Addressing short term heat peaks on the shelf life of minced meat

K. Schmidt[1], T. Lettmann[2], R. Stamminger[2]
[1]University of Bonn, INRES IPE, Karlrobert-Kreiten Str. 13, 53115 Bonn & NEMAPLOT, Bonn
[2]University of Bonn, ILT, Nussallee 5, 53115 Bonn

Presented on the 4th. International Workshop on Cold-Chain-Management at the University of Bonn, Sept. 2010, further information on: http://www.ccm.uni-bonn.de

Email: kai.schmidt@uni-bonn.de
Keywords: shelf life, minced meat, predictive modelling, temperature response function, parameter estimation, initial value problems

Introduction

Minced pork meat decays rapidly as microbiological growth processes continue immediately after production and packing. However the potential shelf life can be extended from two to seven days by the use of MAP ("Modified Atmosphere Packaging") foil under favourable cold conditions from 2 to 4 °C. It is conceivable that food is temporarily exposed to high temperatures up to 50 °C during transport by the consumer. The question arises, how the shelf life of food is affected by such events. A common tool used to estimate shelf life is to model microbial growth as a function of temperature using the Arrhenius equation imbedded in some kind of continuous growth function. This approach is applicable to temperature regimes up to 20°C, but not valid at higher temperatures, as the system would exceed realistic growth rates. In order to consider high temperature exposures, a response model is required with recontoured slopes at higher temperatures.

Material and methods

MAP meat packages, taken directly from the producer, were stored both at constant temperatures in the range from 2 to 20 °C and partly exposed to temperatures of 20/30/50 °C, respectively for 3 hour periods at different points in time. Total microbiological contents (log cfu/g) were measured directly after delivery and continuously monitored in daily intervals for all trials, resulting in different growth dynamics with varying temperature scenarios. The constant temperature trials were imposed to identify the basic influence of temperature on microbiological growth, the latter ones, in total more than 30 combinations, to identify alternative response functions at higher temperatures.

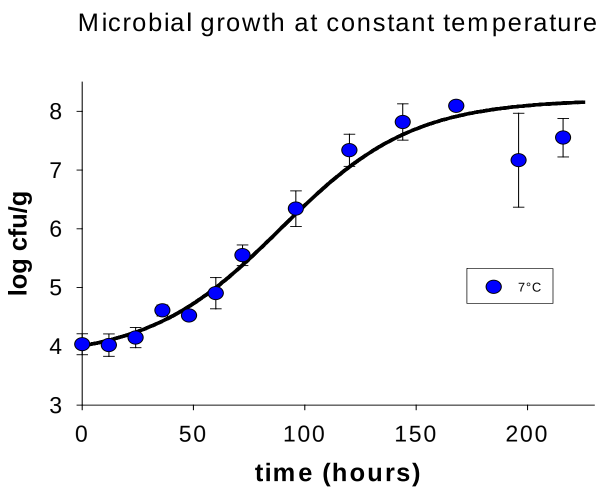


Fig. 1: Common bacterial growth pattern at constant temperatures, here 7 °C

To address the sigmoidal growth pattern of microbia dynamics including the common lag phase a logistical growth model is proposed as a parsimonious approach for modelling the time courses (after Richter, 1985). More complex models, as Richards, Gompertz (Richter, 1985) or Baranyi equations (Baranyi et al, 1993), are possible with respect to expected deviance

$$Log(N_t) = \log\left(N_0 + \frac{(N_{\max} - N_0)}{\left(1 + e^{(\tau_s - \tau)}\right)}\right) \quad \text{Eq. 1}$$

As common, a log scale is used for both presenting the data and the models. The basic equation includes the following parameters: N_t denotes the population density at time t, N_0 the initial density at start of the measurements t=0, N_{max} the upper asymptote, the growth rate as a function of temperature τ and the constant τ_s represents the lag phase. Growth is suppressed while τ is smaller than τ_s.
τ itself is the integral over the searched temperature response function d_r at temperature T and given time t (eq. 2), or simplified, the accumulated heat units with the specific rates of the underlying function.

$$\tau = \int_0^{t_d} d_r(T(t))dt \quad \text{Eq. 2}$$

The following temperature response functions were tested (the related trajectories are depicted in Fig. 2):

1. the widely used Arrhenius equation

$$d_r(T) = k_0 e^{-\frac{E_A}{RT}} \quad \text{Eq. 3}$$

with three parameters k_0, the activating energy E_A, and the universal gas constant R

