On the use of the Gompertz model to predict microbial inactivation behaviour

<u>Maria M. Gil</u> F. Miller, M. Quintas, T.R.S. Brandão and C.L.M. Silva



June 24th-28th, 2006 Orange County Convention Center Orlando, Florida



Objectives





y population size t time a,b,c model parameters



Study of the original Gompertz equation

modifications in order to describe microbial inactivation

re-parameterization of the modified function

biological meaning



Introduction



Mathematical modelling

- Food microbiologists are giving increased attention to microbial kinetics modelling
- The use of mathematical models that properly describe microbial behaviour under specific environmental conditions is important for predictive purposes and process design
- Mathematical models require the definition of <u>parameters</u> (e.g. the rate constant), which should be <u>precisely estimated</u>



Introduction





 $y_{orig}(t) = a \exp(-\exp(b - ct))$

Is an empirical sigmoidal relationship (describe linear and nonlinear curves)

Introduced in food microbiology to describe <u>asymmetrical</u> <u>sigmoidal shape</u> of microbial growth

Can be used to describe microbial <u>inactivation</u> behaviour (*if properly modified*)









information related to function mathematical study and to methodology of re-parameterization is lacking

neglecting parameters biological meaning !

only few works link model parameters to microbiological meaning (growth/survival rate and lag time/shoulder)

drawbacks in microbial kinetic models







Insightful information can be obtained with <u>re-</u> parameterized forms

Microbial survival often presents a lag, a linear phase (corresponding to a maximum inactivation rate, k_{max}) and a residual population (tail)



Those phenomena should be included

in model parameters





Introduction



modify in order to describe inactivation



Gompertz model



Microbial behaviour







Microbial behaviour







Introduction





modify in order to describe inactivation

re-parameterization based on the analytical study of the function

Original

Gompertz model





Introduction



modify in order to describe inactivation re-parameterization based on the analytical study of the function

Original

Gompertz model

test drawbacks/advantages of the re-parameterized forms



Approaches



Two different approaches were studied in order to obtain Gompertz modified model for inactivation kinetics:

the logarithm of the microbial load (log N) → approach 1

>
$$y_{inact}(t) = \log(N) = const - y_{orig}(t)$$
 (1)

EXAMPLE 1 normalized to the initial load (log N/N₀) \rightarrow approach 2

$$y_{inact}(t) = \log\left(\frac{N}{N_0}\right) = -y_{orig}(t)$$
 (2)





Analytical study of the functions

Func	tion	limits

time → ∞	tailing effect
time → 0	initial value





Parameters with microbiological meaning













Model parameters

Maximum inactivation rate

(k_{max})

derived by calculating the 1st derivative at the curve inflexion point







Model parameters

<u>Shoulder</u> (L) determined by the interception of the extrapolated tangent line with initial value (or time-axis - approach 2)







Re-parameterized forms Approach 1

 $y_{inact}(t) = \log(N) = const - a \exp(-\exp(b - ct))$









Re-parameterized forms

Approach 2

$$y_{inact}(t) = \log\left(\frac{N}{N_0}\right) = -a \exp\left(-\exp\left(b - ct\right)\right)$$

$$a = -\log\left(\frac{N_0}{Nres}\right)$$
$$c = -\frac{k_{\max} \exp(1)}{a}$$
$$b = L \ c + 1$$

3 parameters

$$y_{inact}(t) = \log\left(\frac{N_{res}}{N_0}\right) \exp\left(-\exp\left(\frac{k_{max}e}{\log\left(\frac{N_{res}}{N_0}\right)}(L-t)+1\right)\right)$$







Studied approaches were validated on the basis of experimental thermal inactivation data of *Listeria innocua*





Methodology



Kinetic parameters were estimated by non-linear regression analysis of isothermal data

least squares estimation

using STATISTICA TM v 6.0 software





Time (min)





















Gompertz modified model allowed accurate predictions of *Listeria innocua* inactivation in the temperature range considered







	Approach 1		Approach 2	
	$y_{inact}(t) = \log(N) = const$	$-a\exp(-\exp(b-ct))$	$y_{inact}(t) = \log\left(\frac{N}{N_0}\right) = -$	$-a\exp(-\exp(b-ct))$
Regression	R _{adj} ²	0.876	R _{adj} ²	0.970
Analysis	Normality	\checkmark	Normality	\checkmark
	Randomness	\checkmark	Randomness	\checkmark
	Parameter	Error	Parameter	Error
		(%)		(%)
Parameter's	log N _{res} /N ₀	26 - 37	log N _{res} /N ₀	14 - 28
Precision	k _{max}	11 - 17	k _{max}	7 – 13
		43 - 563		16 - 63





	Approach 1		Approach 2		
	$y_{inact}(t) = \log(N) = const - a \exp(-\exp(b - ct))$		$y_{inact}(t) = \log\left(\frac{N}{N_0}\right) = -a\exp\left(-\exp(b - ct)\right)$		
Regression Analysis	R _{adj} ²	0.876	R _{adj} ²	0.970	
	Normality	\checkmark	Normality		
	Randomness	\checkmark	Randomness	\checkmark	
	Parameter	Error (%)	Parameter	Error	
Parameter's	log N _{res} /N ₀	26 - 37	log N _{res} /N ₀	14 - 28	
Precision	k _{max}	11 - 17	k _{max}	7 – 13	
		43 - 563		16 - 63	
		$error = \frac{95\% \text{ con}}{2}$	$\frac{\text{fidence interval}}{2} x \frac{1}{\text{parameter}}$	estimate	

Conclusions



Gompertz allowed accurate predictions of Listeria innocua inactivation in the range considered

Both approaches are quite similar

Parameters were estimated with precision

The quality of regression and parameters estimation were improved if normalized data is used

The use of accurate models is a considerable tool to predict target pathogen's survival





Acknowledgments

The first author acknowledges FLA (Fundação Luso Americana)

fundação LUSO-AMERICANA

and

Escola Superior de Tecnologia do Mar – Instituto Politécnico de Leiria





Thank You!

