

# **Predicting the Troublemakers: Guidance and a Computer Tool for Microbial Growth**

IAFP Webinar: May 15, 2025, 10:30-11:30 AM CST

Moderated by Dr. Abdullatif Tay, PepsiCo

<sup>AT</sup>  
Organized by Modelling and Risk Analysis PDG

# WEBINAR HOUSEKEEPING

- 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.
- All attendees are muted. Questions should be submitted to the presenters during the presentation via the Q&A or Chat section on your screen. Questions will be answered at the end of the presentations.
- This webinar is being recorded and will be available for access by IAFP members within one week.

# Meet Our Expert Speakers



**Dr. Heidi den Besten**

Wageningen University

"How to predict growth of microorganisms?"

Fundamental principles of microbial growth prediction, key factors affecting growth kinetics, and mathematical models



**Dr. Mariem Ellouze**

Ferrero

"Development of an international standard on the determination and use of cardinal values for growth"  
Insights on ISO's standardization efforts for microbial growth prediction



**Dr. Panagiotis Skandamis**

Agricultural University of  
of Athens

"User-friendly, freely available computer tool to predict microbial growth" Demonstration of accessible tools for food safety professionals with practical applications



# How to predict growth microorganisms?

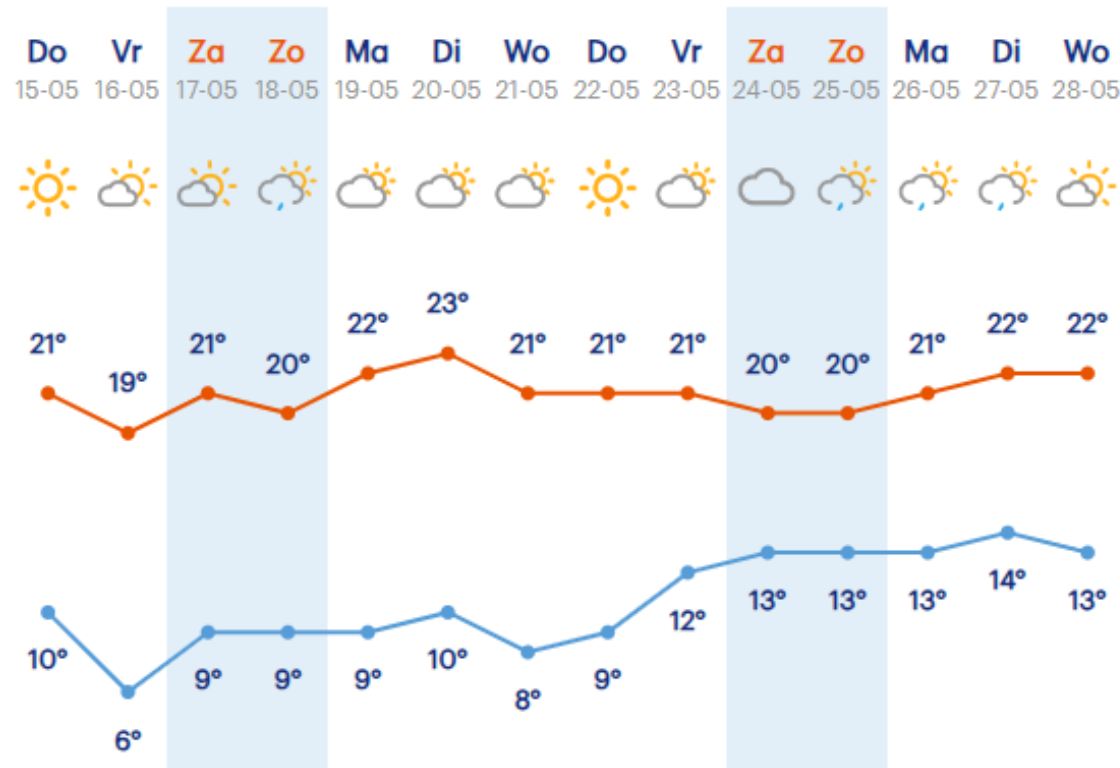
Professor Heidy den Besten, [heidy.denbesten@wur.nl](mailto:heidy.denbesten@wur.nl)

15 May 2025



# Decision **support** system

Buienrader.nl



- All models are wrong ..... some are useful (Box)
- All models are correct ..... but they are not perfect (Zwietering)

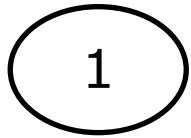
# Growth of microorganisms

- Bacterial growth: 1 – 2 – 4 – 8 – 16 – 32 – .... ( $=2^n$ )
- Generation time: time to generate a new generation



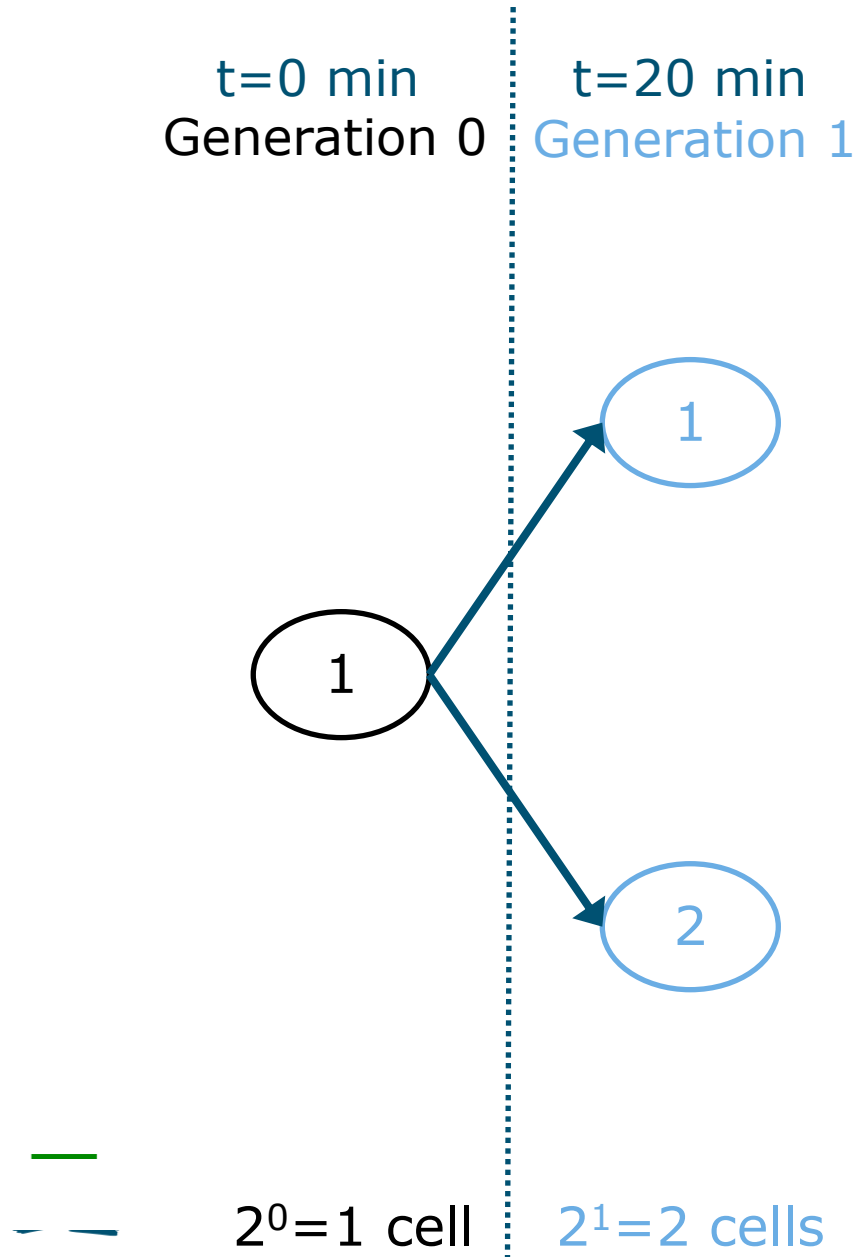
# Example: *Escherichia coli*

t=0 min  
Generation 0



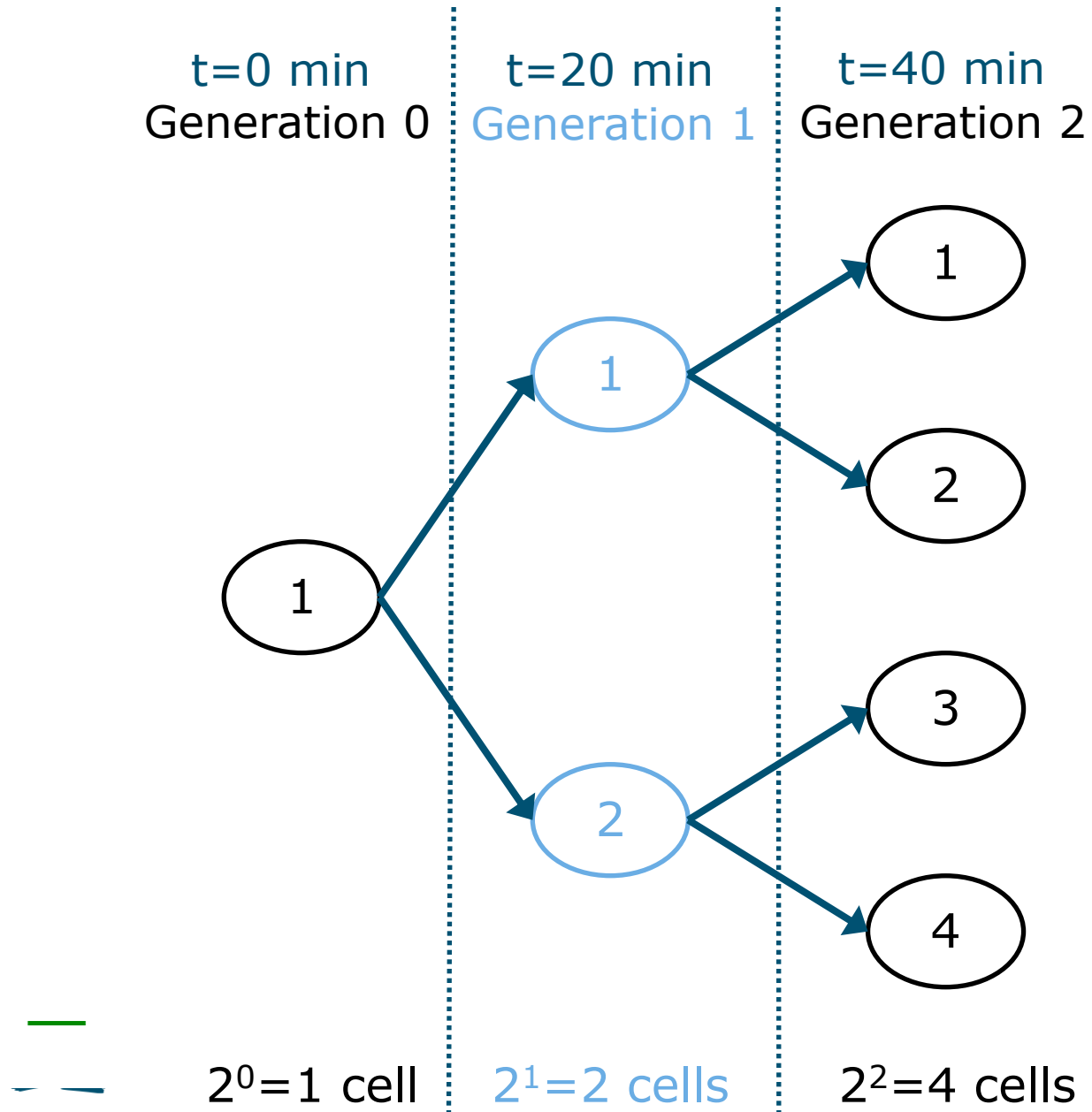
$2^0 = 1$  cell

# Example: *Escherichia coli*

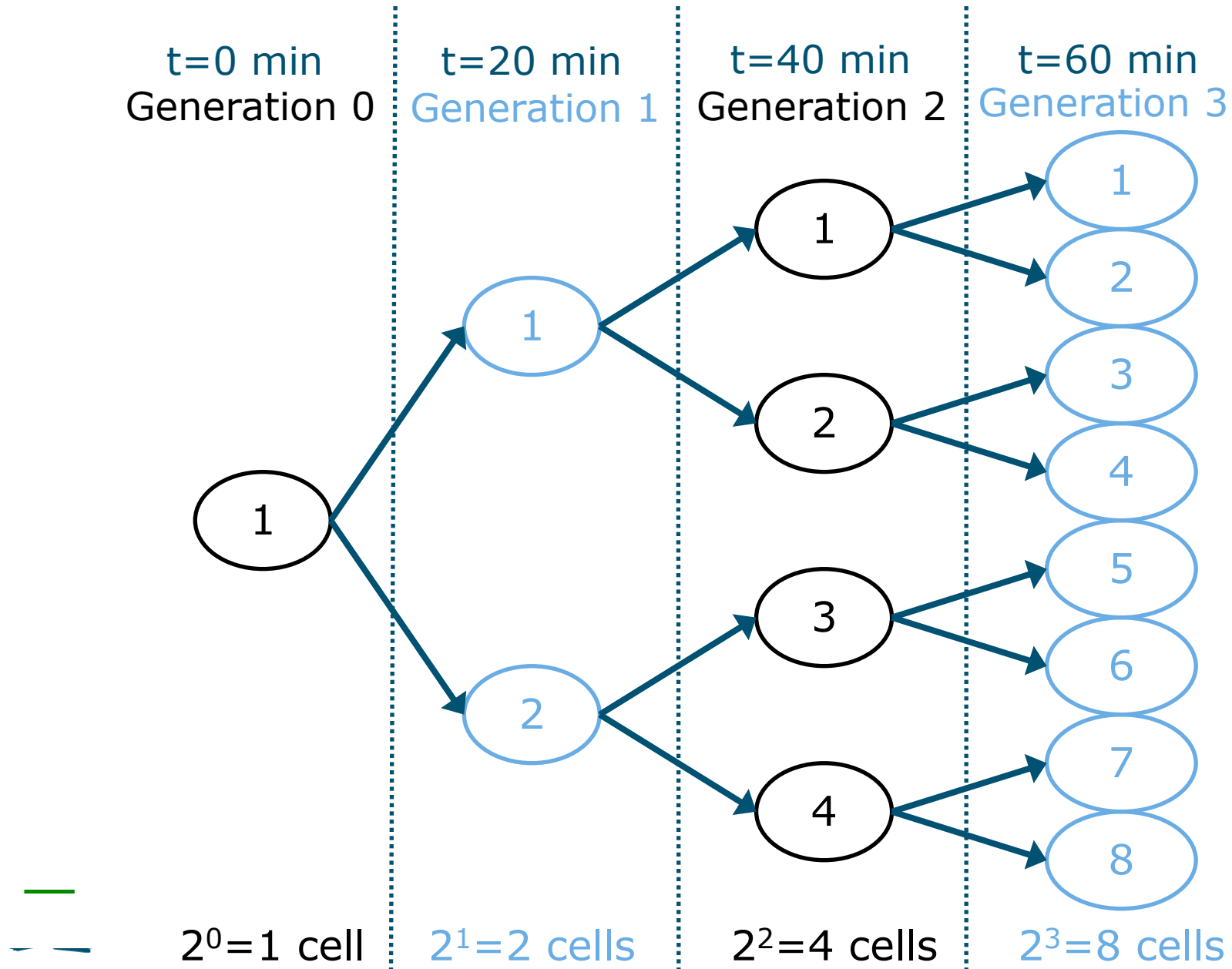




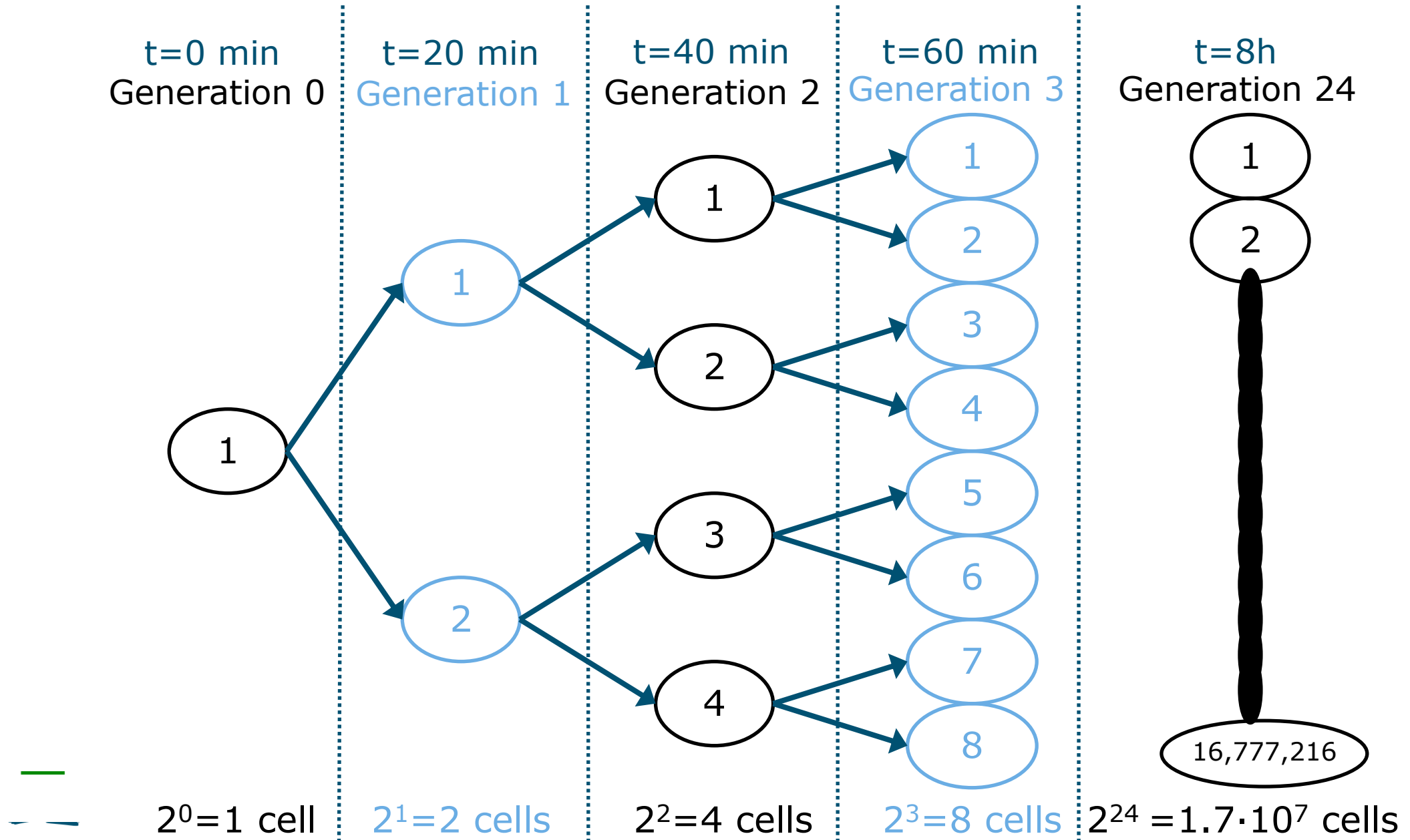
# Example: *Escherichia coli*



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# Example: *Escherichia coli*

