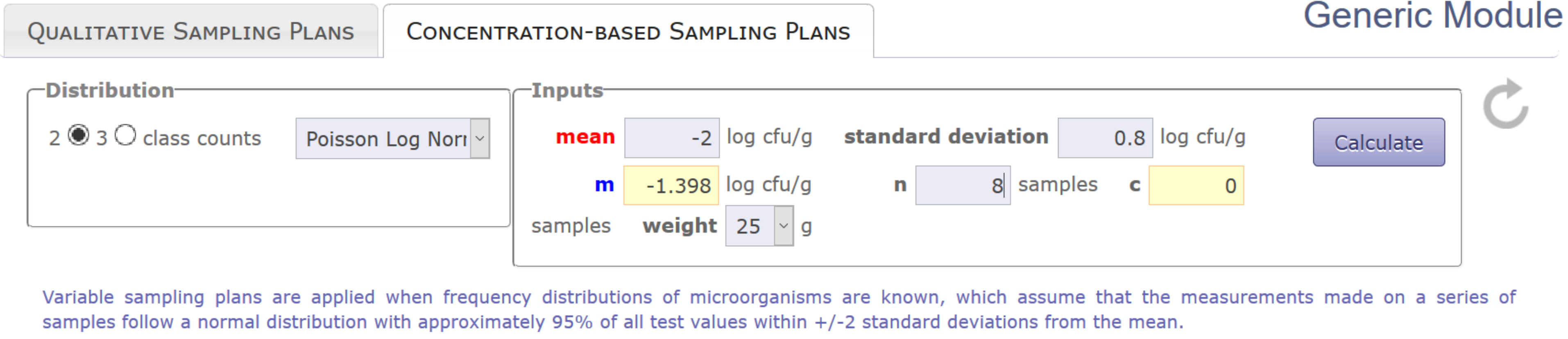
» **GROUP 1**: Very low concentration (< 1cfu/g) non detectable by conventional analytical methods (quantitative)

» **GROUP 2**: Low concentration (< 10 cfu/g) detectable but not countable (which would be representing censored data)

Case studies

Assumed mean concentration = 1 cell/100g = - 2 $\log_{10}$ cfu/g
Standard deviation = 0.8 $\log_{10}$ cfu/g

Poisson-log normal distribution (-2; o.8) $\log_{10}$ cfu/g
Non detectable levels by conventional techniques