2. a non-linear function with a plateau at temperature optimum, for example the O'Neill-function (O'Neill et al., 1972)

$$d_r(T) = k_{\max} \cdot \left(\frac{T_{\max} - T}{T_{\max} - T_{opt}}\right)^x \cdot e^{\frac{x \cdot (T - T_{opt})}{(T_{\max} - T_{opt})}}$$

$$\textit{with}$$

$$x = \frac{w^2 \cdot \left(1 + \sqrt{1 + \frac{40}{w}}\right)^2}{400} \quad \text{Eq. 4}$$

$$\textit{and}$$

$$w = (Q_{10} - 1) \cdot (T_{\max} - T_{opt})$$

with four parameter k_{max}, Q_{10}, T_{opt} and T_{max}.

3. An simple exponential function

$$d_r(T) = a \cdot \exp^{(bT)} \quad \text{Eq. 5}$$

with two parameters a, b

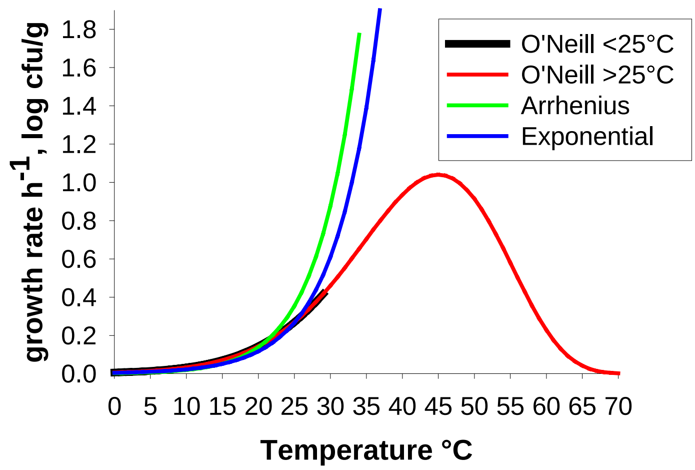
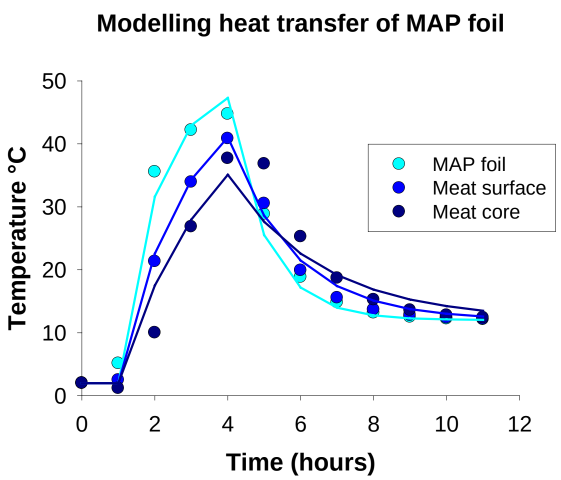


Fig. 2: Potential trajectories of equation 3-5, the O'Neill function is separated to the range up to 25°C and above

Related devices have recorded the temperature to which the samples have been exposed. To achieve realistic temperature exposures of the meat, the heat transfer through MAP foil was measured, providing the parameters of a MAP specific heat transfer function determining the effective temperature. Table 1 summarises an example.



Experiment 2/30/2 °C		
Storage hour	Measured temperature	Effective temperature
72	2	2.000
73	27.11	12.330
74	27.84	18.710
75	28.03	22.544
76	2.37	14.244
77	1.73	9.098
78	1.68	6.045
79	1.62	4.224
80	1.54	3.120
81	1.50	2.452

Fig. 3: Modelling heat transfer of different meat-MAP components and numerical realisation (Tab. 1: Proposed, realised and effective meat surface temperature scenario for heating (3 hours) and cooling)

To solve the regression problem to any of the chosen model combinations, i.e. the logistic growth model including the embedded temperature response function, they were fitted simultaneously to all data of either the constant temperature experiments or/and to the data of the variable temperature experiments. Excel and SPSS were used for the analysis.

Results

To estimate the temperature dependency of microbiological growth rates, different derivates of the logistic growth model in combination with different types of temperature response functions were simultaneously fitted to the observations. The simultaneous fitting procedure diminishes one classical problem: fitted growth curves are biased by the majority of the data from the lower and upper asymptote, while the estimated growth rate parameter is loaded by only few data taken during the exponential growth phase. Any of the chosen models fitted to the data taken from the constant temperature experiments has been of equal precision. Models of higher complexity, as the Richards or the Gompertz equation, were tested, but did not result in any significant better fittings.