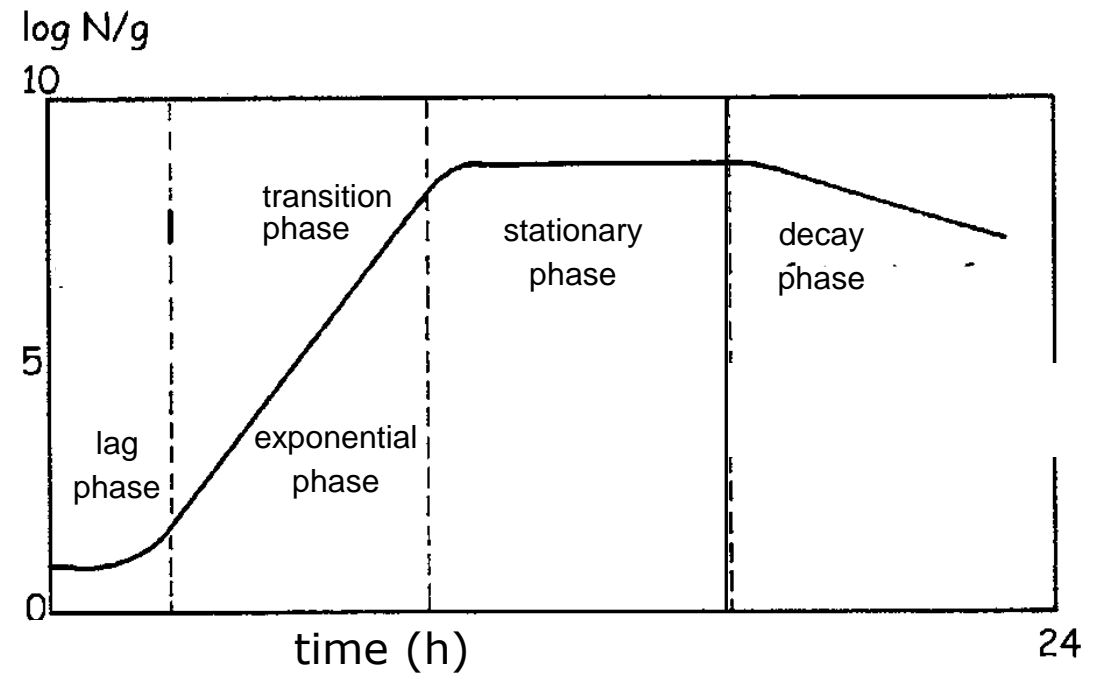
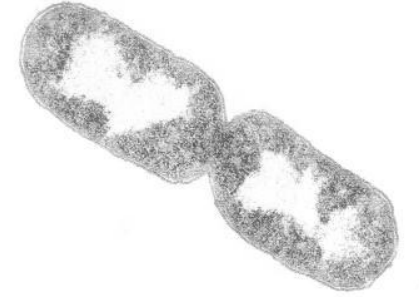


# Growth of bacteria

- Exponential growth: 1 – 2 – 4 – 8 – 16 – 32 – .... ( $=2^n$ )

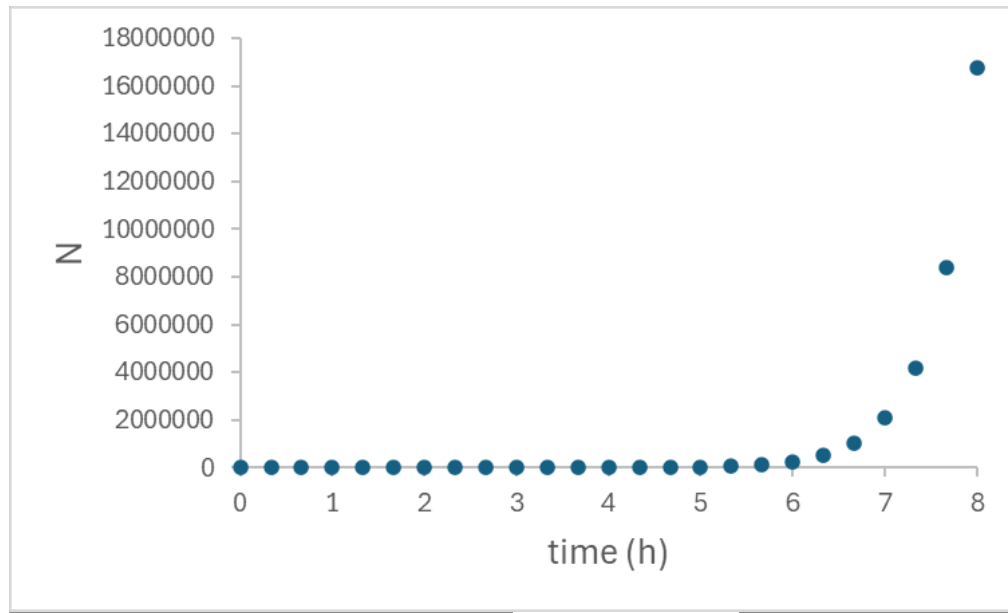
- Growth curve:  $\log N / g$

$N$  = number of cells



# Exponential growth

$$N_t = N_0 \cdot 2^n \rightarrow N_t = N_0 \cdot 2^{\frac{t}{GT}}$$

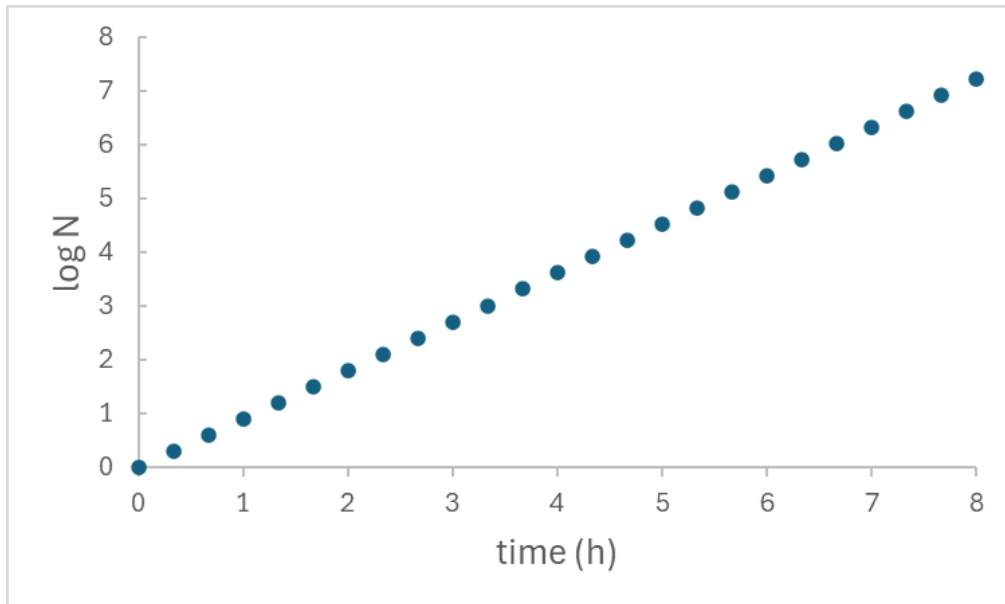


$n$  = number of generations  
 $t$  = time (hour)  
GT = generation time (hour)

# Exponential growth

$$N_t = N_0 \cdot 2^n \rightarrow N_t = N_0 \cdot 2^{\frac{t}{GT}}$$

$$\log N_t = \log( N_0 \cdot 2^{\frac{t}{GT}})$$



$n$  = number of generations

$t$  = time (hour)

GT = generation time (hour)



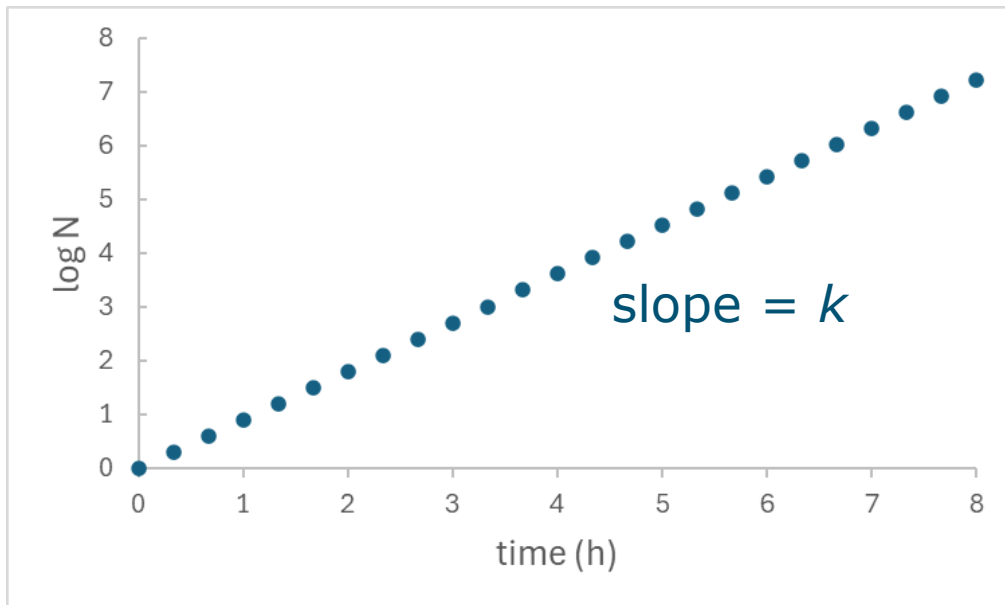
# Exponential growth

$$N_t = N_0 \cdot 2^n \rightarrow N_t = N_0 \cdot 2^{\frac{t}{GT}}$$

$$\log N_t = \log(N_0 \cdot 2^{\frac{t}{GT}})$$

$$\log N_t = \log N_0 + \log(2^{\frac{t}{GT}}) \rightarrow \log N_0 + \frac{t}{GT} \cdot \log(2) \rightarrow \log N_0 + \frac{\log(2)}{GT} \cdot t \rightarrow$$

$$\log N_t = \log N_0 + k \cdot t$$



$n$  = number of generations

$t$  = time (hour)

GT = generation time (hour)

$k$  = growth rate on log-scale ( $\log_{10}/h$ )

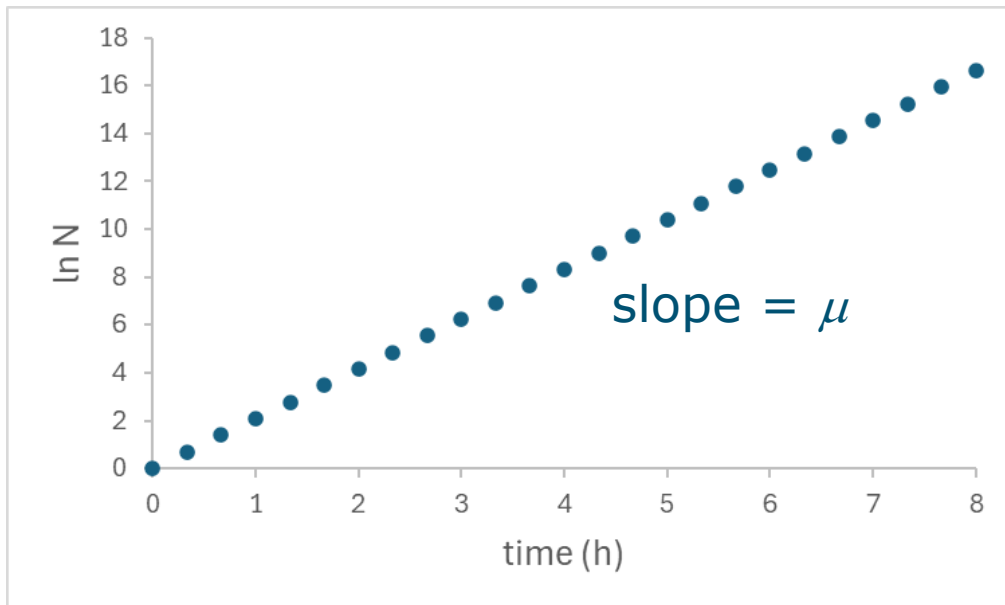
# Exponential growth

$$N_t = N_0 \cdot 2^n \rightarrow N_t = N_0 \cdot 2^{\frac{t}{GT}}$$

$$\ln N_t = \ln(N_0 \cdot 2^{\frac{t}{GT}})$$

$$\ln N_t = \ln N_0 + \ln(2^{\frac{t}{GT}}) \rightarrow \ln N_0 + \frac{t}{GT} \cdot \ln(2) \rightarrow \ln N_0 + \frac{\ln(2)}{GT} \cdot t \rightarrow$$

$$\ln N_t = \ln N_0 + \mu \cdot t$$



$n$  = number of generations

$t$  = time (hour)

$GT$  = generation time (hour)

$\mu$  = growth rate on ln-scale (/h)

$\mu = \ln(10) \cdot k$

# Prediction of $\mu$ using gamma model

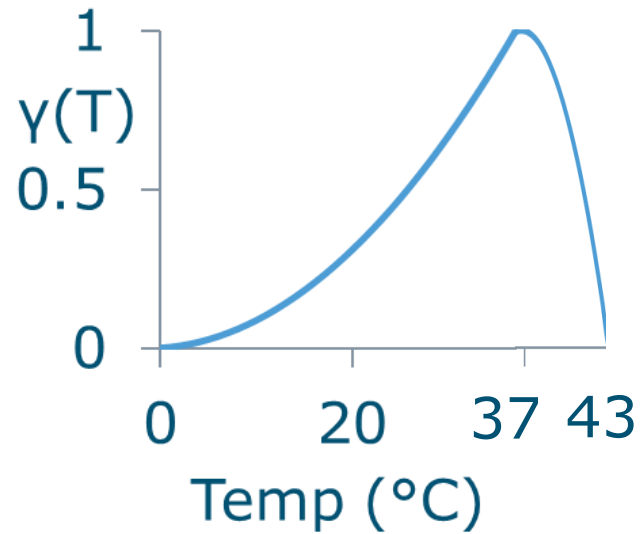
- Growth rate is affected by multiple factors (e.g., Temp, pH, HA,  $a_w$ ) that act independently

$$\mu = \mu_{\text{opt}} \cdot \gamma(T) \cdot \gamma(\text{pH}) \cdot \gamma(\text{HA}) \cdot \gamma(a_w)$$

$$\gamma(\text{condition}) = \frac{\text{growth rate at actual condition}}{\text{growth rate at optimal condition}} \quad \gamma [0-1]$$

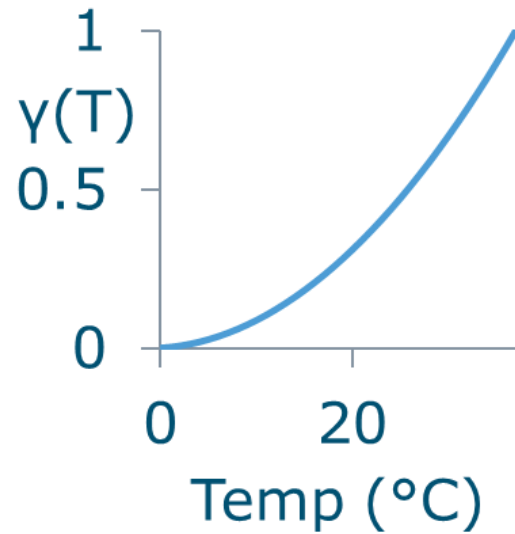
# Gamma model: fraction of growth rate

The fraction of  $\mu_{\text{opt}}$  is termed “ **$\gamma$** ”



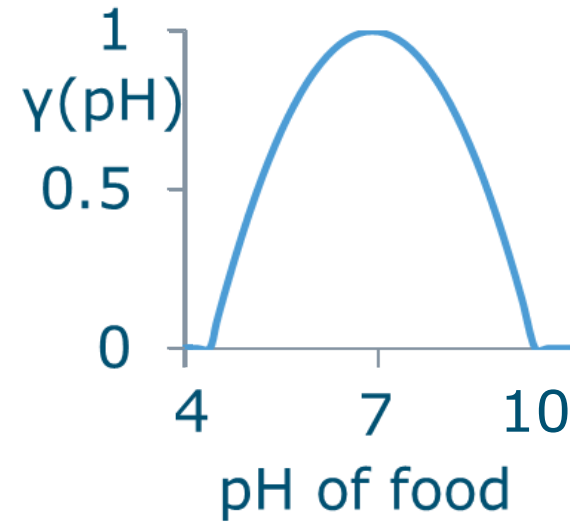
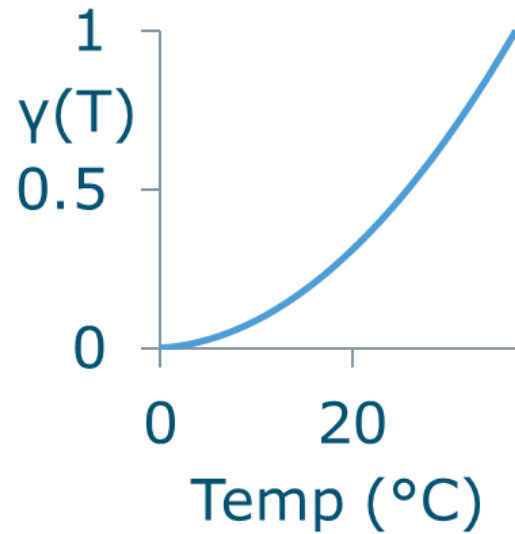
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# Gamma model: fraction of growth rate