Distribution

2 ● 3 ○ class counts — Poisson Log Nor

Inputs

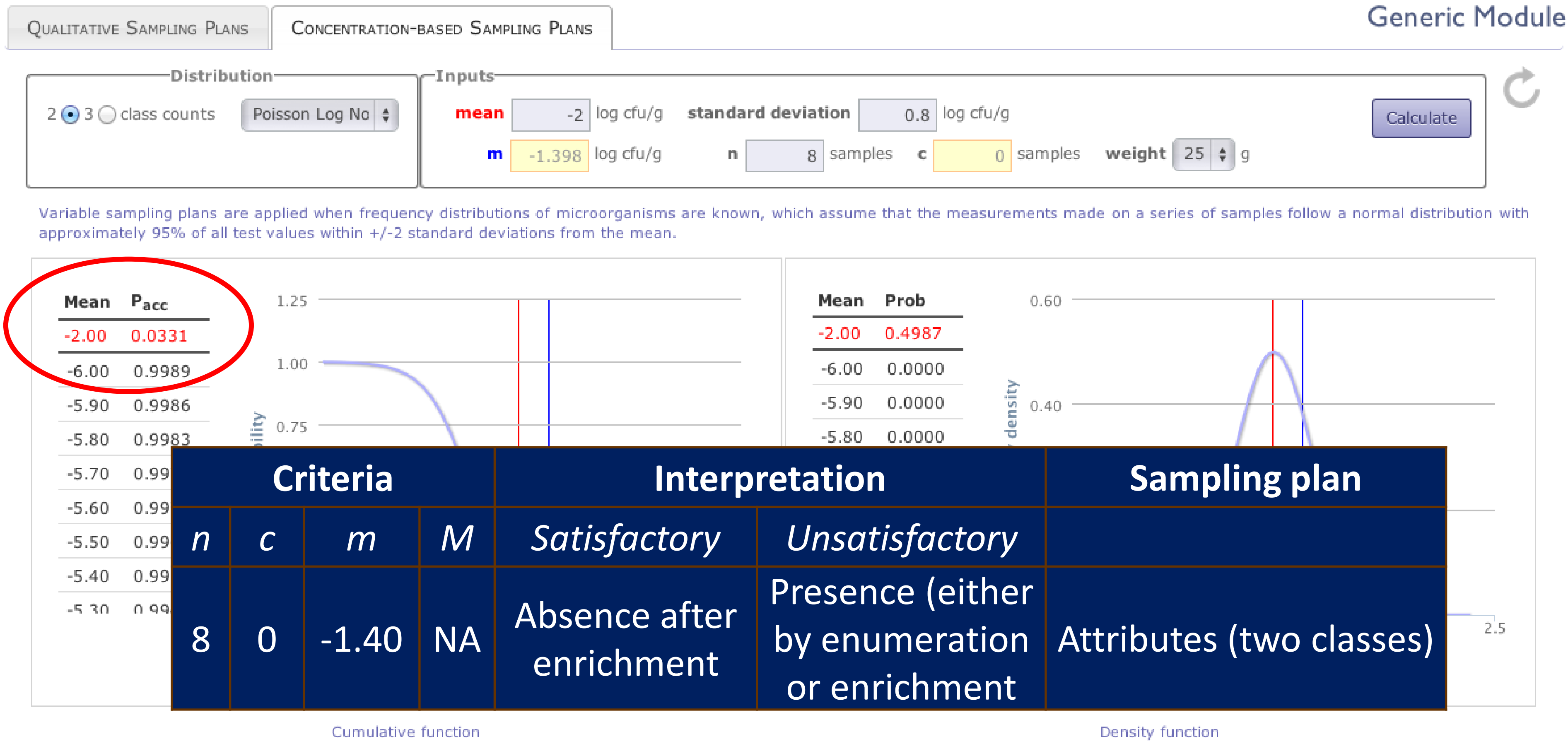
mean -2 log cfu/g — **standard deviation** 0.8 log cfu/g

m -1.398 log cfu/g — **n** 8 samples — **c** 0

samples **weight** 25 g

Variable sampling plans are applied when frequency distributions of microorganisms are known, which assume that the measurements made on a series of samples follow a normal distribution with approximately 95% of all test values within +/-2 standard deviations from the mean.

Case studies



2 ● 3 ○ class counts Poisson Log No

mean -2 log cfu/g **standard deviation** 0.8 log cfu/g

m -1.398 log cfu/g **n** 8 samples **c** 0 samples **weight** 25 g

Variable sampling plans are applied when frequency distributions of microorganisms are known, which assume that the measurements made on a series of samples follow a normal distribution with approximately 95% of all test values within +/-2 standard deviations from the mean.

Mean	P_{acc}
-2.00	0.0331
-6.00	0.9989
-5.90	0.9986
-5.80	0.9983
-5.70	0.99
-5.60	0.99
-5.50	0.99
-5.40	0.99
-5.30	0.99

Mean	Prob
-2.00	0.4987
-6.00	0.0000
-5.90	0.0000
-5.80	0.0000

Cumulative function

Density function

Criteria				Interpretation		Sampling plan
n	*c*	*m*	*M*	*Satisfactory*	*Unsatisfactory*	
8	0	-1.40	NA	Absence after enrichment	Presence (either by enumeration or enrichment	Attributes (two classes)

BASELINE On-line Software Tool

Sampling Plan Report

Example II

Deriving a Microbiological criteria from a Performance Objective that is set as a concentration value of the pathogen

Setting the PO: *"the maximum frequency and / or concentration of a hazard in a food at a specified step in the food chain before consumption that provides or contributes to an Food Safety Objective or an Appropriate Level Of Protection, as applicable"*