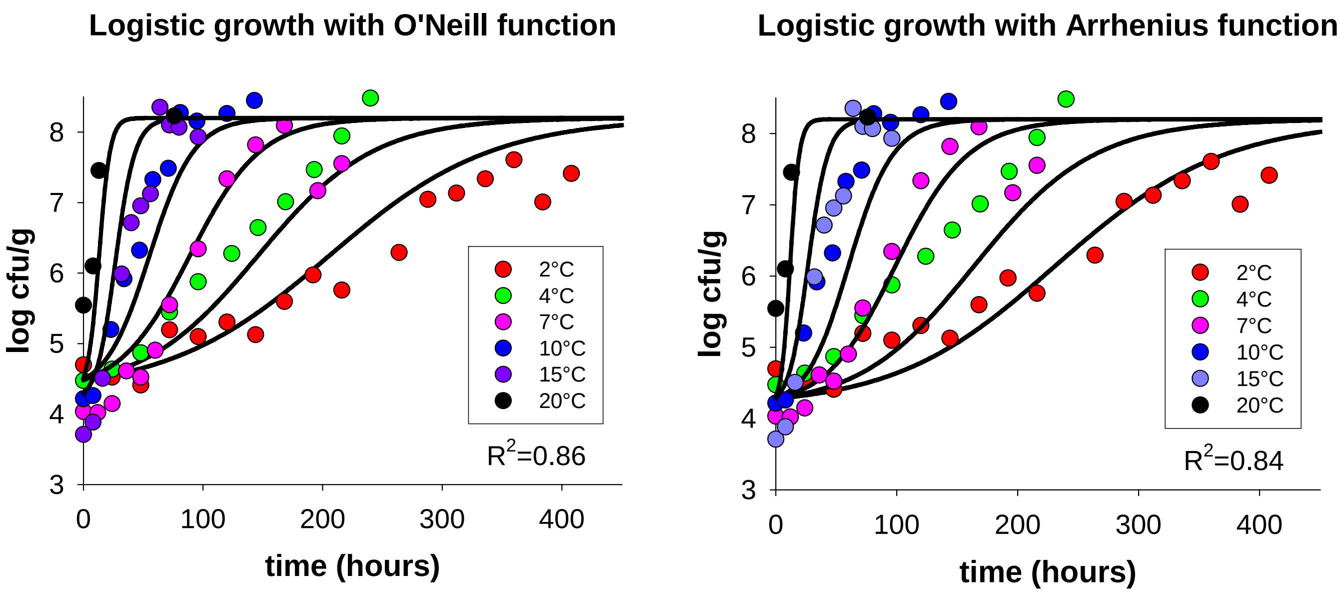


Fig. 4: left: simultaneously fitted O'Neill function; right: simultaneously fitted Arrhenius function

Parameter list for logistic growth model with an O'Neill function were: N_0=4.3, N_{max}=8.2, k_{max}=1, Q_{10}=1.74, T_{opt} and T_{max} were determined from the data taken from the experiments under higher temperatures. The lag phase parameter was found constant for all experiments (τ_s = 3.04)
After identifying the parameter, the real time data were transformed to biological times with respect to the underlying temperature response functions in the range from 2°C up to 20°C. Using the concept of biological times or accumulated heat units as the independent variable transforms the data to a time invariant scale and thus is comparable for different temperatures. The resulting function allows the parameter calibration of the O'Neill temperature response function addressing the higher temperature ranges. Again, all measured data were simultaneously taken into account. The resulting fit determines the parameter T_{opt} = 44.9 and, more extrapolated, the parameter T_{max} = 73.8 as depicted in fig. 1 by the scattered trajectory.