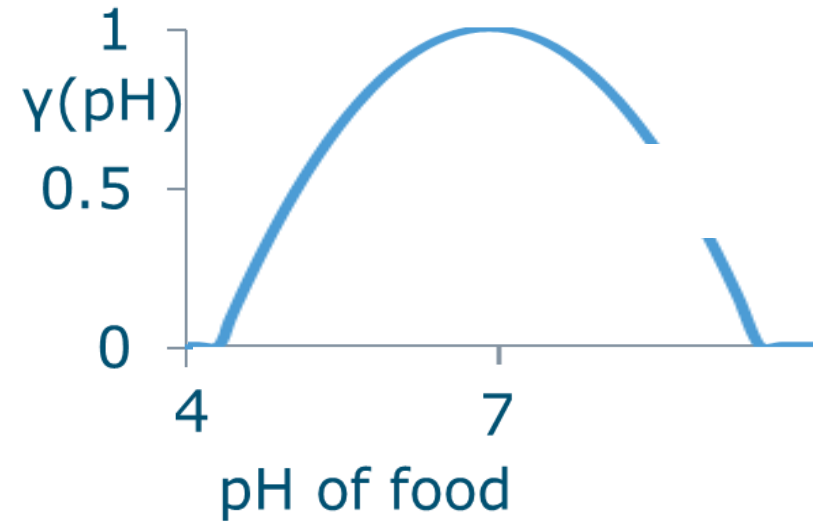
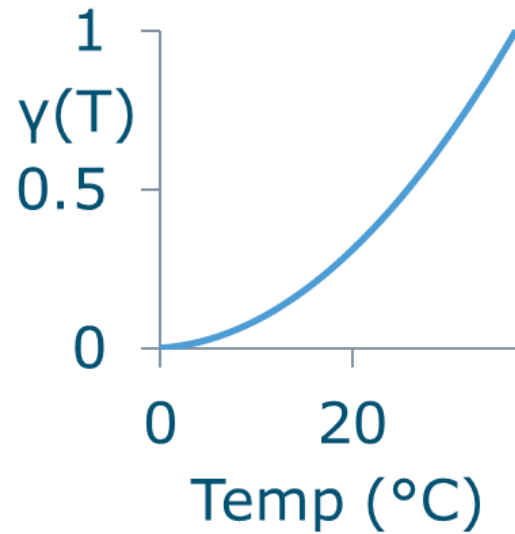
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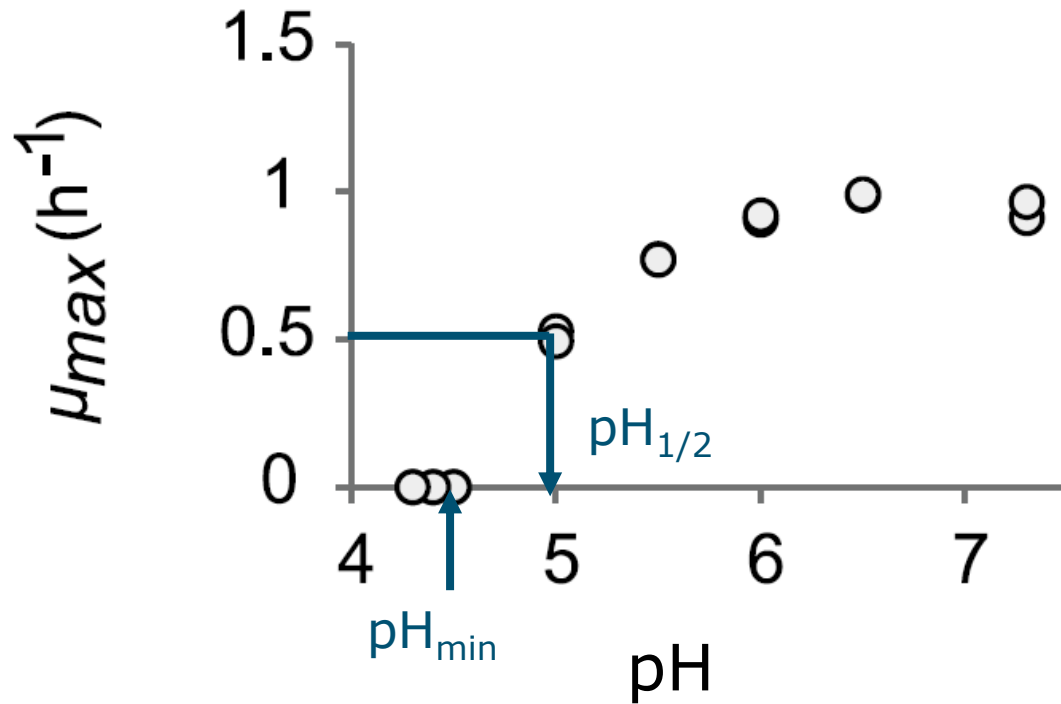


# Gamma model: fraction of growth rate

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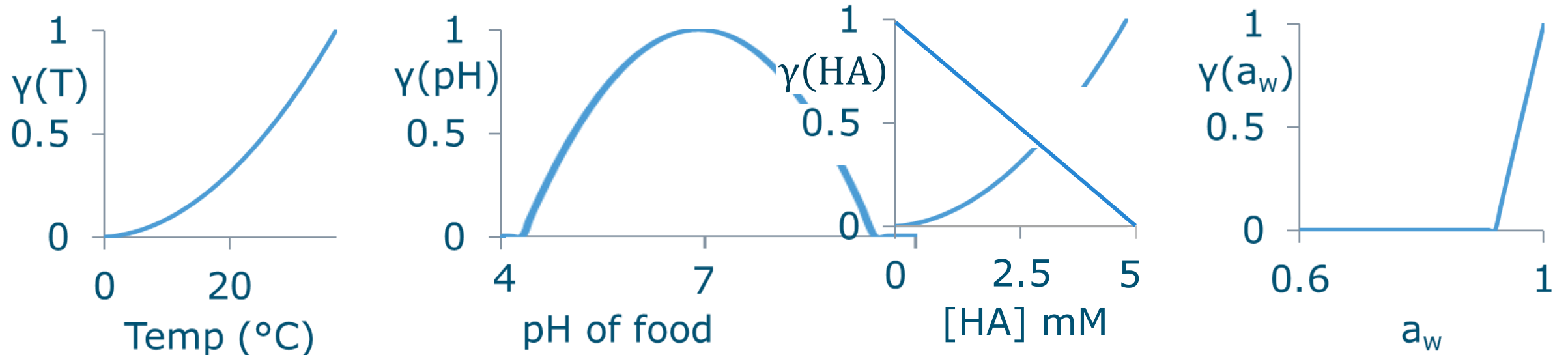
# Gamma model: fraction of growth rate



$$\mu_{max} = \mu_{opt} \left( 1 - 2^{\frac{(pH - pH_{min})}{(pH_{min} - pH_{1/2})}} \right)$$

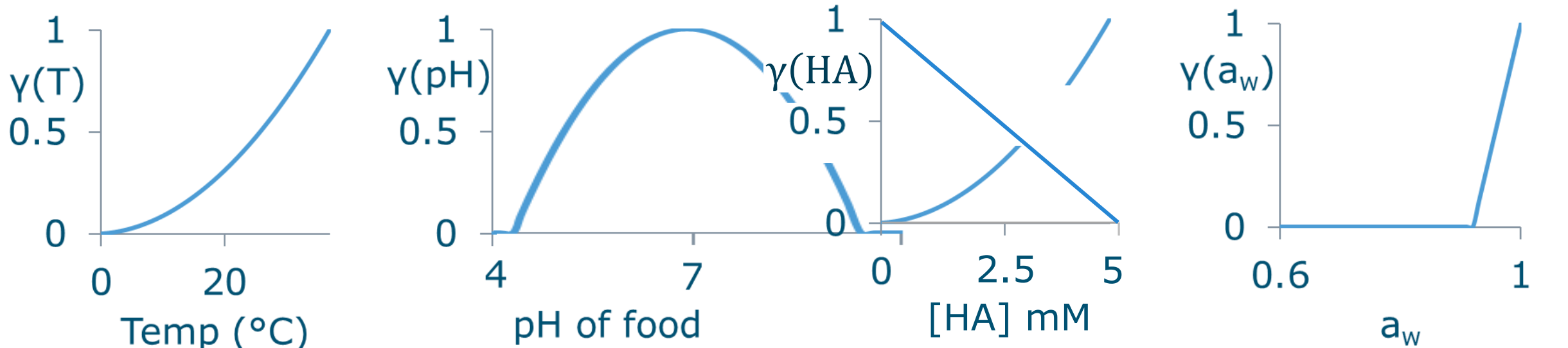
# Gamma model: fraction of growth rate

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# Gamma model: fraction of growth rate

The fraction of  $\mu_{\text{opt}}$  is termed “ $\gamma$ ”



$$\gamma(T) = \left( \frac{T - T_{\min}}{T_{\text{opt}} - T_{\min}} \right)^2$$

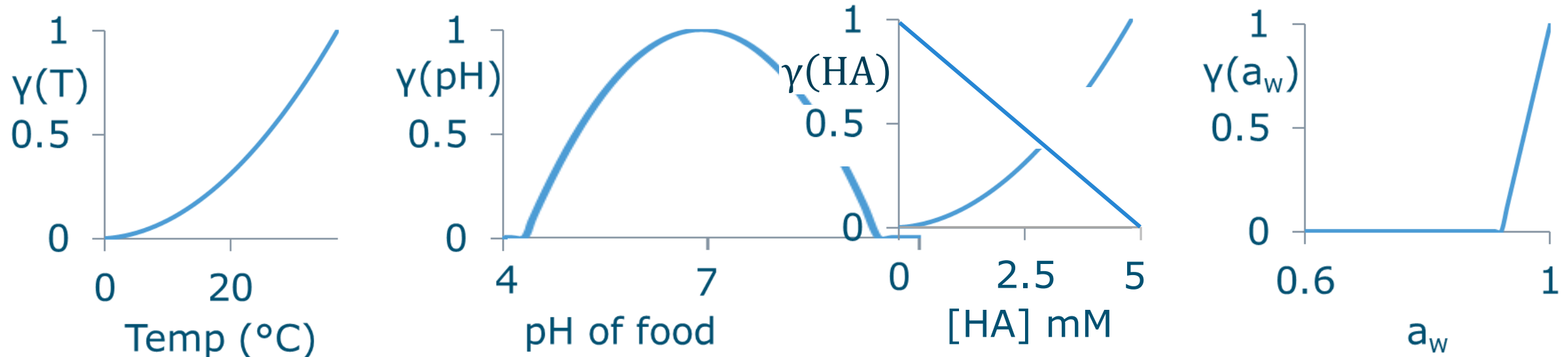
$$\gamma(\text{pH}) = \left( 1 - \frac{(\text{pH} - \text{pH}_{\min})}{2(\text{pH}_{\min} - \text{pH}_{1/2})} \right)$$

$$\gamma(\text{HA}) = 1 - \frac{\text{HA}}{\text{HA}_{\max}}$$

$$\gamma(a_w) = \frac{(a_w - a_{w\min})}{(1 - a_{w\min})}$$

# Gamma model: fraction of growth rate

Cardinal parameters *Listeria monocytogenes*



$\gamma(T)$  Effect temperature

$T_{\min}$ : -1.5

$T_{\text{opt}}$ : 37

$\gamma(\text{pH})$  Effect pH

$\text{pH}_{\min}$ : 4.4

$\text{pH}_{1/2}$ : 5.0

$\gamma(\text{HA})$  Effect [HA]

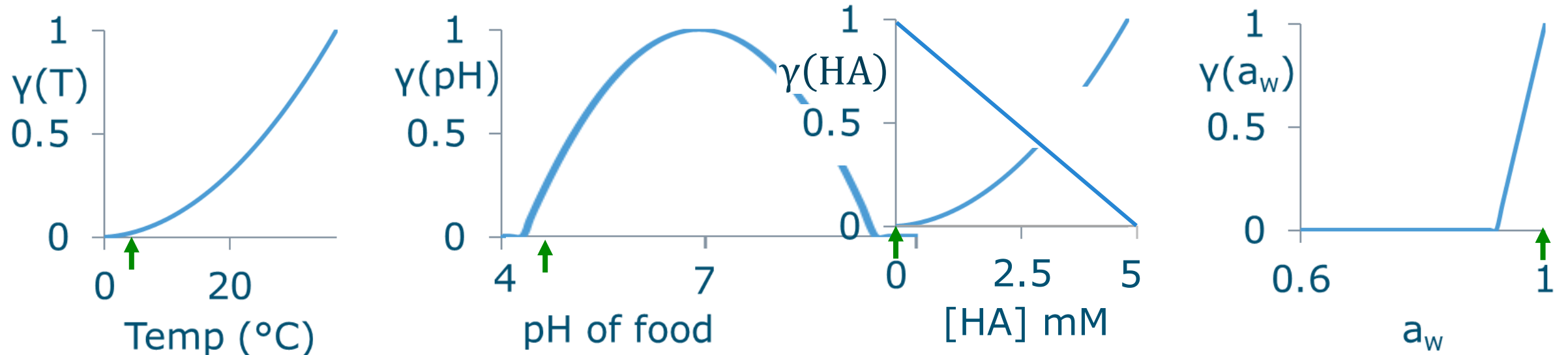
$[\text{HA}_{\max}]$ : 5.0

$\gamma(a_w)$  Effect  $a_w$

$a_{w,\min}$ : 0.92

# Estimation of $\mu$

Vegetable product:  $T=7^{\circ}\text{C}$ ,  $\text{pH}=4.5$ ,  $\text{HA} = 0 \text{ mM}$ ,  $a_w=0.997$



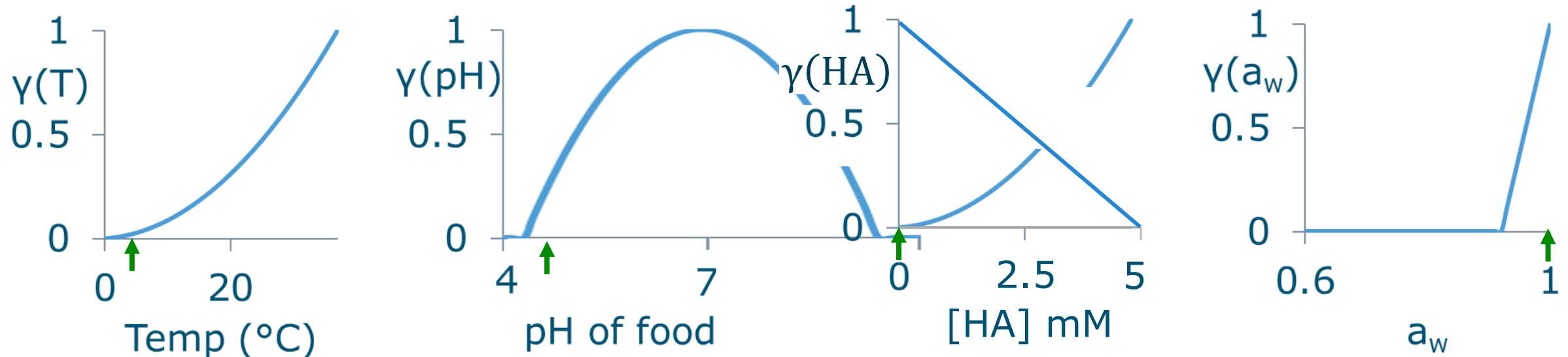
$$\gamma_{\text{tot}} = \gamma(T) \cdot \gamma(\text{pH}) \cdot \gamma(\text{HA}) \cdot \gamma(a_w) = 0.049 \cdot 0.109 \cdot 1 \cdot 0.96 = 0.005$$

$$\mu = \gamma_{\text{tot}} \cdot \mu_{\text{opt}} = 0.005 \cdot 1 = 0.005 \text{ h}^{-1}$$



# Estimation of $\mu$ and ranking of effects

Vegetable product:  $T=7^{\circ}\text{C}$ ,  $\text{pH}=4.5$ ,  $\text{HA} = 0 \text{ mM}$ ,  $a_w=0.997$



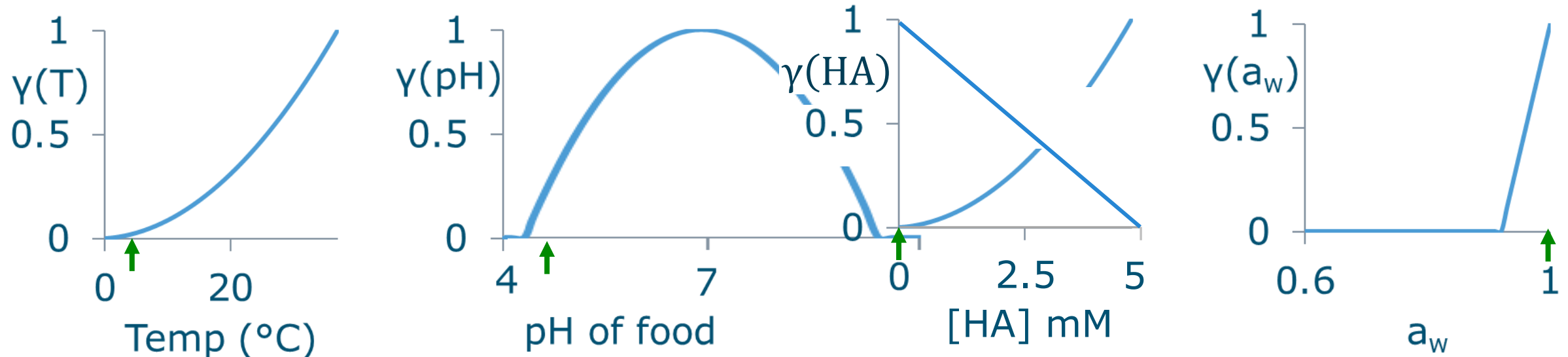
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**reduction factors** Temp: 20.5, pH: 9.2, HA: 1,  $a_w$ : 1.04

# Estimation of $\mu$ and ranking of effects

Vegetable product:  $T=7^{\circ}\text{C}$ ,  $\text{pH}=4.5$ ,  $\text{HA} = 0 \text{ mM}$ ,  $a_w=0.997$



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**reduction factors** Temp: 20.5, pH: 9.2, HA: 1,  $a_w$ : 1.04

$$\text{generation time} = \frac{\ln(2)}{\mu} = 135 \text{ h} \approx 5.6 \text{ days}$$

# Pro of gamma model

- Structured/transparent/simple
- Insight (gamma's: ranking, how to influence)
- Quantitative

# Pro of gamma model

- Structured/transparent/simple
- Insight (gamma's: ranking, how to influence)
- Quantitative

But

All models are correct ..... but they are not perfect

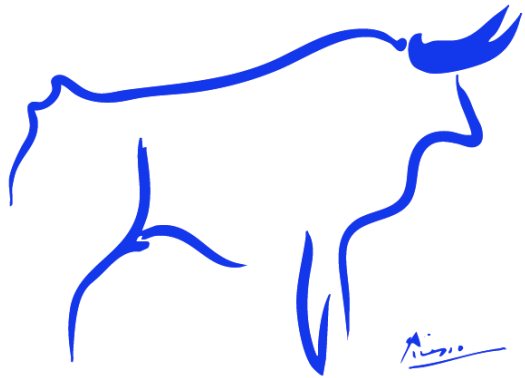
*Development of an international standard on the determination  
and use of cardinal values for growth*

15/05/2025

Mariem Ellouze,

Group Food Microbiology Senior Manager

# Why do we need standardization?



---

From data to  
mathematical models

From descriptive to predictive  
science

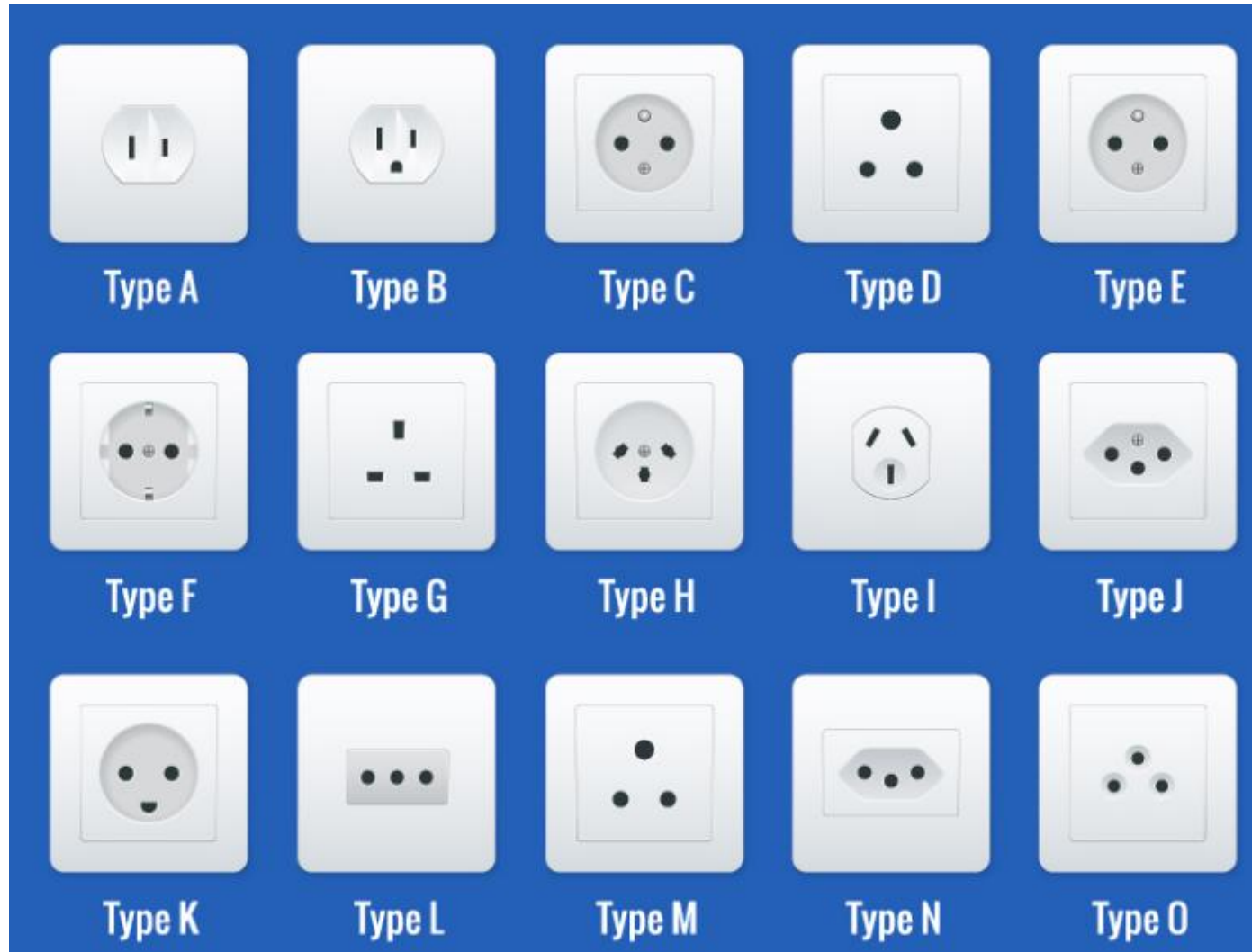
Model: Simplification from  
a certain point of view

What to omit is like an art.