Input Data

» Maximum allowable concentration that should not be exceeded: **3** log cfu/g
» Maximum allowable percentage of units in the lot below the targeted concentration. **95** % [0 - 99.99]
» Mean corresponding to the concentration of the pathogen in the lot: **1.5** log cfu/g
» Standard Deviation corresponding to the concentration of the pathogen in the lot: **0.8** [0 - 3]

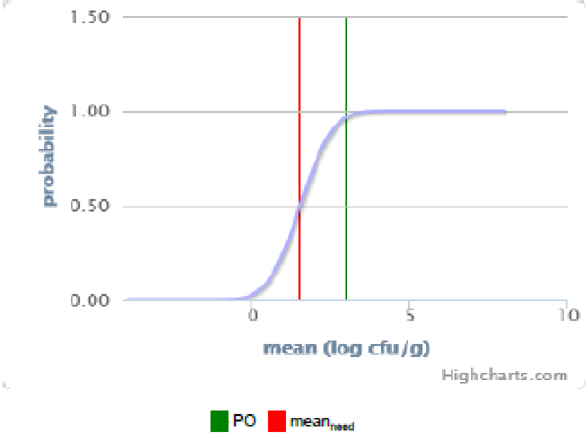
Results

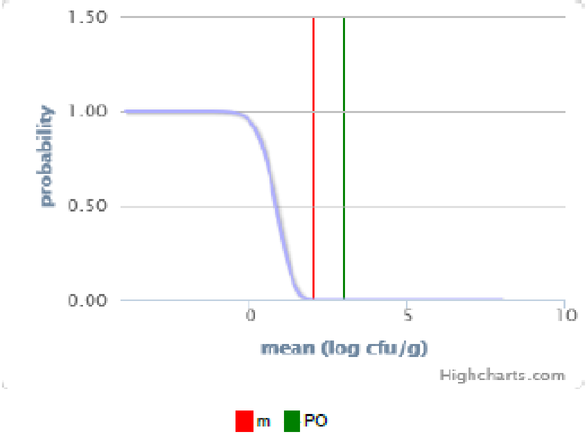
» Percentage of units below targeted concentration (PO): **96.960 %**