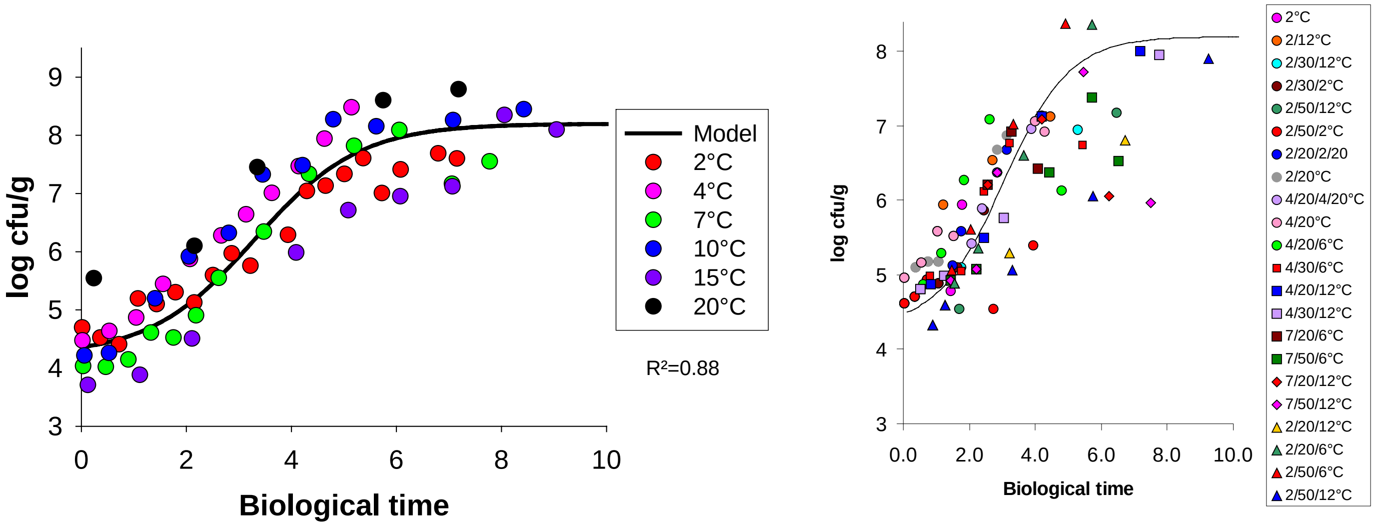
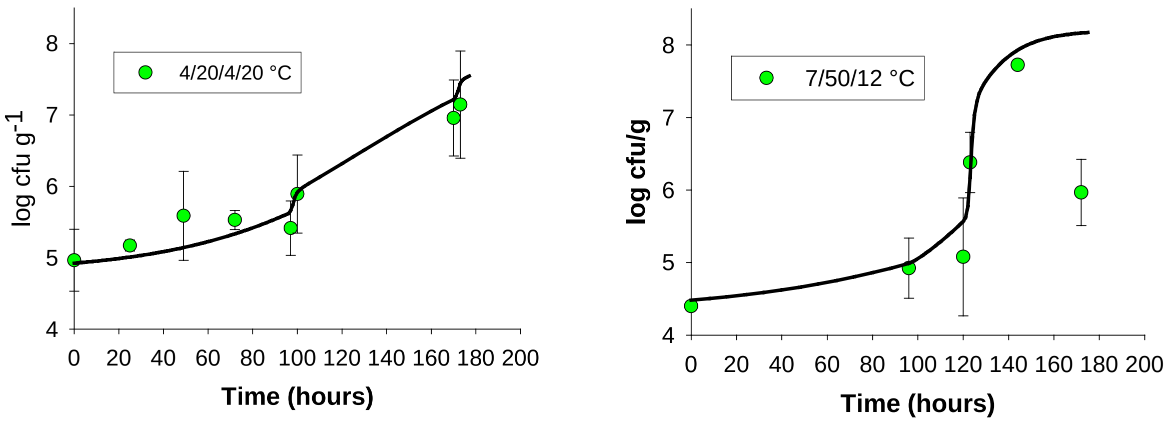


Fig. 5: Time transformed growth dynamics and observations, left: for constant temperature data; right: for variable temperature data

Despite the R^2 values indicates a sufficient accuracy of the models used (Fig. 4), deviance is obvious for the data under variable temperature regimes (Fig. 5, right). Some treatments are repeated satisfactorily by the O'Neill model (Fig. 6, green dots), but the model is not capable with some observations, as the observed growth dynamics are significant over-predicted as density losses are not part of the modelling (Fig. 6, red dots).