- How you standardize the «wet» part is relatively easy
- How you standardize the «dry» part is less straightforward



# Why do we need standardization?

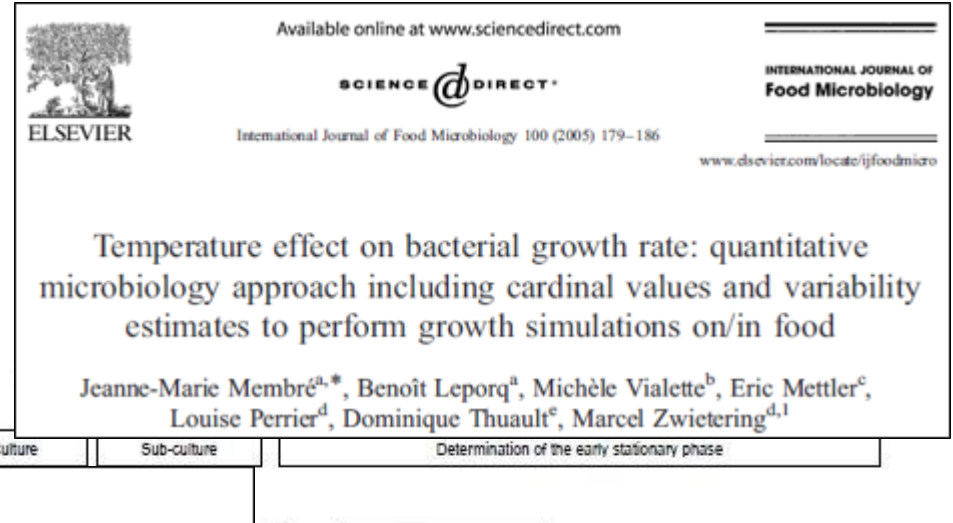


# Why do we need standardization ?

Membré et al. 2002. Food'Micro, Lillehammer, Norway, August 2002. *In* Conference Proceedings. Matforsk Norwegian Food Research Institute, pp. 143-146

**Experimental protocols and strain variability of cardinal values (pH and  $a_w$ ) of bacteria using Bioscreen C : microbial and statistical aspects.**

Jeanne-Marie Membré<sup>1\*</sup>, Benoît Leporq<sup>1</sup>, Michèle Vialette<sup>2</sup>, Eric Mettler<sup>3</sup>, Louise Perrier<sup>4</sup> and Marcel Zwietering<sup>4</sup>.



## Abundant literature on the topic... but great differences!

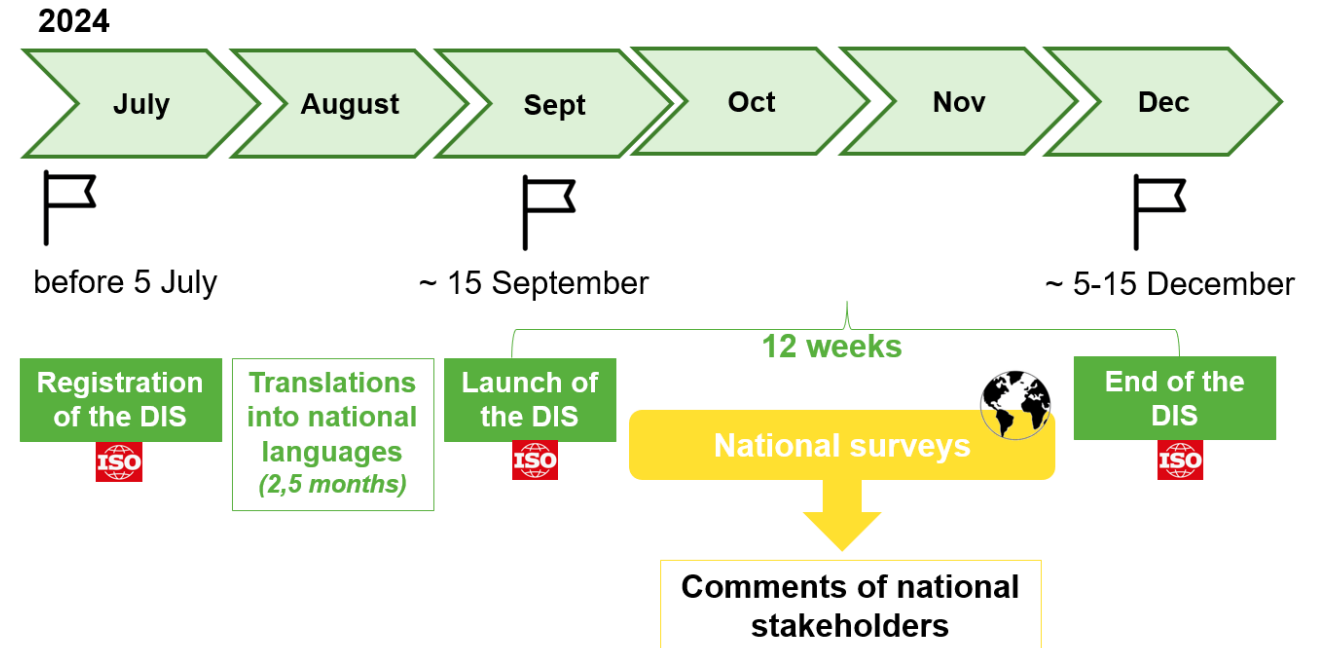
- **Possible methods for measurements** : indirect (OD) vs direct (CFU) and others (conductivity)
- **Conditions of experiments**: static (fixed) conditions vs dynamic (fluctuating) conditions
- **Models used**: cardinal models vs square root model
- **Raw data used**: growth rates vs transformations of the growth rates (sqrt, ln)
- **Experimental design**: a single or several factors tested at a time

→ All this has an influence on the result !! And on the use of predictive microbiology models for industrial applications. Need for harmonization.

# A journey that started in 2017

- **Secretariat:** Marine Huart, AFNOR, **Convenior:** Nicolas Nguyen Van Long, ADRIA, **Project Lead:** Mariem Ellouze, Ferrero
- **Working Group:**

1. Heidy M.W. den Besten, Wageningen University
2. Jeanne-Marie Membre, INRAE / ONIRIS
3. Yvan Le Marc, ADRIA
4. Panagiotis Skandamis, Agricultural University of Athens
5. Rachel Binet, FDA
6. Valérie Stahl, AERIAL
7. Thimo Albert, University of Leipzig
8. Vasilis Valdramidis, National and Kapodistrian University of Athens
9. Jurgen Chardon, RIVM
10. Aldo Evers, Normec Foodcare
11. Paul in't Veld, Netherlands Food and Consumer Product Safety Authority
12. Jiska Oostveen, FoodConsult
13. Ursula Gonzales Barron, CIMO, LA SusTEC, Instituto Politécnico de Bragança
14. Vasco Cadavez, CIMO, LA SusTEC, Instituto Politécnico de Bragança
15. Alberto Garre, Universidad Politécnica de Cartagena
16. Fabio Zuccon, Istituto Zooprofilattico Sperimentale del Piemonte
17. Ruben Barcia Cruz, ANSES
18. Nathalia Buss Da Silva, Nestlé Research



ISO/DIS 23691:2024(E)  
ISO/TC 34/SC 9/WG 19  
Secretariat: AFNOR  
Date: 2025-xx-xx

Microbiology of the food chain — Determination and use of cardinal values

DIS stage

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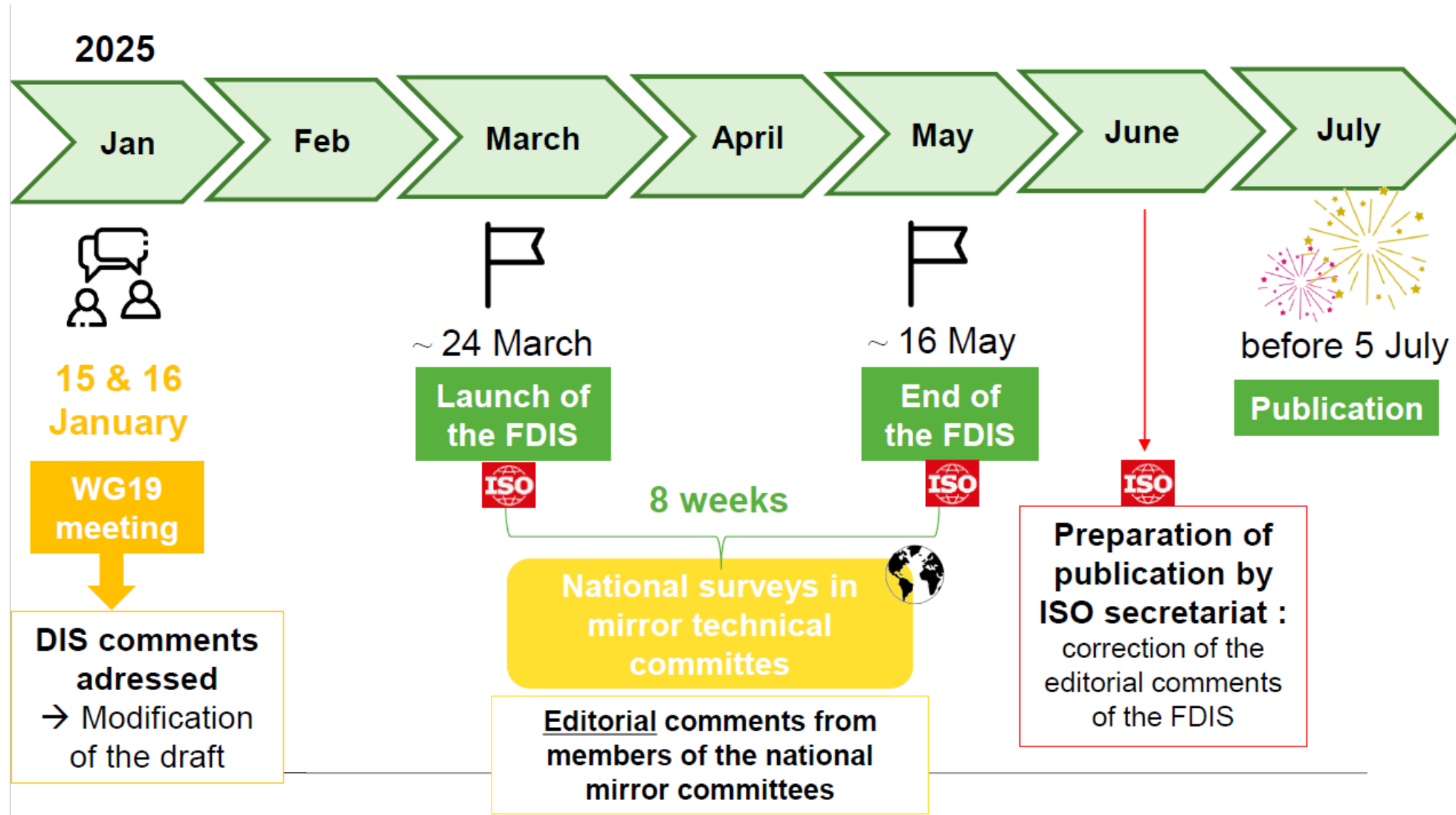
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# The finishing line



*User-friendly, freely  
available computer  
tool to predict  
microbial growth*

**Professor  
Panos N. Skandamis**

*Agricultural University of Athens,  
Greece*

*pskan@aua.gr*








# GROWTH PREDICTOR

<https://skandamis.shinyapps.io/Microbial-Growth-Predictor-Dashboard/>

## Growth Predictor

 User-defined conditions

 Imported 'e-Platon' file

 Modular process Risk model

 Estimation of cardinal values

 Primary model fitting

## Gamma models for the following terms:

T, pH, aw and up to 6 inhibitors

## Available modules

- Fitting (primary/secondary)
- Stochastic growth simulations under static/dynamic conditions
- Variability in:
  - Factors controlling microbial growth
  - Growth limits
  - Lag time (expressed as “ho”=‘the work to be done’)
- QMRA with 4 consecutive modules





# Fitting module Primary & Secondary models

<https://skandamis.shinyapps.io/Microbial-Growth-Predictor-Dashboard/>

# Primary model fitting

$$\frac{dN}{dt} = \frac{q_t}{q_{t+1}} \mu_{\max} \left( 1 - \left( \frac{N_t}{N_{\max}} \right)^m \right) N_t, \quad \text{where } q_t = \frac{P_t}{K_p}$$

$$h_0 = \ln \left( 1 + \frac{1}{q_0} \right) = -\ln(a_0) = \mu_{\max} \lambda$$

## STEP 2: Set starting values for Cardinal Parameters

Y0 (Log CFU/g or ml): starting value

☐ Fixed

Yend (Log CFU/g or ml): starting value

☐ Fixed

muopt: starting value

☐ Fixed

Lag time: starting value

☐ Fixed

Fit the model

Save values

Restore values

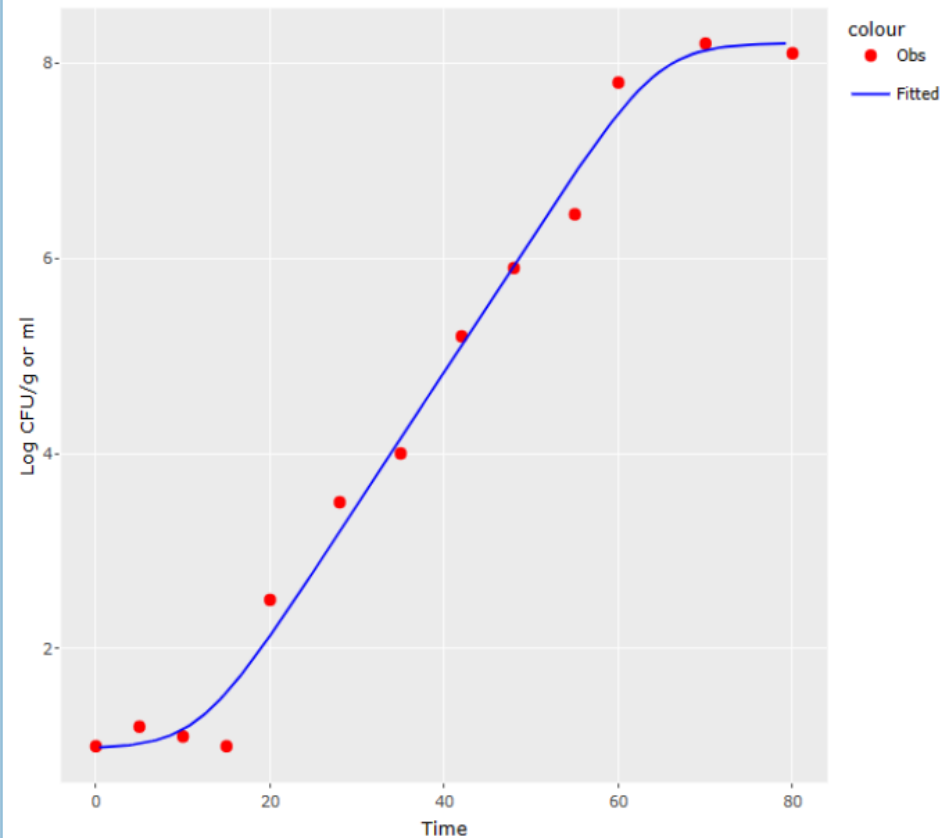
## STEP 1: Upload and plot the data to be fitted

Import data (XL) file acc. to the template

Browse... Time\_vs\_LogN.xlsx

Upload complete

[Click here to download an XL Template](#)

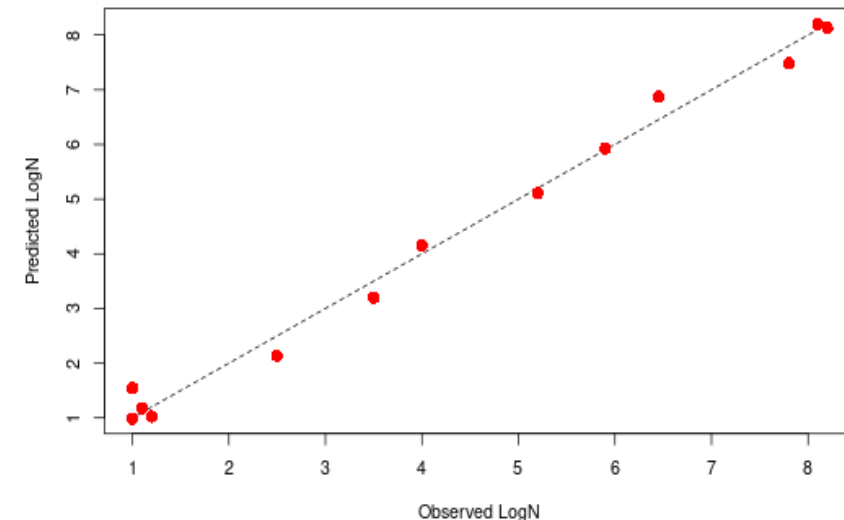


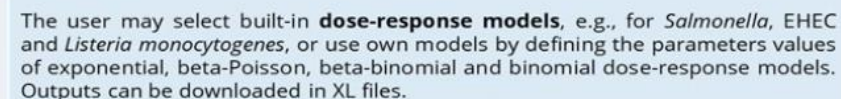
Clear dataset

## STEP 3. Assess the Parameter Estimates

Parameter	Estimate	Std_Error	Percent_Rel_Std_Error
Y0	2.276	0.4934	21.68
Ymax	18.893	0.5606	2.97
mu <sub>max</sub>	0.315	0.0197	6.26
lag	11.863	2.7659	23.32

## STEP 5. View the Predicted vs Observed plot





# Fitting Secondary (cardinal) models

# Gamma terms

$$\mu_{\max} = \mu_{\text{ref}} \cdot \left[ \frac{(T - T_{\min})}{T_{\text{ref}} - T_{\min}} \right]^2 \cdot \frac{(a_w - a_{w \min})}{(a_{w \text{ opt}} - a_{w \min})} \cdot \left[ 1 - 10^{(\text{pH}_{\min} - \text{pH})} \right] \cdot \left( 1 - \frac{[\text{LAC}_U]}{[\text{MIC}_U \text{ lactic acid}]} \right) \cdot \frac{(P_{\max} - P)}{P_{\max}}$$

$$\cdot \left[ \frac{(\text{NIT}_{\max} - \text{NIT})}{\text{NIT}_{\max}} \right]^2 \cdot \frac{(\text{CO}_2_{\max} - \text{CO}_2_{\text{equilibrium}})}{\text{CO}_2_{\max}} \cdot \left( 1 - \sqrt{\frac{[\text{DAC}_U]}{[\text{MIC}_U \text{ diacetate}]}} \right) \cdot \left( 1 - \sqrt{\frac{[\text{AAC}_U]}{[\text{MIC}_U \text{ acetic acid}]}} \right) \cdot \xi$$

$$CM_n(X) = \begin{cases} 0, & X \leq X_{\min} \\ \frac{(X - X_{\max})(X - X_{\min})^n}{(X_{\text{opt}} - X_{\min})^{n-1} \left\{ (X_{\text{opt}} - X_{\min})(X - X_{\text{opt}}) - (X_{\text{opt}} - X_{\max}) [(n-1)X_{\text{opt}} + X_{\min} - nX] \right\}}, & X_{\min} < X < X_{\max} \\ 0, & X \geq X_{\max} \end{cases}$$

$$\gamma(\text{pH}) = 1 - 2^{\frac{(\text{pH} - \text{pH}_{\min})}{(\text{pH}_{\min} - \text{pH}_{1/2})}}$$

$$\left[ 1 - \left( \frac{C_i}{\text{MIC}_i} \right)^{n1} \right]^{n2}$$



# Secondary model fitting

## STEP 2: Set starting values for Cardinal Parameters

### T gamma term

Cardinal

### pH gamma term

Cardinal

Cardinal

pH1/2-Aryani

pHmin-Presser

0,452

☐ Fixed

### Tmin: starting value

0

☐ Fixed

### Topt [or Tref]: starting value

37

☐ Fixed

### Tmax: starting value

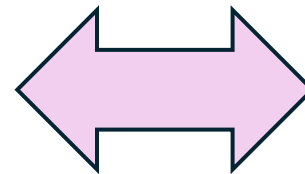
52

☐ Fixed

### pHmin: starting value

1. Select gamma terms to be fitted

2. Set the initial estimates of gamma parameters (depending on the cardinal terms)



Import data (XL) file acc. to the template

Browse...

