ComBase Predictor Update
December 2025

Introduction

ComBase Predictor (see https://combase.errc.ars.usda.gov), is a collection of predictive models based on bacterial growth, survival, and inactivation data generated for various micro-organisms in culture media, using experimental designs specifically prepared to estimate the kinetic parameters of the organism. It integrates primary and secondary models, the first describing the variation of bacterial cell concentration as a function of time in a constant environment (see Appendix), the second describing the variation of the primary model parameters (especially the maximum specific growth rate) as a function of environmental factors such as temperature, pH, water activity and possibly a fourth factor such as nitrite, CO_2 or organic acids. The possible mathematical formulae for primary models are well analyzed and established in the literature, but the approaches to secondary modelling are still subject to research.

Secondary modelling in ComBase Predictor

A secondary model describes change in a primary model parameter (or, in a generic sense, some properties of primary model parameters), as a function of environmental factors (such as temperature, or pH, or water activity, etc).

ComBase Predictor uses the natural logarithm as a link-function for the maximum specific growth rate, denoted by μ_{max} here, and the $Ln(\mu_{max})$ values are modelled as a quadratic polynomial of the (possibly rescaled) environmental factors. The canonical form of the formula, for a three-factor core-model, is

$$Ln(\mu_{max}) = \\ = a_0 + a_1 \cdot T_r + a_2 \cdot p_r + a_3 \cdot b_w + a_4 \cdot T_r \cdot p_r + a_5 \cdot T_r \cdot b_w + a_6 \cdot p_r \cdot b_w + a_7 \cdot T_r^2 + a_8 \cdot p_r^2 + a_9 \cdot b_w^2$$

where T_r, p_r and b_w are (possibly rescaled versions of) temperature, pH and water activity. The following rescaling transformations are used for all models:

$T_r = T$	(temperature; no rescaling)
$p_r = pH$	(no rescaling)
$b_w = \sqrt{(1-A_w)}$	(A_w being the water activity, which is algebraically calculated from the NaCl content and the levels of levels or other solutes, if present)

If the water activity had been set by NaCl added to the medium (as is the case for most datasets), then the formula of Resnik and Chirife (1988) is used:

$A_w = 1 - (\%NaCl) \cdot (5.2471+0.12206 \cdot (\%NaCl)\ ) / 1000$

Therefore, b_w can also be considered as a direct rescaling of the %NaCl concentration.

When creating a secondary model, the polynomial above was fitted to the $Ln(\mu_{max})$ values that had been estimated by fitting a primary model to the log-counts data. Hence, establishing the a_i coefficients is a linear regression problem with a_0 being the intercept, a_1-a_3 the coefficients of the linear terms, a_4-a_6 are the coefficients of the cross-products and a_7-a_9 are those of the quadratic terms. With 10 coefficients per organism, such three-factor models represent the ComBase core-models.

Most laboratory experiments recorded in the ComBase database were specifically designed to generate these core-models. It has been assumed that any further "fourth factor", denoted by ef_4 in what follows, such as CO_2, added nitrite or organic acid (effects of which were studied for growth only), can only decrease the specific growth rates under any other defined set of environmental conditions. Note that

other conditions have also been recorded in the ComBase database but not used to modify the core model predictions.

When the effect of a fourth factor is also considered, ComBase Predictor extends the above core model in a way that the values of the three-factor model coefficients are retained and only the new coefficients describing the effect of the fourth factor are estimated:

$$\mathrm{Ln}(\mu_{max}) = \text{core-prediction} + f_4 =$$
$$a_0 + a_1 \cdot T_r + a_2 \cdot p_r + a_3 \cdot b_w + a_4 \cdot tr \cdot p_r + a_5 \cdot T_r \cdot b_w + a_6 \cdot p_r \cdot b_w + a_7 \cdot t_r^2 + a_8 \cdot p_r^2 + a_9 \cdot b_w^2 +$$
$$+ ef_4 \cdot (a_{10} + a_{11} \cdot T_r + a_{12} \cdot p_r + a_{13} \cdot b_w + a_{14} \cdot ef_4)$$

The difference between this form and that of the gamma-concept of Zwietering *et al.* (1996) is that, in the case of non-significant interaction terms, only an expression of the form $ef_4 \cdot (a_{10} + a_{14} \cdot ef_4)$ is allowed for the ef_4-effect.

The a_{10} , a_{11} , a_{12} , a_{13} , a_{14} coefficients describe the effect of the (possibly rescaled) fourth environmental factor:
a_{10}, is for the linear term, ef_4
a_{11}, a_{12}, a_{13} are for the cross-product terms of ef_4, i.e. $ef_4 \cdot T_r$, $ef_4 \cdot p_r$ and $ef_4 \cdot b_w$
a_{14} is for the square of the fourth factor, ef_4^2.

Via the above formula, the task is simplified to linearly regressing the coefficients of the fourth factor only, that is fitting the "$\mathrm{Ln}(\mu_{max})$ - (core-prediction)" difference by

$$ef_4 \cdot (a_{10} + a_{11} \cdot T_r + a_{12} \cdot p_r + a_{13} \cdot b_w + a_{14} \cdot ef_4)$$

where the $\mathrm{Ln}(\mu_{max})$ observed data can be obtained from those measurements where the fourth factor was not zero. This is linear regression indeed, without the intercept term, and the result is the estimates of the coefficients a_{10} ... a_{14}.