Resulting probabilities of having a negative sample at different values of n

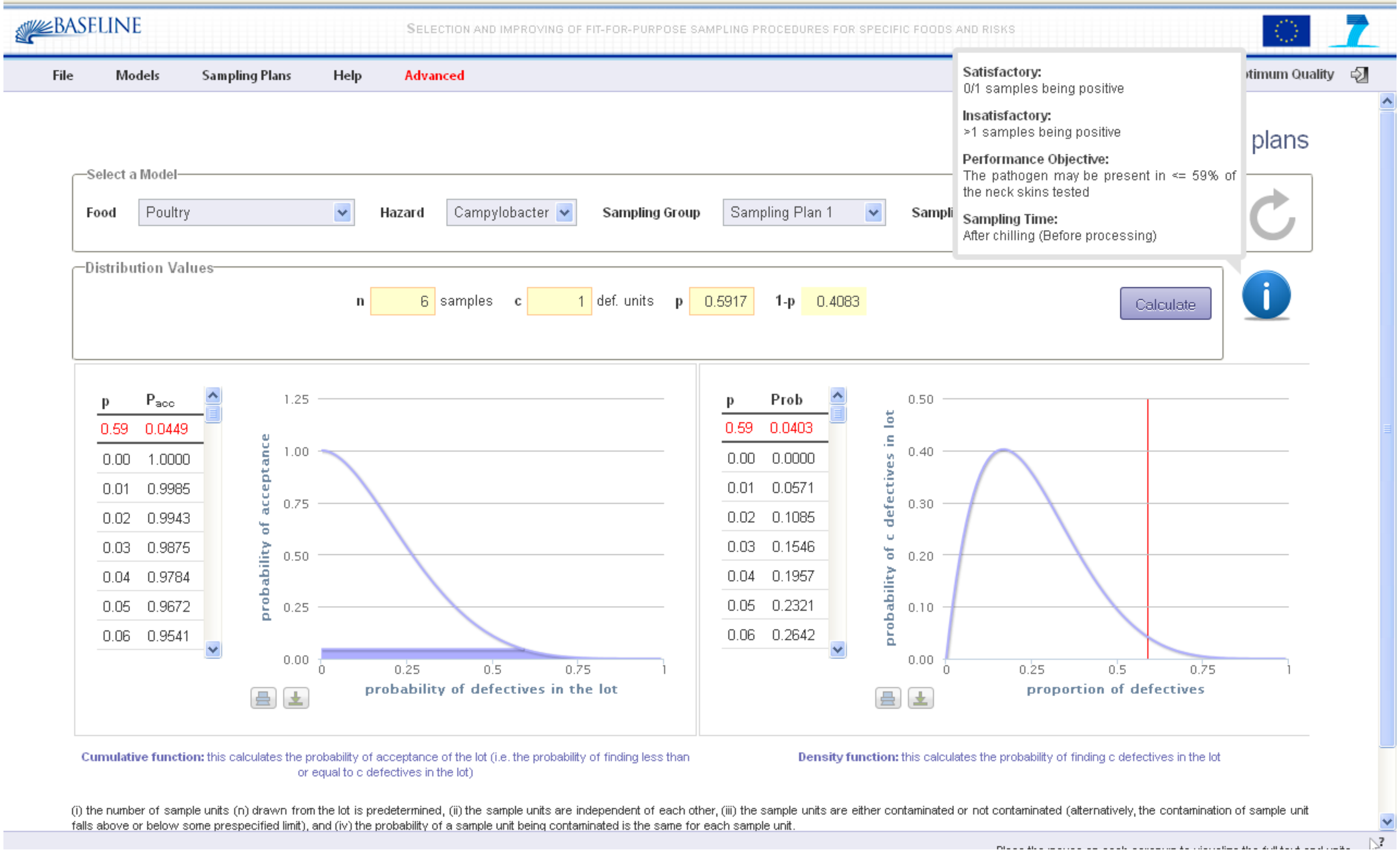
Sampling Plan Data

» m, microbiological limit log cfu/g: **2** log cfu/g
» n, number of units comprising the sample to be taken: **10** samples
» c, allowable number of sample units giving values below m: **0** samples





Specific sampling plans



Satisfactory:
0/1 samples being positive

Insatisfactory:
>1 samples being positive

Performance Objective:
The pathogen may be present in <= 59% of the neck skins tested

Sampling Time:
After chilling (Before processing)

Select a Model

Food Poultry **Hazard** Campylobacter **Sampling Group** Sampling Plan 1

Distribution Values

n 6 samples c 1 def. units p 0.5917 1-p 0.4083

p	P_{acc}
0.59	0.0449
0.00	1.0000
0.01	0.9985
0.02	0.9943
0.03	0.9875
0.04	0.9784
0.05	0.9672
0.06	0.9541

p	Prob
0.59	0.0403
0.00	0.0000
0.01	0.0571
0.02	0.1085
0.03	0.1546
0.04	0.1957
0.05	0.2321
0.06	0.2642

Cumulative function: this calculates the probability of acceptance of the lot (i.e. the probability of finding less than or equal to c defectives in the lot)

Density function: this calculates the probability of finding c defectives in the lot

(i) the number of sample units (n) drawn from the lot is predetermined, (ii) the sample units are independent of each other, (iii) the sample units are either contaminated or not contaminated (alternatively, the contamination of sample unit falls above or below some prespecified limit), and (iv) the probability of a sample unit being contaminated is the same for each sample unit.

Conclusions

The Baseline software tool:

- predicts microbial behavior of different pathogens and food matrices with validated models
- makes possible the addition of new models as well as data are being gathered
- provides an easy derivation of Microbiological Criteria and Sampling plans from previously established risk-based metrics
- offers a tools menu to perform scenario analyses
- includes decision-support system to help non experienced users to choose the suitable option

THANK YOU FOR YOUR ATTENTION!!

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Questions

- **Questions**

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- **Keep your browsers open to complete the survey !!**

Next webinar

- Dose response for *Listeria monocytogenes*
- Prof. Dr. Fernando Pérez Rodríguez (Cordoba)
- Dr. Régis Pouillot (formerly FDA)

- Thursday June 1st, 2017
- 10:00 -11:00 am U.S. Central Time

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