Secondary\_Model\_File.xlsx

Upload complete

Select plot variable

T

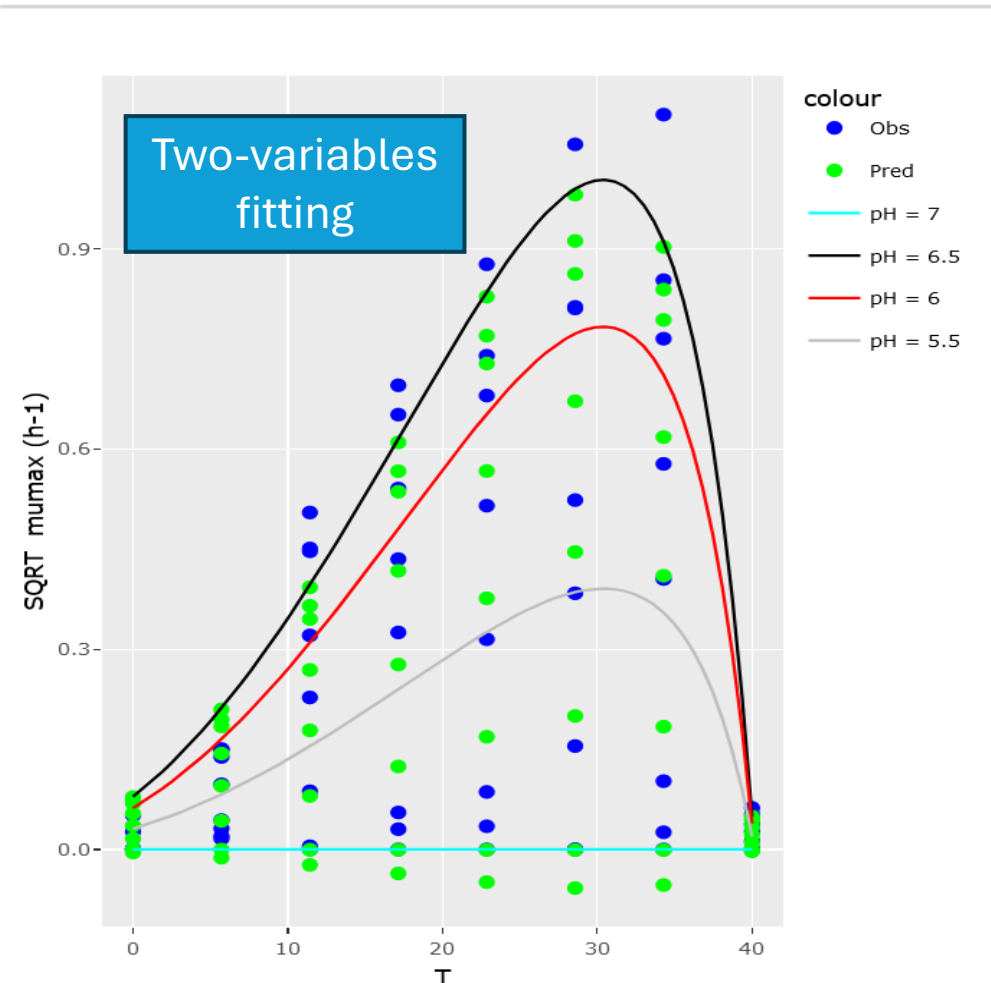
mumax transformation

☐ none

☒ SQRT

☐ Log (ln)

[Click here to download an XL Template](#)



# Fitting outputs

## STEP 3. Assess the Parameter Estimates

Parameter	Estimate	Std_Error	Percent_Rel_Std_Error
SQRT mumax (h-1) or muref	1.00	0.02606	2.5966
Tmin	-8.64	1.91517	-22.1783
Topt	30.38	0.58475	1.9246
Tmax	40.16	0.12899	0.3212
pHmin	5.06	0.03118	0.6158
pHopt	6.51	0.03275	0.5029
pHmax	7.00	0.00477	0.0682

## STEP 4. Assess the Goodness-of-Fit criteria

RMSE	R2	AIC	BIC
0.0649	0.956	-152.45	-135.17

About

User-defined conditions

Imported 'e-Platon' file

Modular process Risk model

Estimation of cardinal values

Primary model fitting

[Click here for user guide files](#)

## Welcome to Growth Predictor

A predictive modelling and QMRA software based on gamma concept models

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The tool is comprised of three modules: primary and secondary model fitting, growth simulations and QMRA.

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The QMRA is comprised of **4 consecutive modules** from primary production until consumption. In addition to prevalence, the modules may also consider partition, mixing and cross-contamination (i.e., changes in prevalence and levels). **Variability** can be introduced through a *variety of probability distributions*, for initial contamination, or re-contamination, storage time and temperature, product characteristics, serving size and maximum population density. Fixed or variable log reductions during cooking, may be introduced as user-defined values or probability distributions, respectively, or estimated by a Bigelow thermal inactivation model.

Variability in the cardinal values can be addressed in this module, too. **Log change upwards (growth) or downwards (reduction)** is described as a fixed value, or a normal distribution, or estimated with growth models. The *trilinear primary growth model* is used for estimating log changes, based on  $\mu_{max}$  obtained by gamma models. The QMRA outputs include graphical distribution of ingested dose and probability of illness ( $P_{ill}$ ), as well as tabular estimates of the average dose and  $P_{ill}$  mode and the 5 and 95 percentiles of the corresponding distributions.

The user may select built-in **dose-response models**, e.g., for *Salmonella*, EHEC and *Listeria monocytogenes*, or use own models by defining the parameters values of exponential, beta-Poisson, beta-binomial and binomial dose-response models. Outputs can be downloaded in XL files.



# Growth simulation module

$$\mu_{\max} = \mu_{\text{ref}} \cdot \left[ \frac{(T - T_{\min})}{T_{\text{ref}} - T_{\min}} \right]^2 \cdot \frac{(a_w - a_{w \min})}{(a_{w \text{ opt}} - a_{w \min})} \cdot [1 - 10^{(\text{pH}_{\min} - \text{pH})}] \cdot \left( 1 - \frac{[\text{LAC}_U]}{[\text{MIC}_U \text{ lactic acid}]} \right) \cdot \frac{(P_{\max} - P)}{P_{\max}} \cdot \left[ \frac{(\text{NIT}_{\max} - \text{NIT})}{\text{NIT}_{\max}} \right]^2 \cdot \frac{(\text{CO}_2_{\max} - \text{CO}_2_{\text{equilibrium}})}{\text{CO}_2_{\max}} \cdot \left( 1 - \sqrt{\frac{[\text{DAC}_U]}{[\text{MIC}_U \text{ diacetate}]}} \right) \cdot \left( 1 - \sqrt{\frac{[\text{AAC}_U]}{[\text{MIC}_U \text{ acetic acid}]}} \right) \cdot \xi$$

$$CM_n(X) = \begin{cases} 0, & X \leq X_{\min} \\ \frac{(X - X_{\max})(X - X_{\min})^n}{(X_{\text{opt}} - X_{\min})^{n-1} \left\{ (X_{\text{opt}} - X_{\min})(X - X_{\text{opt}}) - (X_{\text{opt}} - X_{\max})[(n-1)X_{\text{opt}} + X_{\min} - nX] \right\}}, & X_{\min} < X < X_{\max} \\ 0, & X \geq X_{\max} \end{cases}$$

$$\gamma(\text{pH}) = 1 - 2^{\frac{(\text{pH} - \text{pH}_{\min})}{(\text{pH}_{\min} - \text{pH}_{1/2})}}$$

$$\left[ 1 - \left( \frac{C_i}{\text{MIC}_i} \right)^{n1} \right]^{n2}$$

# Gamma terms

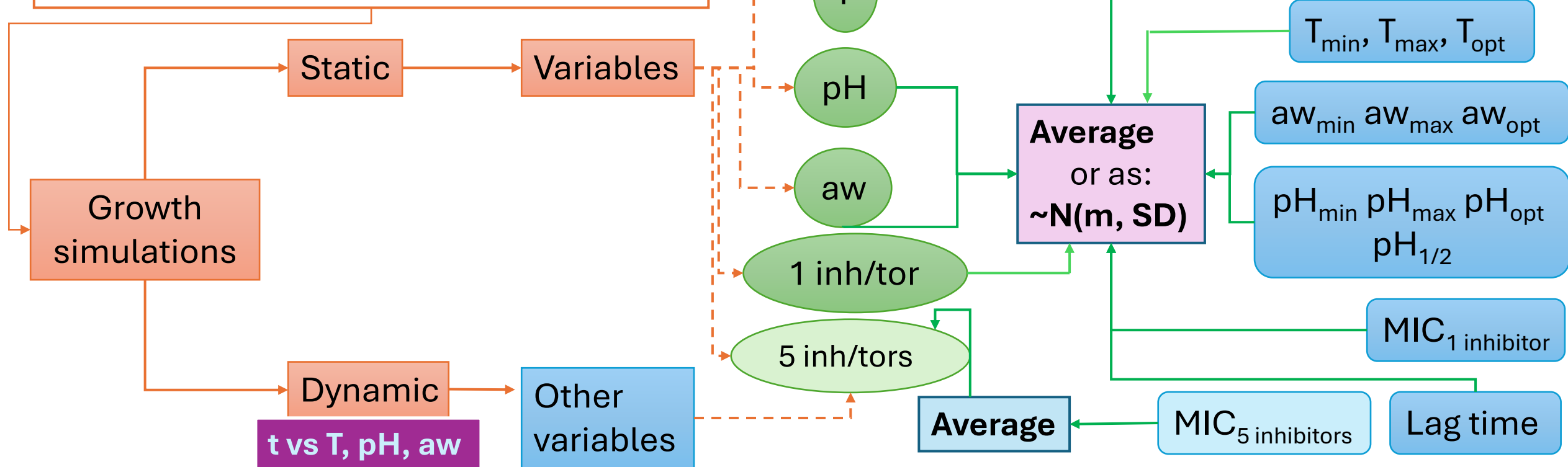
Intr/Extrinsic factors	Cardinal values	Module
<b>Deterministic vs stochastic growth limits</b>		
Fixed value ▼		
<input type="checkbox"/> Rosso model for T°C	<input type="checkbox"/> Rosso model for pH	
<input type="checkbox"/> Rosso model for aw	<input type="checkbox"/> pH12 model for pH	
<input checked="" type="checkbox"/> Including the xsi interaction term		

Intr/Extrinsic factors	Cardinal values	Module
<b>Deterministic vs stochastic growth limits</b>		
Fixed value ▼		
<input type="checkbox"/> Rosso model for T°C	<input checked="" type="checkbox"/> Rosso model for pH	
<input checked="" type="checkbox"/> Rosso model for aw	<input type="checkbox"/> pH12 model for pH	
<input type="checkbox"/> Including the xsi interaction term		

# Selecting gamma terms

Applicable both for fitting & growth simulations

# Stochastic growth simulation module: The backbone



# Defining cardinal values

You may calibrate the model to different foods or strains via this parameter

T, pH, aw

muref (or muopt) 1/h

0,413

Tmin

-0,92

Tref (or Topt)

25

Tmax (when Rosso model is enabled)

48

pHmin

4,4

pHopt (when Rosso model is enabled)

7

pHmax (when Rosso model is enabled)

8

pH12 (when pH12 model is enabled)

5,1

awmin

0,915

awopt or awref

1

awmax

1

Inhibitors

ppm or % of CO<sub>2</sub>, or O<sub>2</sub> in the product

0

Phenolics (ppm, mM, %, or else)

0

Lactate or citrate (ppm, mM, %, or else)

0

Acetate or citrate (ppm, mM, %, or else)

0

Sorbate, benzoate, or diacetate (ppm, mM, %, or else)

0

Intr/Extrinsic factors

Cardinal values

Module

Intr/Extrinsic factors

Cardinal values

Module

MIC CO<sub>2</sub>, or O<sub>2</sub>

3140

Exp. 1 of CO<sub>2</sub> or O<sub>2</sub> term

0.5

Exp. 2 of CO<sub>2</sub> or O<sub>2</sub> term

1

MIC Phenolics

20

Exp. 1 of phenolics term

1

Exp. 2 of phenolics term

1

MIC Lactate or Citrate

50000

Exp. 1 of Lact/Citr. term

1

Exp. 2 of Lact/Citr. term

1

MIC Acetate or Citrate

15000

Exp. 1 of Acet/Citr. term

0.5

Exp. 2 of Acet/Citr. term

1

MIC Sorbate, benzoate or diacetate

2500

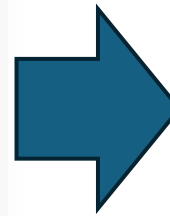
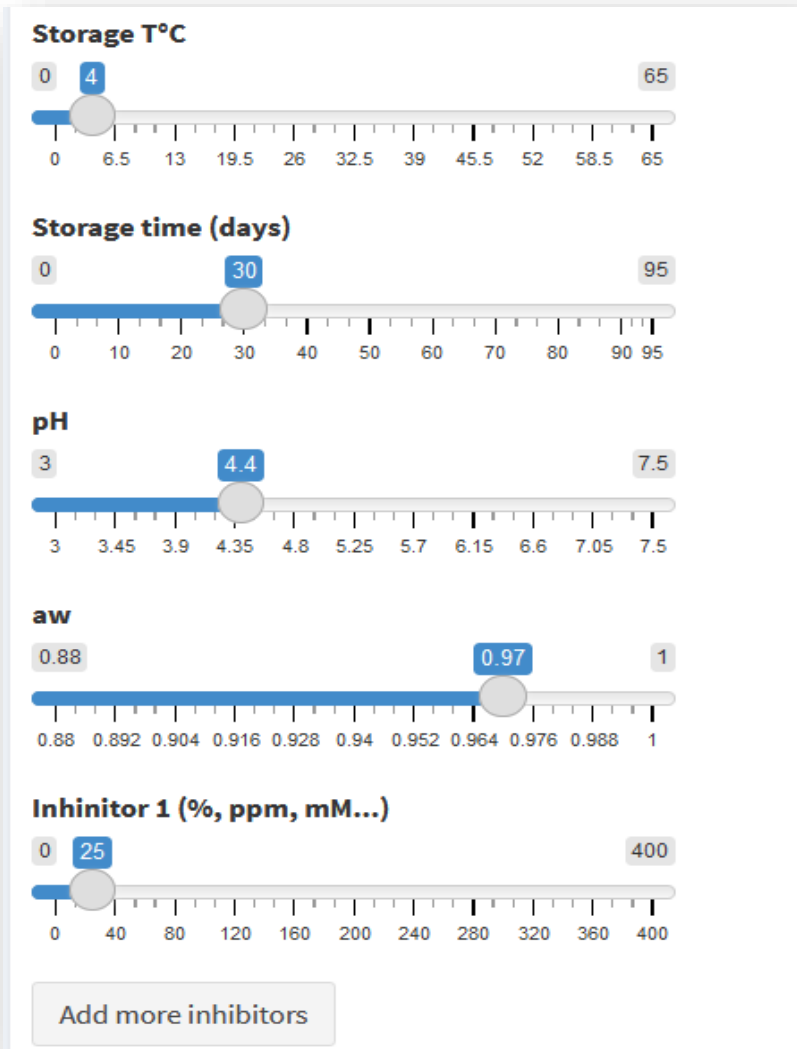
Exp. 1 of Sorb/benz/DA term

0.5

Exp. 2 of Sorb/benz/DA term

1

Use this panel to define the **mean value** (as point estimate) or as the mean value of the distribution



Use this panel to define the **SD** of each factor for use in the **normal distributions**

This panel includes tabs for "Intr/Extrinsic factors", "Cardinal values", and "Module".

**Static vs Dynamic conditions**: A dropdown menu set to "Isothermal".

**Time units**: Radio buttons for "Days" (selected) and "Hours".

**SD of Temp. distr.**: A numeric input field with the value 0.

**SD of Time distr.**: A numeric input field with the value 0.

**SD of pH. distr.**: A numeric input field with the value 0.

**SD of aw distr.**: A numeric input field with the value 0.

**SD of Inhibitor1 distr.**: A numeric input field with the value 0.

**Num. of iterations**: A numeric input field with the value 1.

Use this panel to if you want to use ONLY the **mean value** of cardinal parameters

Cardinal values

Deterministic vs stochastic growth limits

Fixed value

☐ Rosso model for T°C (n=2) ☐ Rosso model for pH (n=1)

☐ Rosso model for aw (n=2) ☐ pH12 model for pH

☒ Including the xsi interaction term

muref (or muopt) 1/h

0.419

Tmin

-2.83

Tref (or Topt)

25

Tmax (when Rosso model is enabled)

48

pHmin

4.97

pHopt (when Rosso model is enabled)

7

pHmax (when Rosso model is enabled)

8



Use this panel to define the **SD** cardinal parameters following **normal distributions**

Cardinal values

Deterministic vs stochastic growth limits

Normal dist.

