Deeper insight into stochastic microbial inactivation

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Introduction

Traditional deterministic inactivation models do not consider the heterogeneity in the resistance of individual cells to a lethal stress. Lately, single cell individuality has attracted the scientific interest and several approaches have highlighted its importance leading to stochastic inactivation models. In a previous work of ours a statistical modeling approach was applied based on probability distributions for the description of individual cell time to death and the evaluation of population inactivation dynamics using simulation techniques (Aspridou and Koutsoumanis, 2015). In practice, food industry is interested in knowing the probability of surviving populations after the application of a treatment.

For this, an approach for the estimating the distribution of treatment times leading to zero survivals was developed.

Concept

Let assume an exponential inactivation model (Fig 1.) where variability in single cell inactivation time is taken into account. Given the binomial process, the probability of having zero survivors $p(0)$ is given by Eq. 1.

$$p_0 = \left(1 - e^{\frac{-t ln(10)}{D}}\right)^{N_0}$$

It can be analytically found that, for high N_0, the treatment times, leading to zero survivors, aka the *maxima* can be described by an Extreme Value Distribution of Type 1 (Gumbel). The proof of concept is given in Fig 2.

- The effect of temperature on the kinetic parameter *D* value using the *z* - value secondary model (Pochet et al., 2005), originally proposed by Bigelow (1921) can be employed using this approach
- The variability of the initial population level N_0 can be also taken into account

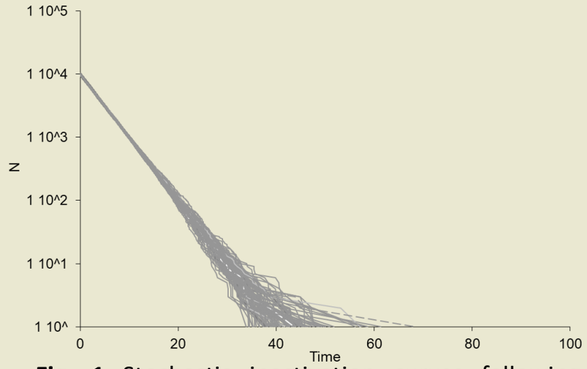

Fig. 1 Stochastic inactivation curves following exponential distribution of individual cell time of death.

$$p_0 = \left(1 - e^{\frac{-t\,ln(10)}{D}}\right)^{N_0} =>$$

$$p_0 = \left(1 - \frac{1}{N_0} e^{\frac{-t\ln(10)}{D} + lnN_0}\right)^{N_0} =>$$

$$p_0 = \left(1 - \frac{1}{N_0} e^{\frac{-t\ln(10)}{D} + \frac{D\,lnN_0}{D}}\right)^{N_0} =>$$

$$p_0 = \left(1 - \frac{1}{N_0} e^{\frac{-t\ln(10) + \log N_0 \ln(10) D}{D}}\right)^{N_0} =>$$

$$p_0 = \left(1 - \frac{1}{N_0} e^{\frac{-t + \log N_0 D}{\frac{D}{\ln(10)}}}\right)^{N_0} =>$$

By setting $t = x$, $\mu = D\ logN_0$, $\beta = D/ln(10)$

$$p_0 = \left(1 - \frac{1}{N_0} e^{\frac{-(x-\mu)}{\beta}}\right)^{N_0} =>$$

$$e^{-e^{\frac{-(x-\mu)}{\beta}}}$$

CDF of Gumbel distribution

Fig. 2 Proof of concept that the probability distribution of treatment times leading to zero survivals converges to an Extreme Value Distribution (Gumbel). μ location, β scale par.

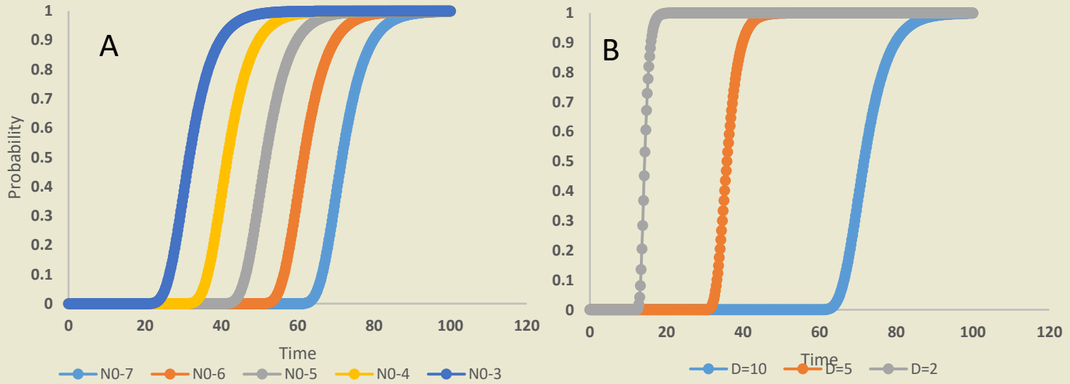

Fig. 3 Effect of ***D*** value and initial population level N_0 on the Gumbel distribution describing the treatment times leading to zero survivals. For A: *D*= 10. For B: N_0 = 10^7.

- Initial population level affects μ (location parameter)
- *D* value affects μ and β (scale parameter)

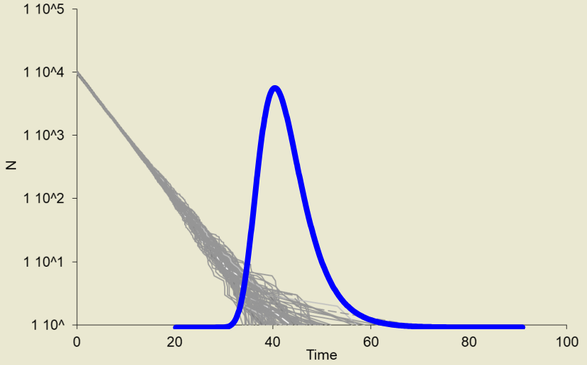

Fig. 4 Comparison of treatment times leading to zero survival based on Extreme Value distribution and Monte Carlo simulation results based on Exponential distribution of individual cell times of inactivation.

Practical importance for the food industry

If *D* value and initial population level N_0 are known, then by using the following Eq. the treatment time leading to zero survivors can be estimated for a desired confidence level.

$$t = D\ logN_0 - \frac{D}{\ln(10)} * \ln(-\ln(p))$$

Example
Initial population: 10000 cfu
D value: 10 time units
Confidence level 99.99%

$t_{0.9999}$ = 80 time units = 8 * D

References Aspridou Z., Koutsoumanis K. 2015. Individual cell heterogeneity as variability source in population dynamics of microbial inactivation. *Food Microbiol 45,2016-221/* Poschet F. et al. 2005. Assessing the optimal experiment setup for first order kinetic studies by Monte Carlo analysis. *Food Control* 16, 873-882/ Bigelow W. 1921. The logarithmic nature of thermal death time curves. *J. Infec. Dis. 26, 528-536*