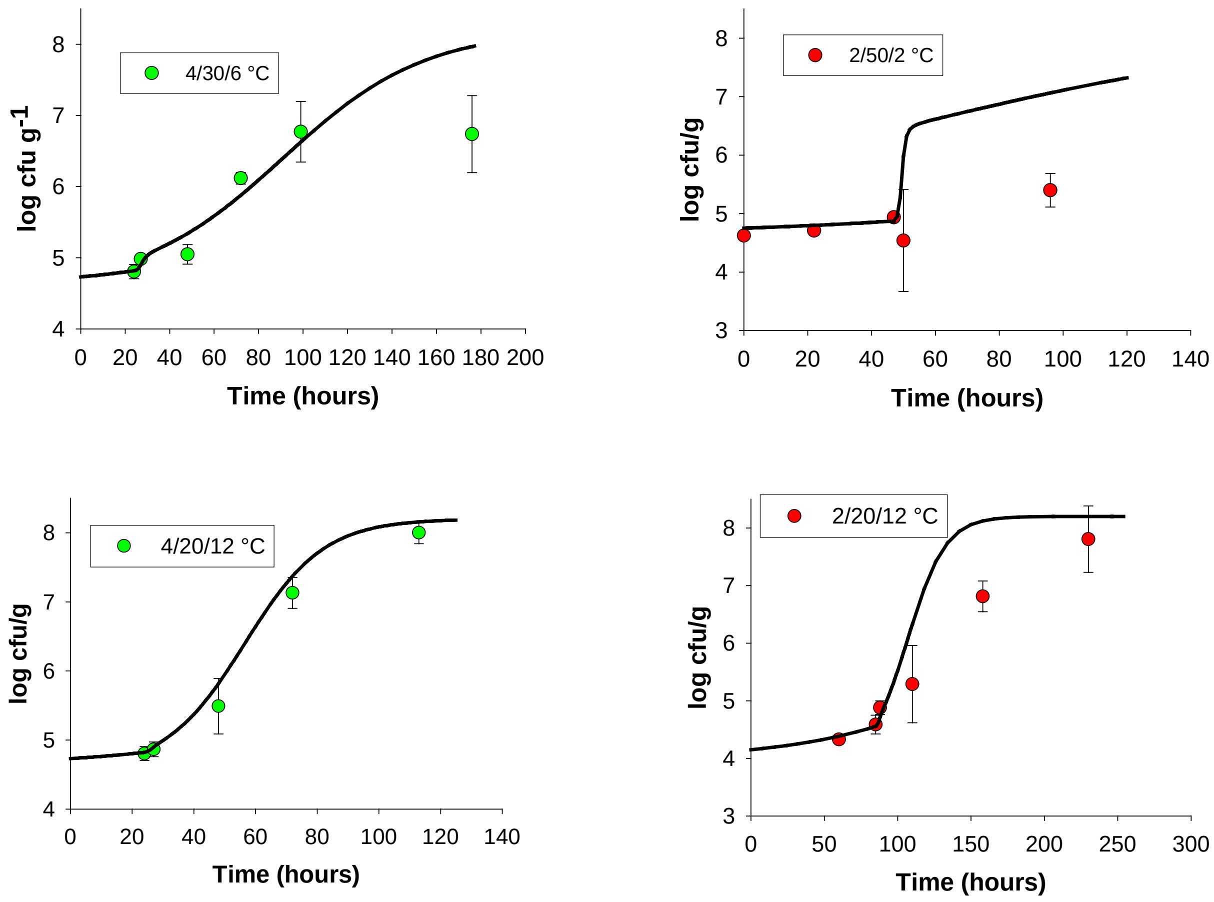


Fig. 6: green dots: sufficient model comparisons and observations; red dots: model failure

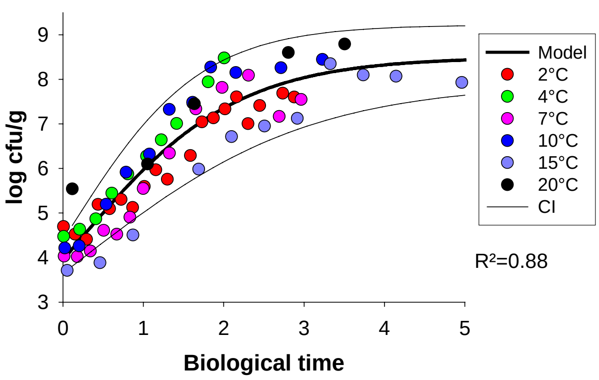


Fig. 7: Transformed logistic growth model without lag phase and 95% confidence intervals (CI) for constant temperature data

Searching for better alternatives it was assumed that the simplicity of a constant lag phase parameter τ_s might be too simple and should be addressed by a similar temperature response functions as developed for the growth rate. Contradicting, with respect to these data, it was of advantage to omit the lag phase completely without losing accuracy (R^2=0.88). Fig. 7 shows an example for a logistic growth model with an exponential temperature response function (eq. 5) fitted to the constant temperature data. Calculating the 95% confidence interval concerning the data shows that at the critical densities of log 6 to 7 cfu/g covers a wide range in terms of the biological times. The observed interval for the given density log cfu/g 6 varies from 0.5 to 2 units. The source of the variance is not an insufficient model approach but the observed initial values, N_0 in equation 1. The variance of the initial contamination maintains throughout the exponential growth dynamics.