☐ Rosso model for T°C (n=2) ☐ Rosso model for pH (n=1)

☐ Rosso model for aw (n=2) ☐ pH12 model for pH

☒ Including the xsi interaction term

Average muref(muopt)	SD muref(muopt)
0.419	0

Average Tmin	SD Tmin
-2.83	0.5

Average Topt	SD Topt
25	0

Average Tmax (when Rosso model is enabled)

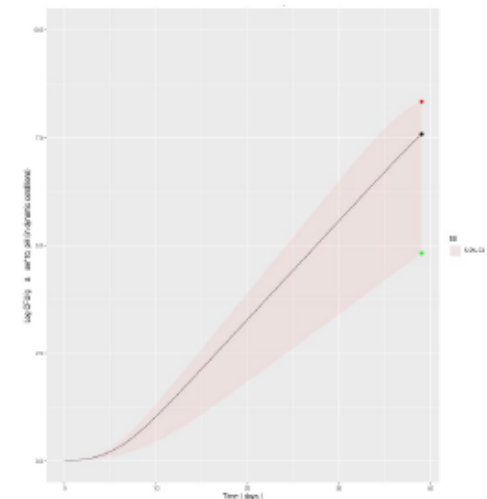
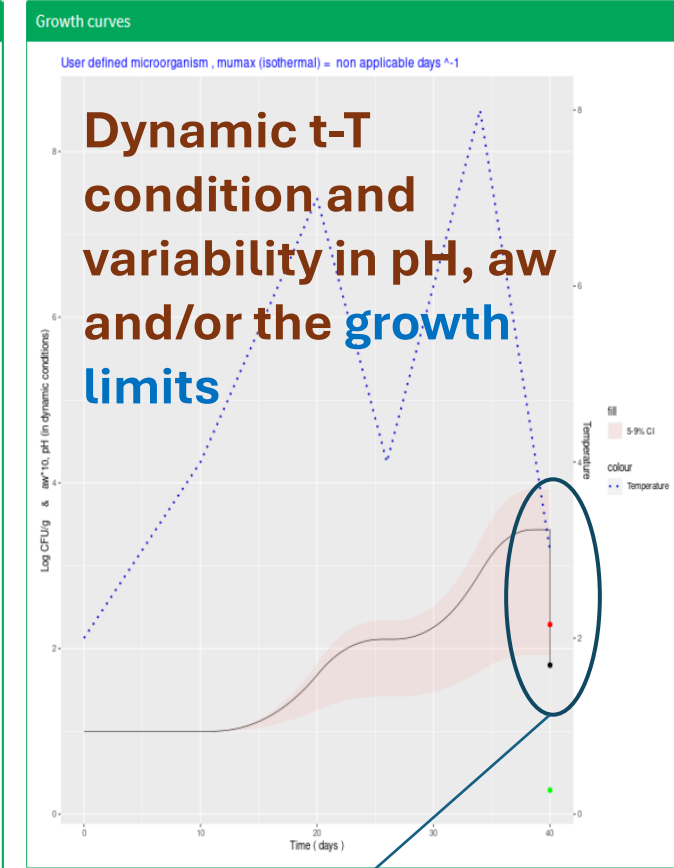
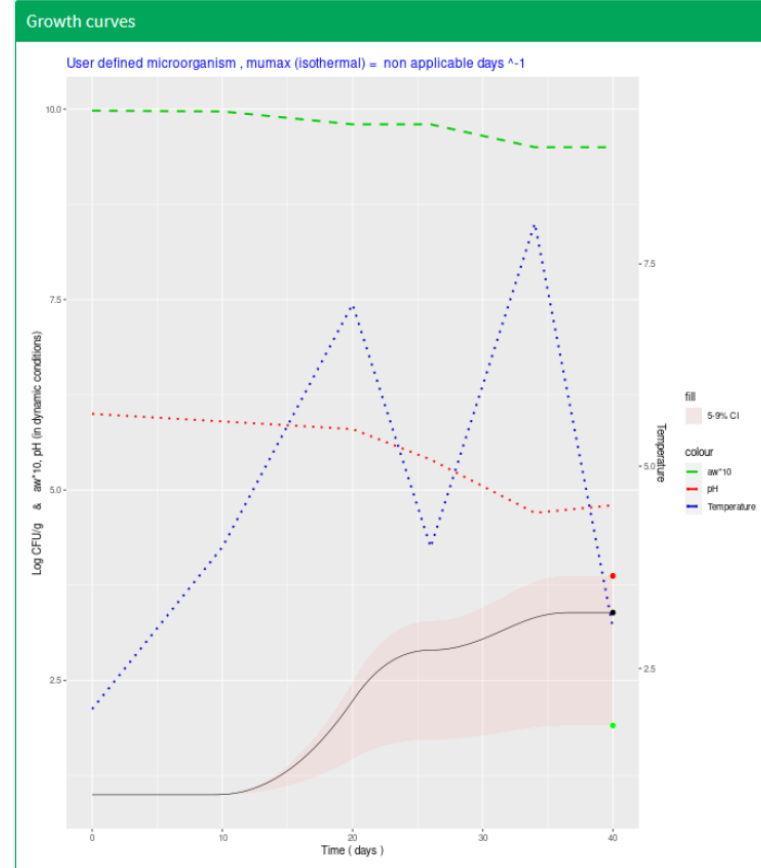
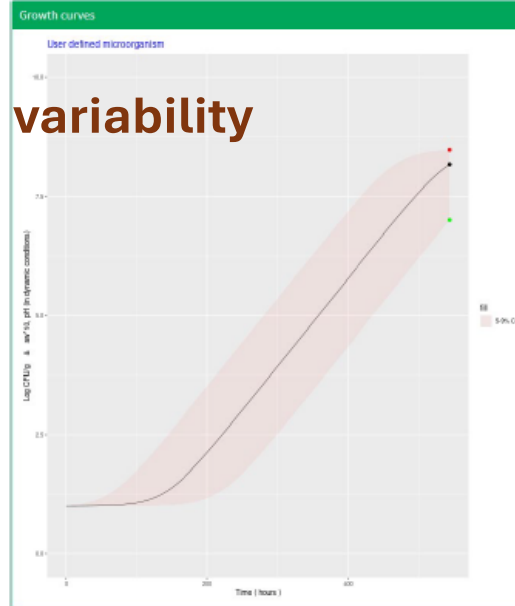
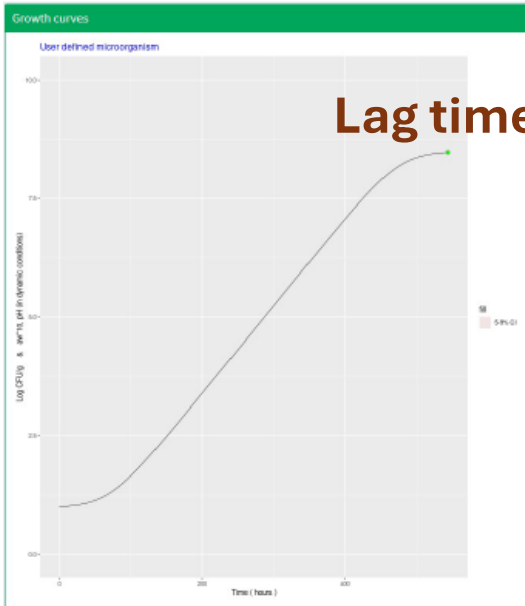
48

SD Tmax (when Rosso model is enabled)

0

Average pHmin	SD pHmin
4.97	0

# Representative graphical outputs (also capturing strain-to-strain variability)



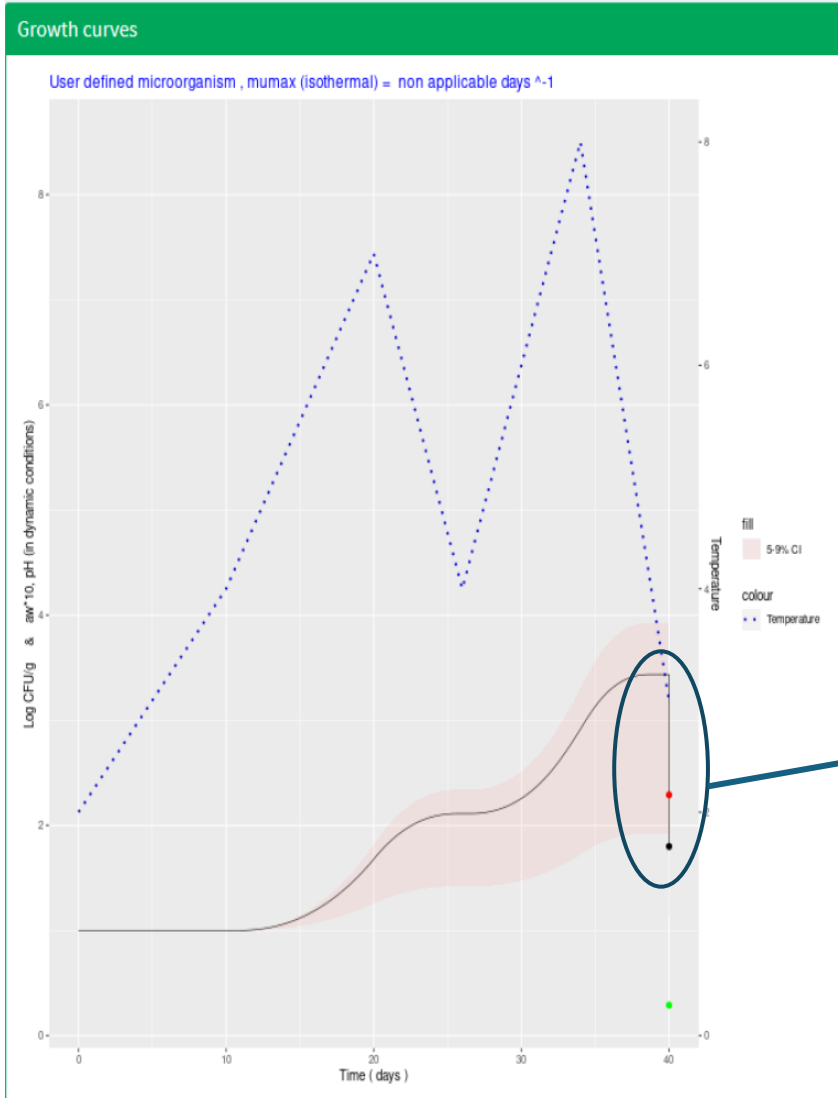
Variability in lag time and/or storage T°C, pH, aw, or inhibitor and/or growth limits

Dynamic t-T-pH-aw conditions & variability in the growth limits

Thermal inactivation (e.g., cooking) after growth



# Digging further to thermal inactivation module



Thermal inactivation  
(e.g., cooking) after  
growth acc. to the  
input panel on the  
right

## Select modules

- ☐ Growth
- ☒ Growth & Inactivation

## Dref (min)

38

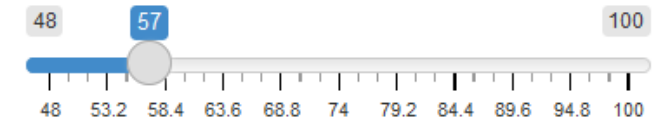
## Tref

52

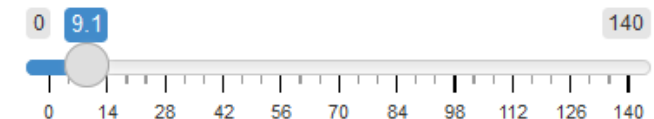
## Z

7

## Heating Temp



## Heating time (min)



1.  
Simulations under **static**  
conditions,  
*deterministically or stochastically*

About

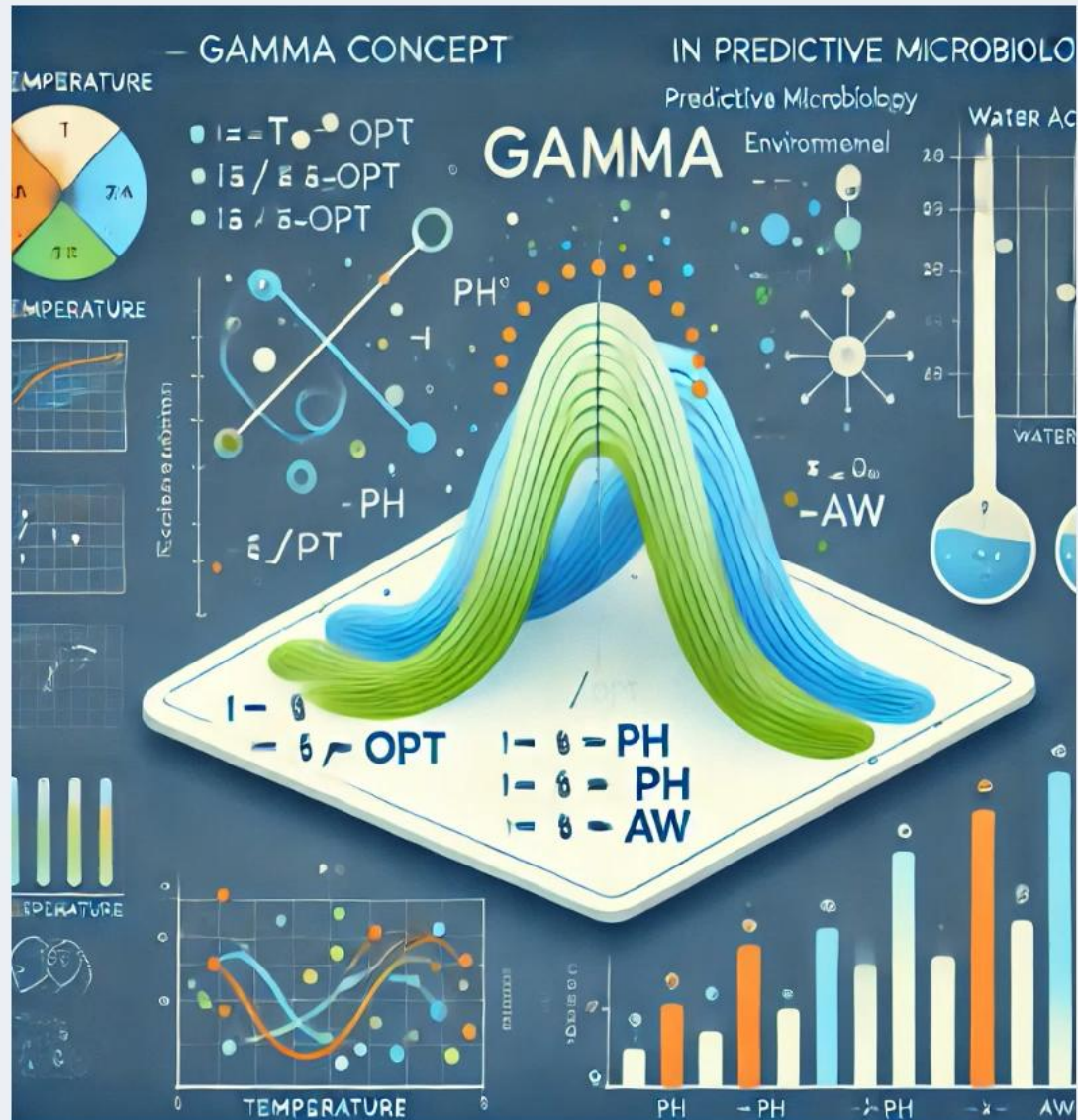
User-defined conditions

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2a.  
Simulations under **dynamic**  
**conditions,**  
*deterministically or stochastically*  
*(STARTING FROM A TABLE)*





2b.  
Simulations under **dynamic**  
conditions,  
*deterministically or stochastically*  
*(STARTING FROM A FILE)*



About

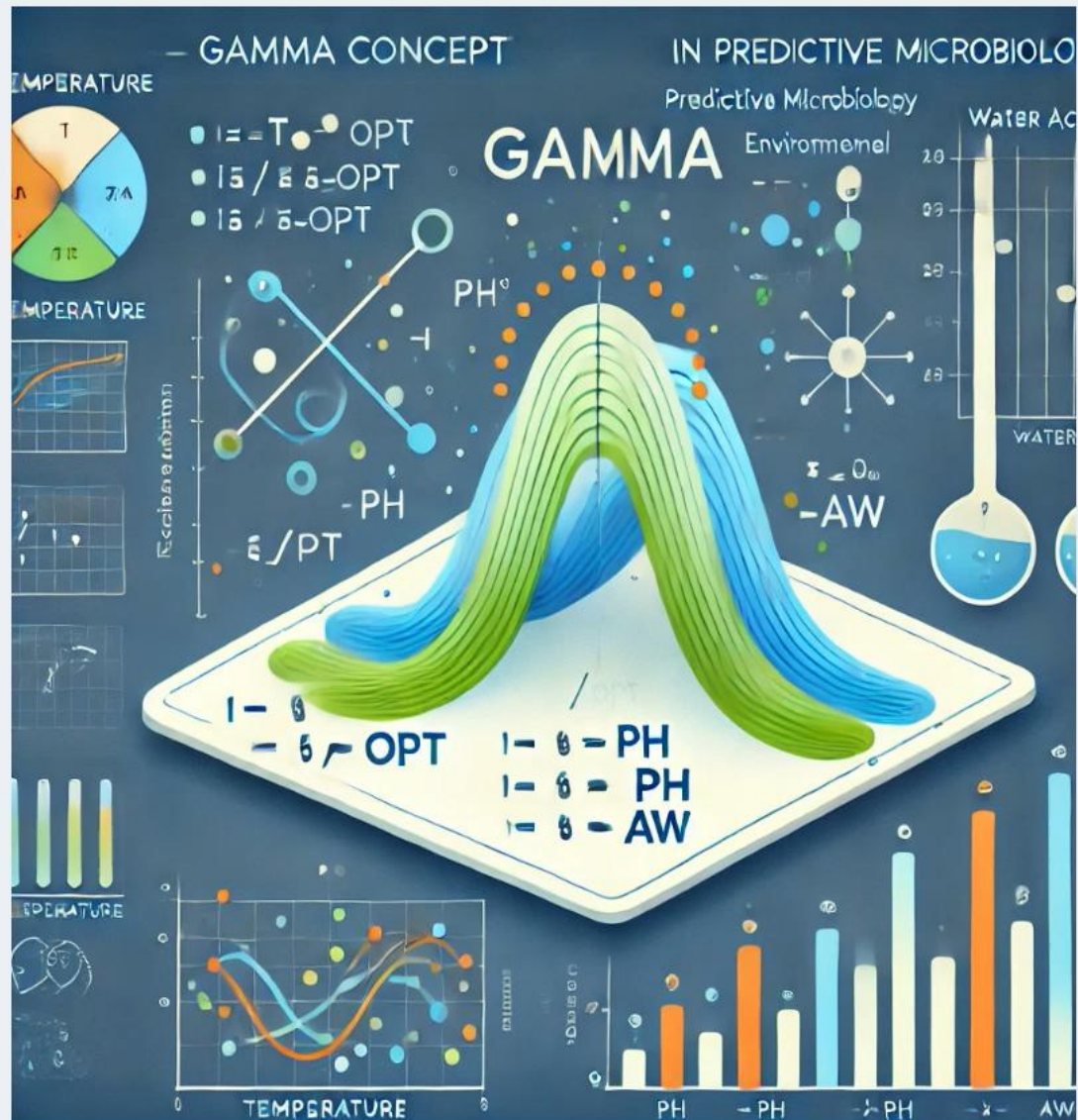
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# Growth/**No Growth** interface based on gamma concept



- About
- User-defined conditions
- Imported 'e-Platon' file
- Modular process Risk model
- Estimation of cardinal values
- Primary model fitting

Click here for user guide files

Intr/Extrinsic factors   Cardinal values   Module

Static vs Dynamic conditions

Isothermal

Time units

Days  
Hours

SD of Temp. distr.