As ef_4 always exhibits inhibitory effects, a_{10} was restricted to negative or zero values. If any of the a_{11} … a_{13} coefficients are positive, then it is possible that the effect of ef_4 is NOT inhibitory at certain combinations of the core factors. This should happen only when extrapolating beyond the 'true' range of the data, considering the 'minimum convex polyhedron', discussed further below.

When estimating these coefficients by linearly fitting measured $\mathrm{Ln}(\mu_{max})$ values, one or more of the estimates may not be significant, i.e. (as a rule of thumb), the standard error of a parameter may be larger than 50% of the estimate itself. After omitting these terms, and with the regression done again, the term with the highest relative error can be eliminated. Repeating this procedure makes only significant (p<5%) terms remain. This procedure is called backward elimination.

ComBase Predictor 1.0 (old version) for four factors
Coefficients and interpolation boundaries

Strictly speaking, predictions should not be made outside the region of observations (such predictions are called extrapolation). As exemplified later, in multiple dimensions, determining the true "interpolation region" is not straightforward.

Below, Table 1 shows the boundaries for those "organism + environmental factor" pairs for which a four-factor model exists.

Table 1. The nominal interpolation region of the environmental factors for each four-factor growth model according to the old ComBase Predictor 1.0. The core variables are temperature, pH, and sodium chloride (%NaCl); the fourth factor (ef_4) can be either $\%CO_2$, nitrite, or an organic acid, but not a combination of two or more.

Data ranges for core growth models with *ef₄*	***Temperature (°C)***		***pH***		***NaCl****	***ef4****
	lowest	***highest***	***lowest***	***highest***	***highest***	***highest***
Bacillus cereus with **ef_4=CO_2**(%)	5	34	4.9	7.4	9.5	60
Escherichia coli with **ef_4=CO_2**(%)	10	42	4.5	7.5	6.5	100
Listeria monocytogenes/innocua with **ef_4=CO_2**(%)	1	40	4.4	7.5	11.5	100
Listeria monocytogenes/innocua with **ef_4=Nitrite**(ppm)	1	40	4.4	7.5	11.5	200
Listeria monocytogenes/innocua with **ef_4=Lactic**(ppm)	1	40	4.4	7.5	11.5	20000
Listeria monocytogenes/innocua with **ef_4=Acetic**(ppm)	1	40	4.4	7.5	11.5	10000
salmonellae with **ef_4=CO_2**(%)	7	40	3.9	7.4	4.6	100
salmonellae with **ef_4=Nitrite**(ppm)	7	40	3.9	7.4	4.6	200
Yersinia enterocolitica with **ef_4=CO_2**(%)	-1	37	4.4	7.2	7	80
Yersinia enterocolitica with **ef_4=Lactic**(ppm)	-1	37	4.4	7.2	7	10000

*For each organism and model the lower limit of NaCl is 0.4. For ef_4, the minimum is always zero.

User-reported controversies with ComBase Predictor v1.0

As discussed above, users of ComBase 1.0 have reported that, in some cases, an increase in the fourth factor (that is supposed to be always inhibitory) caused an increase in the growth rate.

Thanks to such user-reports, it was realized that, when the coefficients of the four-factor models had been estimated, the above-described backward elimination algorithm had not been applied to every microorganism dataset, and the non-significant terms resulted in illogical and unjustifiable trends in extrapolation regions or where the measured data were scarce. These happen, for example, outside the minimum convex hull (polyhedron) of the experimental design, even if the test point is still inside the nominal interpolation region; see Figures below, also Baranyi et al (1996). In such regions, consequently, it is possible that the old ComBase Predictor predicted higher growth rate at higher value of ef_4, which trend is not correct.

The points below give possible reasons for such scenarios:

1. The effect of the fourth factor was frequently studied ONLY at values close to the optimum of the other factors (mainly at optimum pH and NaCl). This could make the cross-product terms omittable. However, if the backwards elimination procedure was not carried out, then the cross-product terms remained in the model, which can cause unreasonable trends in regions where there are no, or just few data.
2. Remember that the above model-extension method determined the effect of the fourth factor by means of the rearrangement
   $\text{Ln}(\mu_{max})$ - core-prediction =
   $= a_{10}\cdot ef_4 + a_{11}\cdot T_r\cdot ef_4 + a_{12}\cdot p_r\cdot ef_4 + a_{13}\cdot b_w\cdot ef_4 + a_{14}\cdot ef_4^2$
   Sometimes the experimental design only studied the effect of the fourth factor at fixed values of the other factors (this was generally the case with the experiments with the fourth factors). The result is an ill-posed estimation problem for estimation of the cross-product terms, for similar reasons as above.

In summary, non-reasonable trends can be detected most frequently outside the convex hull of the observations (strict interpolation region), which is typically less than half of the NOMINAL interpolation region (which can be envisioned as the "brick" whose edges are at the minimum and maximum environmental factor values where measurements were carried out – see Baranyi et al., 1996 and Masana-Baranyi, 2000).