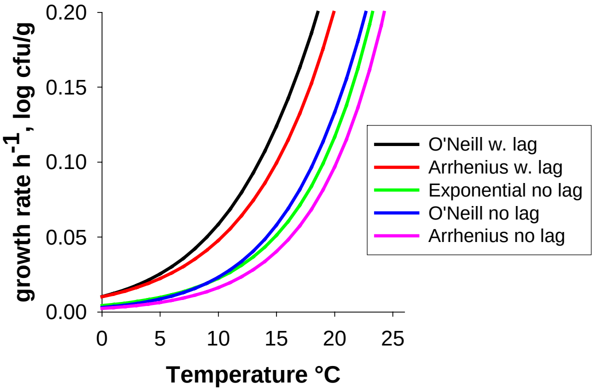


Fig. 8: Comparison of growth rates based on the combination of underlying model and embedded temperature response function

Summarising the tested model combinations revealed different response functions for the same data set (Fig. 8). Minor differences are caused by the fitting procedure, but a single consideration of the identified temperature response function is not feasible for any application, as the parameters changes with the underlying model. Here a logistic growth model with and without lag phase was tested. Using more complex models as the Richards, Gompertz or Baranyi equation will also change the curve of the embedded response functions. Hence, using such temperature response functions in a predictive mode, the underlying model has to be taken into account as well. Both, the growth model and the temperature response function must be seen as one unit for any application.

Discussion

A logistic growth model can be adequately fitted to microbiological growth data of minced meat stored at constant temperatures. The need for more complex models was not justified by the data used here. Using fitting procedures simultaneously over all experiments overcame potential lack of data during the exponential growth periods, putting the growth rate parameter on a sound data base. The growth rate was not parameterised itself, but was modelled by the integral over different temperature response functions.

All tested temperature response functions were applicable for the range up to 20°C without differences in precision or gaining enhanced information. Addressing higher temperatures and short-term heat peaks the O'Neill function was the only one, which can deal with the problem by its given nature of curvature. Due to its advanced flexibility and wider range of validity, model types like the O'Neill function are much more recommended than the usual exponential functions. Nevertheless, the overall fit is certainly not as good as achieved in the experiments under constant temperatures. The comparison of observations and model output of individual experiments revealed partly plausible consensus, but also complete failures. Those deviances indicate that the underlying microbiological processes are not as straightforward as the simple, continuous models might imply. Those types of models might basically be used to identify temperature dependencies, as it was done here, but are certainly of limited use for predictive applications. Discrete models which take into account the different composition of microbiological populations over time and temperature are more suitable. Although obvious, the findings of altered response functions with varying model complexity make it difficult to transfer the results, ie. model parameters, to other situations. The alteration applies also for the concept of the biological time. So represents 400 hours in real time an equivalent of 10 biological time units for the model with lag phase (fig. 5), but only 5 for the model without lag parameter (fig 7). Regarding both model components as one unit might be a solution, if such results provide a basis for the calibration of monitoring devices, for example time-temperature integrators.

The most important problem in modelling microbiological growth is not the deviance or uncertainty in the model itself, but the very large variance in the initial log cfu/g values. The variance is maintained throughout the growth processes (fig. 7). That fact causes serious constrains which nearly eradicate any efforts of predicting shelf life of meat by modelling. Further research has to emphasise on alternatives in the detection of initial microbiological concentrations by rapid and cost efficient techniques early in time.

Literature

Baranyi, J., Roberts, T.A. and McClure, P.J. (1993). A non-autonomous differential equation to model bacterial growth. Food Microbiol. 10, 43-59.

O'Neill, R.V., Oldstein, R.A., Shugart, H.H. & J.B. Makin (1972) Terrestrial ecosystem energy model. Eastern deciduous forest biome memo report, No. 72-19: 38 pp.

Richter, O. (1985) Simulation des Verhaltens ökologischer Systeme, Mathematische Methoden und Modelle, VCH Weinheim, 219 pp.