0

SD of Time distr.

0

SD of pH. distr.

0

SD of aw distr.

0

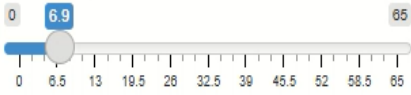
SD of Inhibitor1 distr.

0

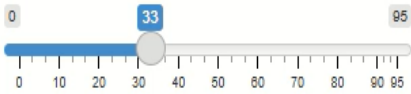
Num. of iterations

1

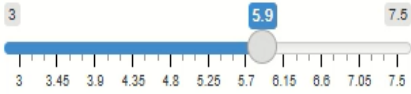
Storage T°C



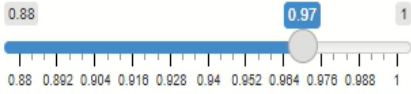
Storage time (days)



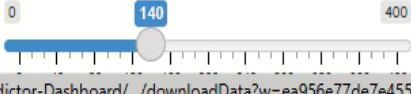
pH



aw

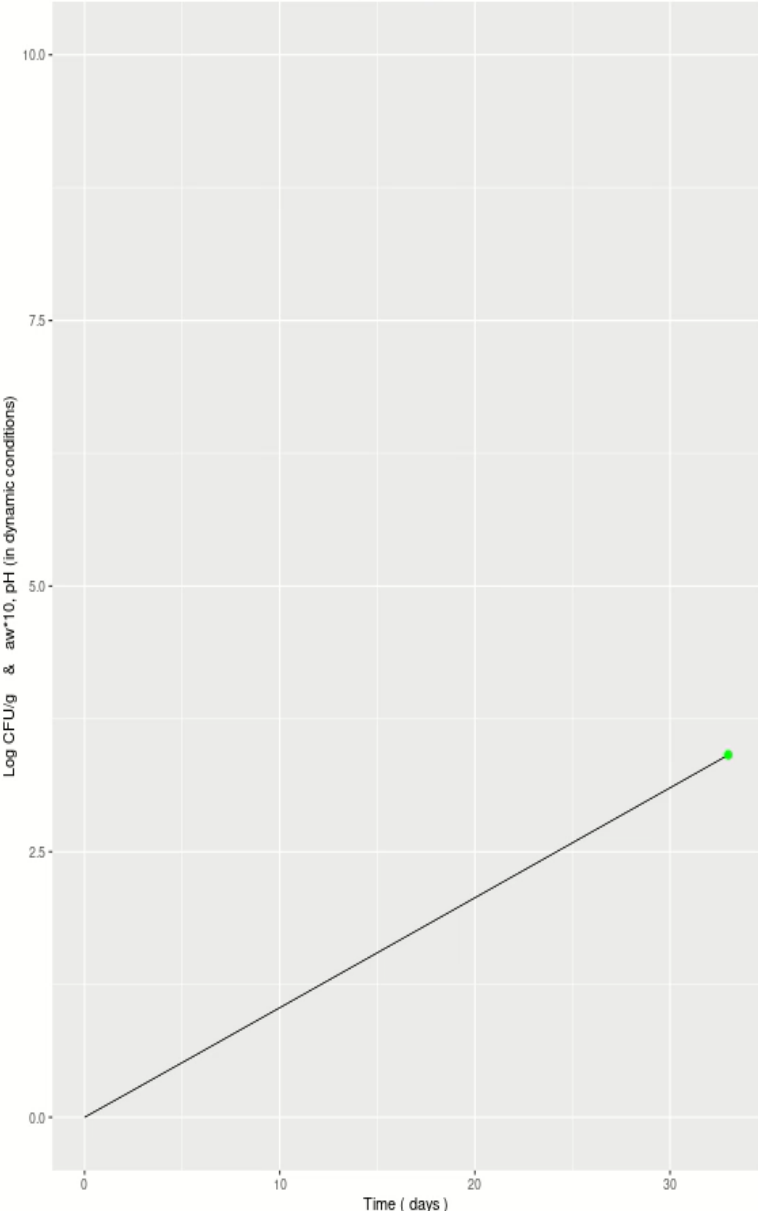


Inhinator 1 (% , ppm, mM...)



Growth curves   Growth/No growth interface

User defined microorganism , mumax (isothermal) = 0.2384 days ^-1



Import/Export data

Independent data

Choose one of the following

Download Model Outputs

Built-in dbase models

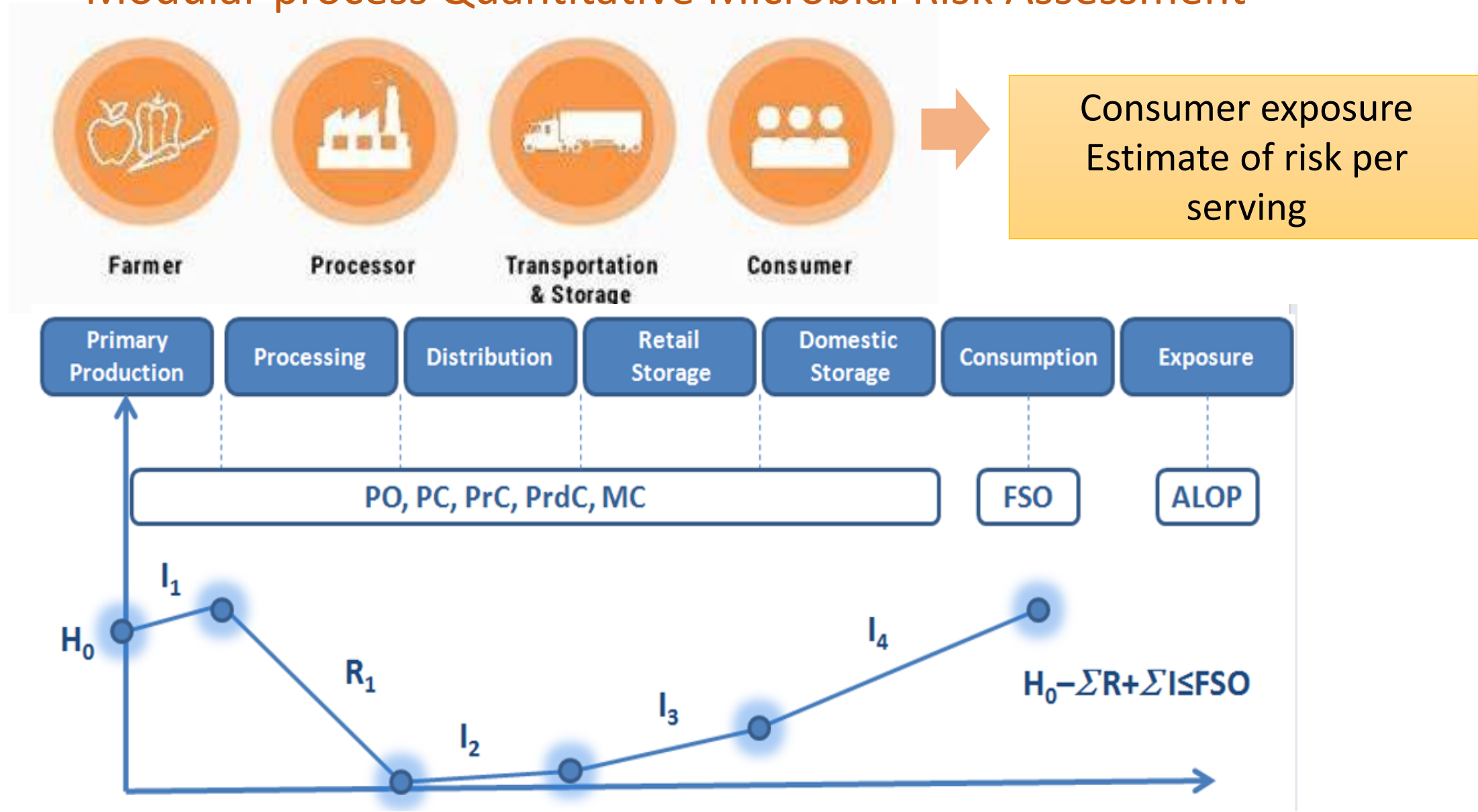
Microorganism	pHmin	pH12	Tmin	Tmax	awmin	awopt	awmax
Salmonella	4.50	5.10	7.20	48.00	0.93	1.00	
STEC	4.50	5.50	9.20	48.00	0.94	1.00	
Bacillus cereus	4.30	5.90	10.30	55.00	0.95	1.00	

Estimating time for certain log increase

Log increase	From	To	Average
3	29.2 days	29.2 days	29.2 days

# QMRA Module

## Modular process Quantitative Microbial Risk Assessment



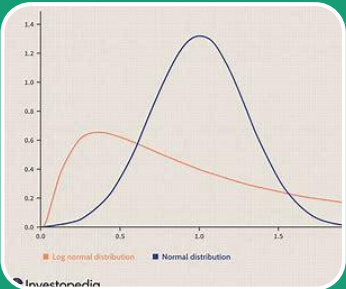
# Specific features



Partitioning (0-1)

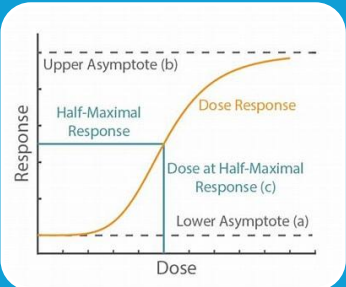
Mixing (Initial + Added mass)

Cross-contamination (P, levels)



Variability (Probability dist/tions)

- Initial contamination
- Time, T, ho, Cardinal values, Growth/reduction
- Serving size + **uncertainty in prevalence (Beta distr.)**



Dose response

- Built-in (literature) DR models
- User-defined models
- Beta-Poisson, (Beta-)Binomial, Exponential

Partitioning

☒ No partition

☐ Partition

☐ Mixing

Initial mass (g: 0-infinity)

1

Added mass (g: 0-infinity)

1

P cross-contamination (0-1)

0

Cross- (re-)contamination levels

Pert

Need

Concept-Design

Interactive tool

On-line demo

# Modular process Quantitative Microbial Risk Assessment



Farmer



Processor



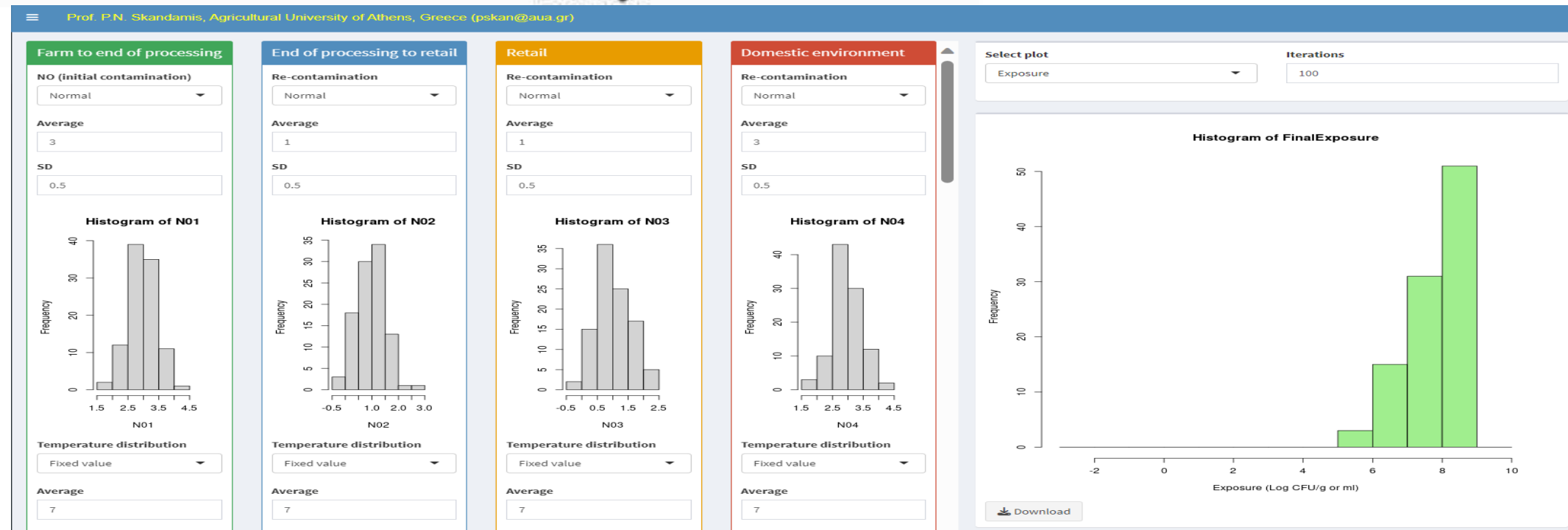
Transportation  
& Storage



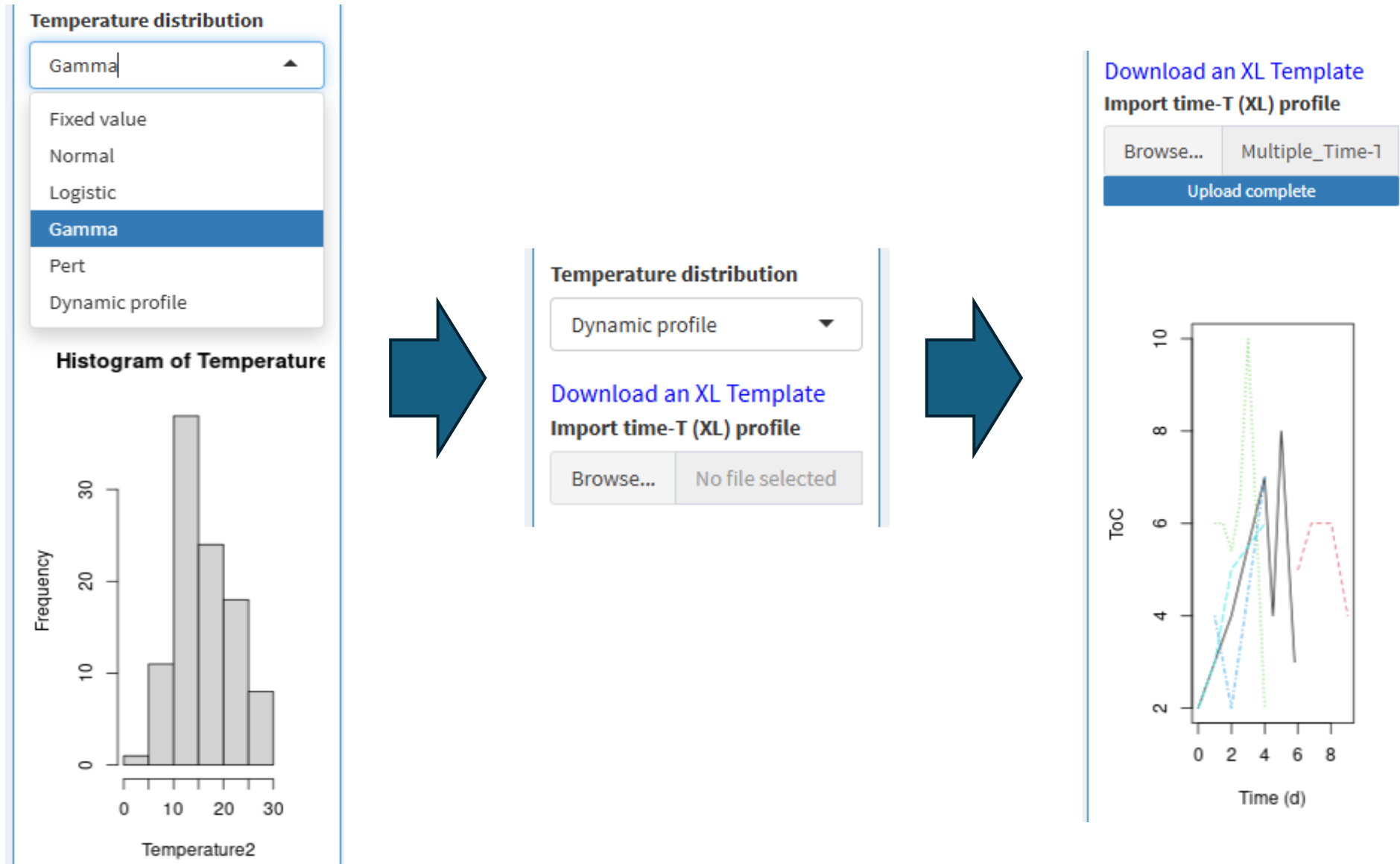
Consumer



Consumer exposure  
Estimate of risk per  
serving



# Integrating time-T profiles in QMRA for 3 modules



## Annual number of services

1

## Risk Table

Exposure_Metrics	LogCFU_per_g_OR_ml	Illness_Metrics	Estimate
Average Dose per serving	5.7	Average Pill per serving	6.036e-07
-	-	Cases per annum	6.036e-07
Mode	5.5	Mode	3.162e-07
p5	4.6	p5	4.972e-08
p50	5.62	p50	5.233e-07
p95	6.89	p95	9.611e-06

## Select plot

Probability of illness

## Iterations

1000

## Serving size (g)

61

## Serving Size Distr/tion

Gamma

## alpha of gamma dist.

4

## beta of gamma dist.

12

## Initial Prevalence (0-1)

0

## Dose response

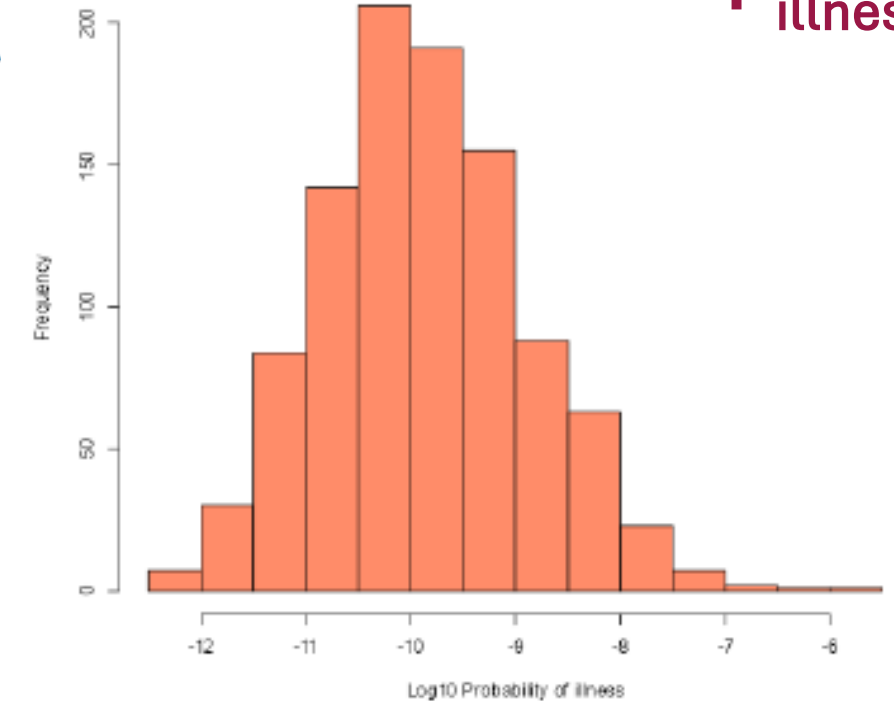
L. monocytogenes susceptible

FDA, 2014

Please FIRST read the DISCLAIMER

Click to render Plot or resample

Histogram of P\_of\_illness



Pillness

## Select Mode

Exposure

## Iterations

100

## Serving size (g)

25

## Serving Size Distr/tion

Gamma

## alpha of gamma dist.

4

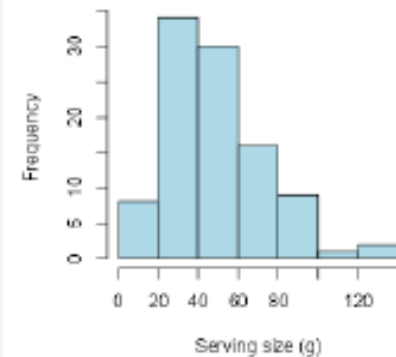
## beta of gamma dist.

