Comparison of the modified Gompertz model with the Baranyi model for fitting *Listeria monocytogenes* growth curves in three different food matrices

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Introduction and objectives

Objectives:
- Simplify the understanding of predictive microbiology.
- Compare the performance of two well-known models for estimating the growth parameters of *Listeria monocytogenes* in three different matrices.
- Learn how to implement curve-fitting in R programming and to interpret the statistical results.

Hypothesis:
The Gompertz and the Baranyi models have similar fitting capabilities based on their extensive use in literature.

Methodology

The data were collected from the database Combase and were fitted by means of a regression with the non-linear least squares using the Gauss-Newton algorithm in Rstudio.

Table 1: Description and intrinsic and extrinsic characteristics of the processed data for each food matrix selected from the Combase database.

Food Category	Temperature	pH	aw	Number of count data
Beef ham	4ºC, 6ºC, 8ºC,10ºC, 12ºC	6.8	0.98	20
Pork ham	6ºC, 8ºC, 15ºC	6.4	0.987	32
Custard	2ºC, 5ºC	6.9	0.999	14

The selected models for the fitting analysis were;

Modified Gompertz equation

$$Y(t) = Y_0 + (Y_{max} - Y_0)exp\left\{-\exp\left[\frac{2.71\mu_{max}(t_{lag}-t)}{Y_{max}-Y_0} + 1\right]\right\}$$

Baranyi equation

$$\begin{cases} Y(t) = Y_0 + \mu_{max}A(t) - \ln\left[1 + \frac{\exp(\mu_{max}A(t))-1}{\exp(Y_{max}-Y_0)}\right] \\ A(t) = t + \frac{1}{\mu_{max}}\ln[\exp(-\mu_{max}t) + \exp(-\mu_{max}t_{lag}) - \exp(-\mu_{max}t - \mu_{max}t_{lag})] \end{cases}$$

Where; *y(t)* is the logarithm of the cell concentration at time t (log10 CFU/g), *y0* is the logarithm of the cell concentration at t = 0 (log10 CFU/g), *ymax* is the logarithm of the maximum cell concentration (log10 CFU/g), *μmax* is the maximum specific growth rate (log10 CFU/g/h), *A(t)* is the gradual growth retardation over time and the *tlag* is the lag phase duration (h).

Results

The performance of the models was evaluated through: the residual sum of squares (*RSS*), the root-mean-square error (*RMSE*), the mean square error (*MSE*), the residual standard error (*RSE*), the Aikake Information Criterion (*AIC*), the Bayesian information criterion (*BIC*) and the analysis of variance (*ANOVA*).
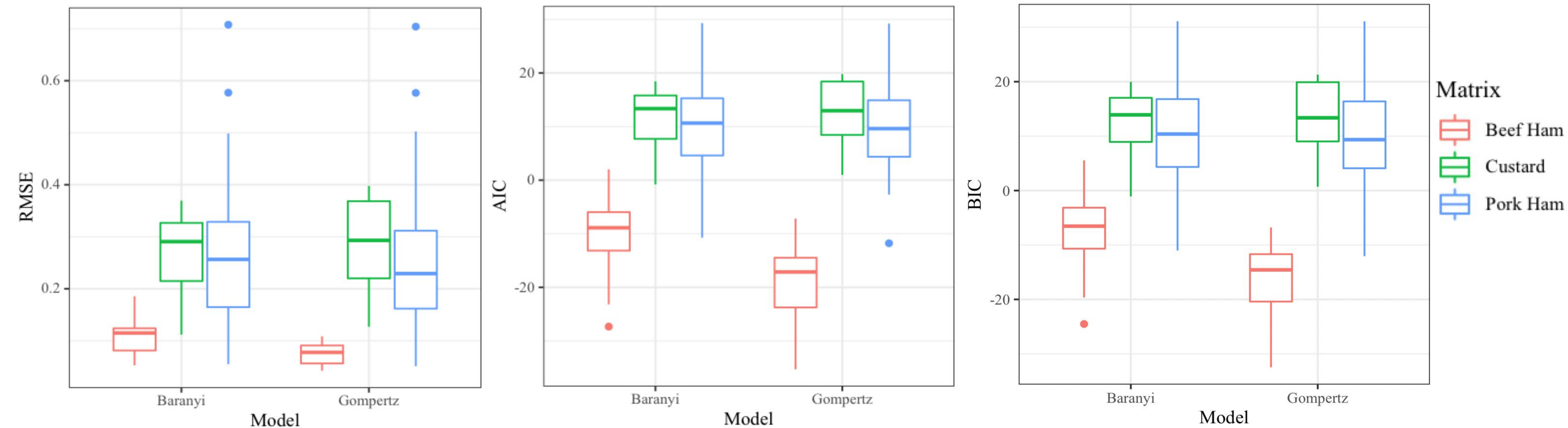

Figure. 1. Box plot of the RMSE, AIC and BIC indicators' results. The orange color represents beef ham, green represents custard, and blue represents pork ham.

Table 2: Anova test for the comparison of RMSE, MSE, RSE and RSS performance indicators obtained from the fitting analysis of Gompertz and Baranyi models for beef ham, pork ham and custard matrices by Rstudio.

Matrix	p value			
	RMSE	**MSE**	**RSE**	**RSS**
Beef ham	0.0006	0.0002	0.0002	0.004
Pork ham	0.850	0.721	0.900	0.950
Custard	0.470	0.268	0.460	0.480

Conclusions

- Both models had a good fitting performance for the growth curves of *Listeria monocytogenes* in the studied matrices.
- None of the models produced the best fit to all the growth curves.
- The Gompertz model fit better for a larger number of growth curves (38 out of 66) and was statistically better for the beef ham matrix, under the conditions in which the results were obtained.
- The interpretation of these results should be done with caution, as the performance and accuracy of the models depend on many factors.
- Predictive microbiology is a very useful tool in the food industry to guarantee food safety and product quality, but the value and the operation of this tool must be understood to implement it and generate value for the industry effectively.

Bibliography

Baranyi, J., & Roberts, T. A. (1995). Mathematics of predictive food microbiology. *International Journal of Food Microbiology, 26*(2), 199–218. https://doi.org/10.1016/0168-1605(94)00121-L

Zwietering, M. H., Jongenburger, I., Rombouts, F. M., & van 't Riet, K. (1990). Modeling of the Bacterial Growth Curve. *Applied and Environmental Microbiology, 56*(6), 1875–1881. https://doi.org/10.1128/aem.56.6.1875-1881.1990