12

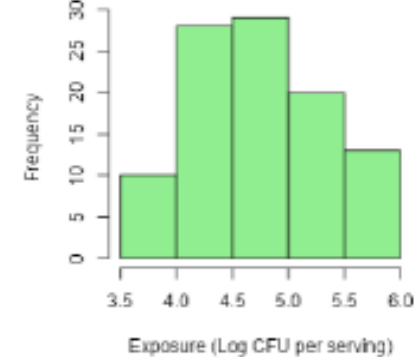
Click to render Plot or resample

Exposure

Histogram of Serving



Histogram of FinalExposure

Risk  
outputs

Download FULL MODEL



- About
- User-defined conditions
- Imported 'e-Platon' file
- Modular process Risk model
- Estimation of cardinal values
- Primary model fitting

Click here for user guide files

Intr/Extrinsic factors   Cardinal values   Module

Static vs Dynamic conditions

Isothermal

Time units

Days  
Hours

SD of Temp. distr.

0

SD of Time distr.

0

SD of pH. distr.

0

SD of aw distr.

0

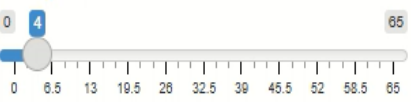
SD of Inhibitor1 distr.

0

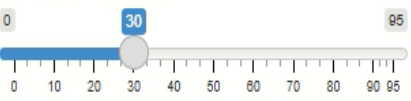
Num. of iterations

1

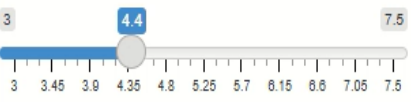
Storage T°C



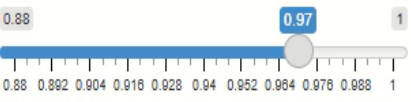
Storage time (days)



pH



aw

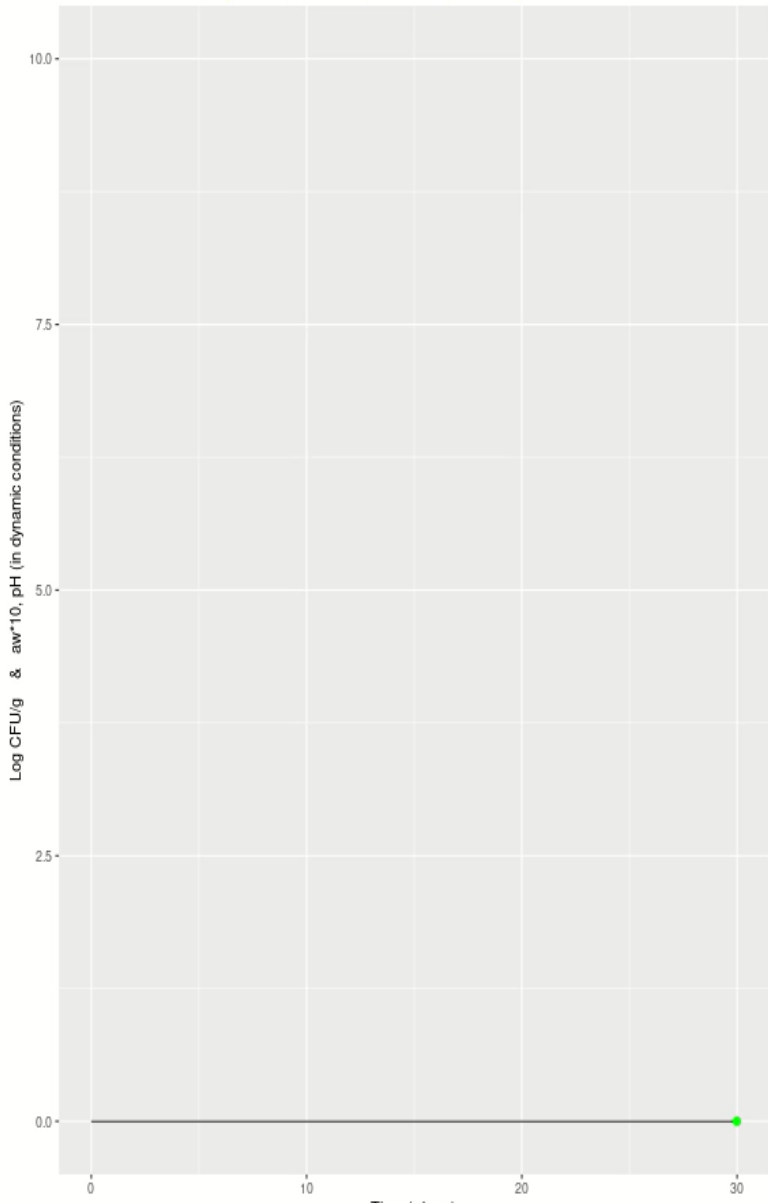


Inhibitor 1 (% , ppm, mM...)



Growth curves   Growth/No growth interface

User defined microorganism , mumax (isothermal) = 0 days ^-1



fill  
5-9% CI

Import/Export data

Independent data

Choose one of the following

Download Model Outputs

Built-in dbase models

Microorganism	pHmin	pH12	Tmin	Tmax	awmin	awopt	awmax
Salmonella	4.50	5.10	7.20	48.00	0.93	1.00	
STEC	4.50	5.50	9.20	48.00	0.94	1.00	
Bacillus cereus	4.30	5.90	10.30	55.00	0.95	1.00	

Estimating time for certain log increase

Log increase	From	To	Average
0	> 30 days	> 30 days	> 30 days



## Correlation type

- ☒ Spearman  
☐ Pearson

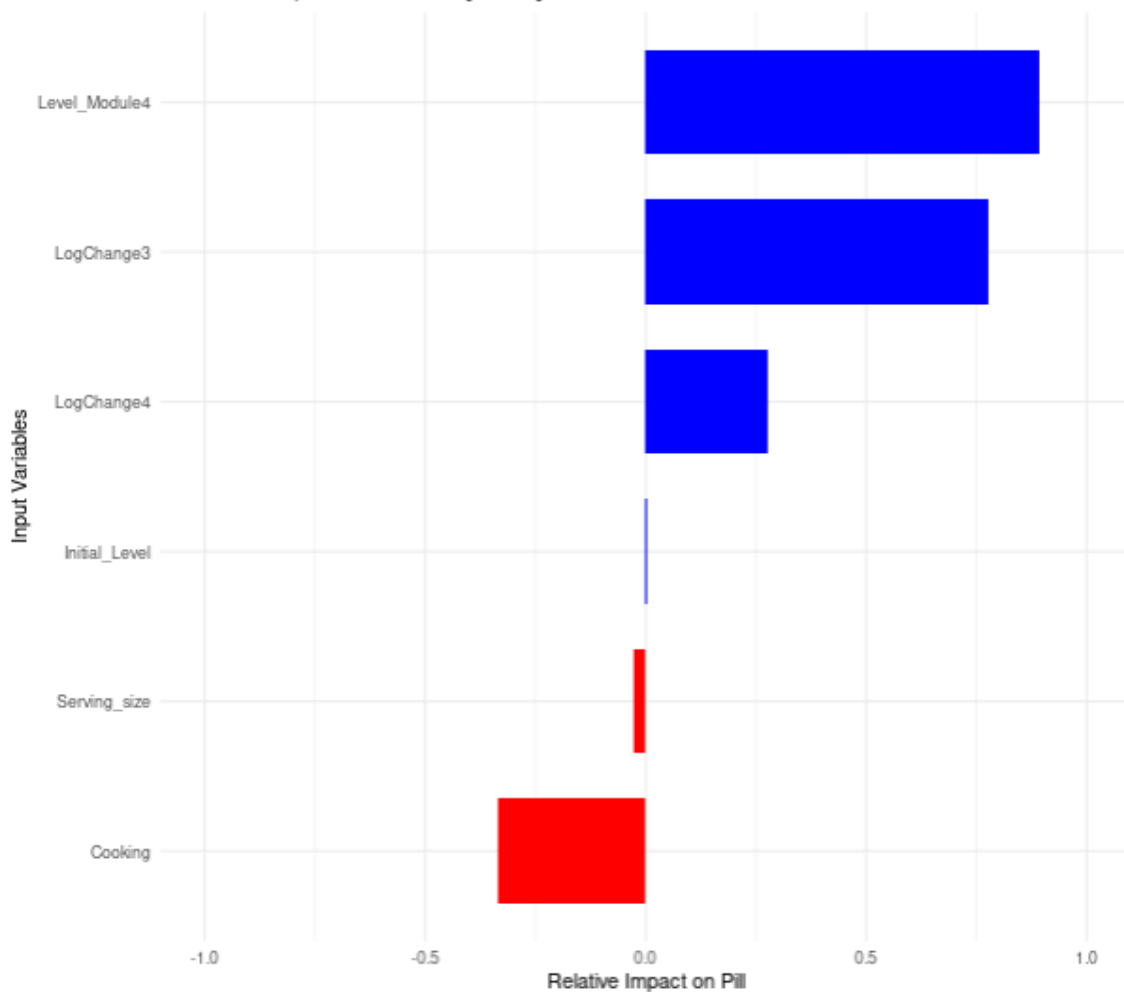
## Variable

- ☒ Pillness  
☐ Exposure

Variables: N01  
LogChange (Incre  
Decontamination



Tornado Graph for Sensitivity Analysis of Pill



# Sensitivity analysis

*Thank you!*

**Professor  
Panos N. Skandamis**

*Agricultural University of Athens,  
Greece*

*pskan@aua.g*



## 1. Load Training Dataset

Browse... No file selected

[Download an XL Template](#)

Specify the number of variables

19

### Independent variable type

- ☒ Continuous (ANN,SVM,PLSR)  
☐ Categorical (PLS-DA)

### Actions for fitting (pre-processing)

- ☒ Log10 transformation of dependent variable  
☐ Savitzky-Golay smoothing  
☒ SNV transf/tion to independent (predictor) variables  
☒ (Auto)-scaling of independent variables for fitting

### Actions for PCA

- ☒ Apply autoscaling for PCA  
☐ Apply rangescaling for PCA

### Machine learning algorithm

- ☐ Artificial Neural Networks (1 hidden layer)  
☐ Random Forest Regression  
☐ Supporting Vector Machines (Linear)  
☐ Supporting Vector Machines (Non Linear)  
☒ Partial Least Square Regression

- ☐ Bootstrapping for CI estimation of PLSR coefficients

[About](#)

[Training Graphs](#)

[PCA](#)

[Testing \(validation\) with independent data](#)

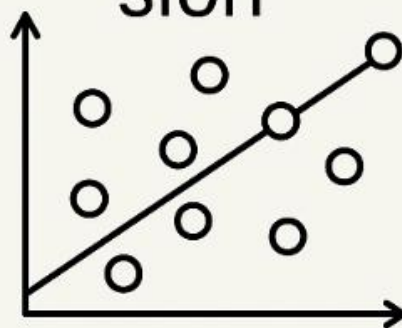
[PLSR summary](#)

[PLS-DA training](#)

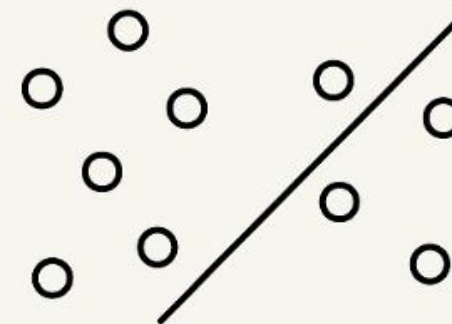
[Random Forest Regression GoF](#)

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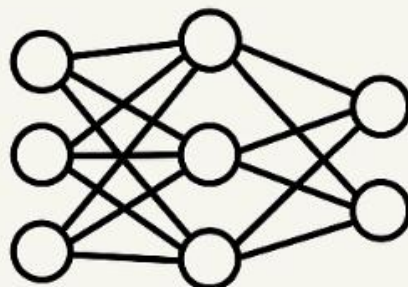
## Partial Least Squares Regression



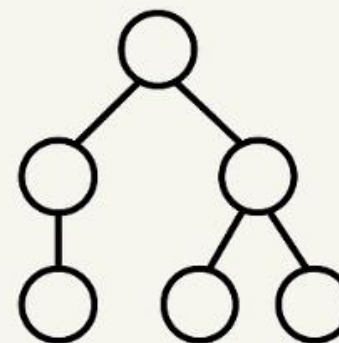
## Support Vector Machines



## Artificial Neural Networks



## Random Forest Regression





## 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 <sup>a</sup>, Annemarie Gunvig <sup>b</sup>, Claus Borggaard <sup>b</sup>, Jesper Blom-Hanssen <sup>b</sup>, Lyndal Mellefont <sup>c</sup>, Tom Ross <sup>c</sup>, Francoise Leroi <sup>d</sup>, Tony Else <sup>e</sup>, Diana Visser <sup>e</sup>, Paw Dalgaard <sup>a,\*</sup>

$$\mu_{\max} = \mu_{\text{ref}} \cdot \left[ \frac{(T - T_{\min})}{T_{\text{ref}} - T_{\min}} \right]^2 \cdot \frac{(a_w - a_{w \min})}{(a_{w \text{opt}} - a_{w \min})} \cdot \left[ 1 - 10^{(\text{pH}_{\min} - \text{pH})} \right] \cdot \left( 1 - \frac{[\text{LAC}_U]}{[\text{MIC}_U \text{ lactic acid}]} \right) \cdot \frac{(P_{\max} - P)}{P_{\max}}$$

$$\cdot \left[ \frac{(\text{NIT}_{\max} - \text{NIT})}{\text{NIT}_{\max}} \right]^2 \cdot \frac{(\text{CO}_2_{\max} - \text{CO}_2_{\text{equilibrium}})}{\text{CO}_2_{\max}} \cdot \left( 1 - \sqrt{\frac{[\text{DAC}_U]}{[\text{MIC}_U \text{ diacetate}]}} \right) \cdot \left( 1 - \sqrt{\frac{[\text{AAC}_U]}{[\text{MIC}_U \text{ acetic acid}]}} \right) \cdot \xi$$

## Need

## Concept-Design

## Interactive tool

## On-line demo

Handbooks/textbooks, review articles,  
Expert knowledge, certification

Laboratory analysis,  
technical papers

Scientific publications, data  
bases, statistical process control

Spatio-temporal illustration,  
interactive tools, cloud-  
based applications, **(AI),**  
**ChatGPT**

Information

Data  
!

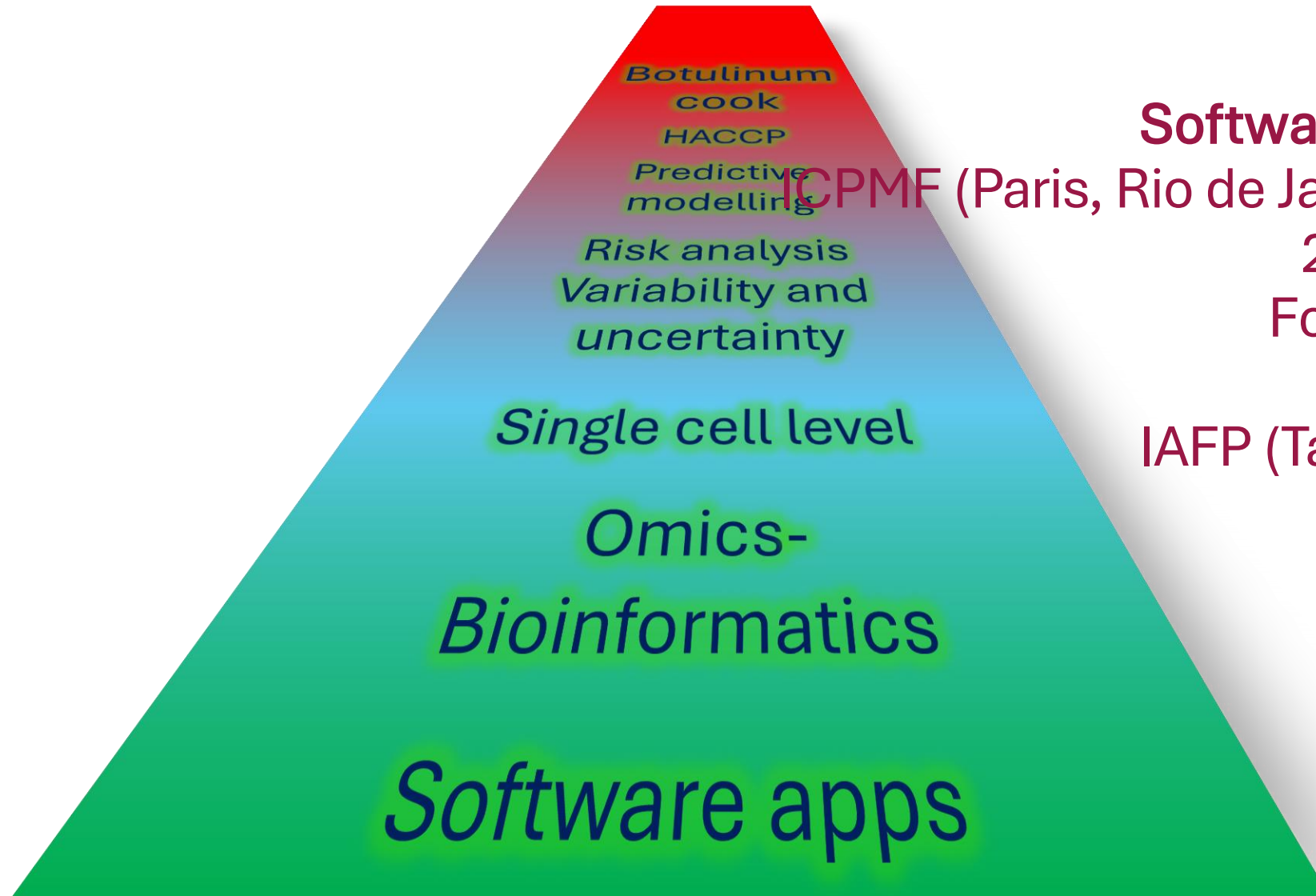
Knowledge !!

Wisdom  
!!!(?)

*“...From **humancene** (‘ανθρωπόκαινο’), Gaea Theory, to **Novacene** (καινόκαινο) of hyper-intelligence ...”. James Lovelock*



# Roadmap of quantitative microbiology



## Software Fair sessions:

ICPMF (Paris, Rio de Janeiro, Braganca):

2011, 2015, 2019

FoodMicro (Berlin):

2018

IAFP (Tampa, Louisville):

2017, 2019

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- June 3, 2025    Sanitation Break: Legal Interpretation and Industry Practice
- June 3, 2025    Risk-Based Approaches to Sanitation in Dry Processing Environments
- June 5, 2025    Hygienic Design & Monitoring Strategies to Prevent In-Process Contamination in Food and Beverage Applications

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