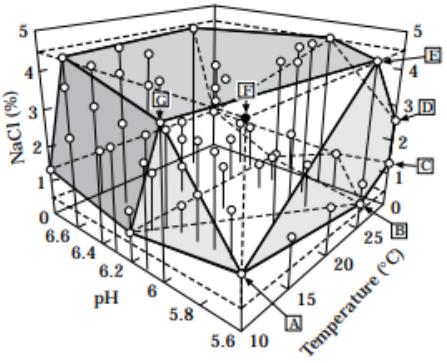


Fig. 1. Strict interpolation region: the Minimum Convex Polyhedron (convex hull) of the points, where experiments were carried out. This could be just a small portion of the nominal interpolation region (i.e. the brick produced by the product of the ranges of all individual variables). From Baranyi et al, 1996.

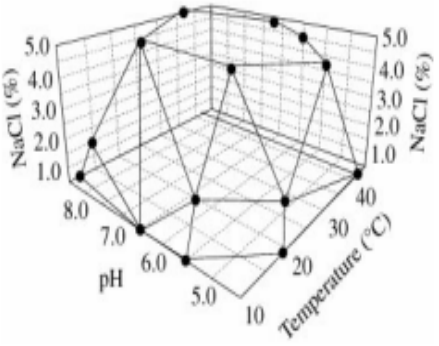


Fig. 2. The ratio between the volume of the convex hull of the experimental test points and the nominal interpolation region (brick) is the probability that a random test point is interpolation. From Masana-Baranyi, 2000.

ComBase Predictor update (v1.1)

- The backward elimination procedure mentioned above has now been undertaken systematically.
- The wrong trend cannot occur if all the retained coefficients are negative. It may still happen if the $p_r\cdot ef_4$ or $b_w\cdot ef_4$ terms have positive coefficients (in red, see the table below).
- The (a_{10}...a_{14}), coefficients have been changed for the four-factor models, accordingly, see below. The 10 coefficients of the respective core-model remain unamended. This means that three-factor core-predictions have not changed.
- The lower limit of NaCl is 0.5, and the upper limit for pH is 7.1.

	OLD Four-factor-model coefficients					**NEW Four-factor-model coefficients**				
	a_10	a_11	a_12	a_13	a_14	**a_10**	**a_11**	**a_12**	**a_13**	**a_14**
	ef_4	ef_4*temp	ef_4*pH	ef_4*bw	ef_4^2	**ef_4**	**ef_4*temp**	**ef_4*pH**	**ef_4*b_w**	**ef_4^2**

Bc_CO2	0	0	-0.0018	0.059994	0	**0**	**0**	**-7.339E-4**	**0**	**0**
Ec_CO2	0.01195	0.000203	-0.00174	-0.01484	-8.2E-05	**0**	**0**	**-4.268E-4**	**0**	**0**
Lm_CO2	0	0.00013	-0.00197	0	0	**0**	**0**	**-1.712E-3**	**0**	**0**
Lm_Nitr	-0.02086	-6.4E-06	0.002849	0.001953	-2.1E-06	**-2.115E-2**	**0**	**2.852E-3**	**0**	**0**
Lm_Lact	-3.5E-05	-3E-07	0.000009	-0.00014	-1.2E-09	**0**	**0**	**0**	**-1.297E-4**	**0**
Lm_Acet	0	3.5E-06	0.000262	-0.03473	0	**-1.776E-3**	**0**	**2.484E-4**	**0**	**0**
Ss_CO2	0	0.00064	-0.00299	0	0	**0**	**0**	**-1.265E-3**	**0**	**0**
Ss_Nitr	-0.04993	-0.00089	0.00807	0	0	**-8.636E-2**	**0**	**1.205E-2**	**0**	**0**
Ye_CO2	-0.0152	0.00035	-0.00106	0.02002	6.3E-05	**0**	**0**	**-1.753E-3**	**0**	**0**
Ye_Lact	0	0	0	0	0	**-1.652E-5**	**0**	**0**	**0**	**0**

Secondary model for the 'lag time'

After predicting Ln(μ_{max}), the product $h_0 = \mu\lambda$ was modelled by a species-specific constant, independently of the environment. As $1/\mu_{max}$ is ca. the generation time in the exponential phase, what h_0 expresses is equivalent to the ratio between the lag and the generation time (also called the relative lag time in the literature). Its value was taken as a representative constant, estimated by the multiplicative average of its values obtained from the primary model fitting. Then the lag (or shoulder, for survival curves) was calculated by $\lambda=h_0/\mu_{max}$. As h_0 depends on the history of the cells (which, in turns, depends on the experimenter/experimental design), it is a free parameter, just as the inoculum level. In ComBase v1.0, its default value was obtained by taking the multiplicative average of its estimates from the primary modelling.

A rescaling of h_0, namely $\alpha_0 = \exp(-h_0)$ is also frequently used in the literature. It is another quantification of the "history" of the cells; it expresses their "suitability" to the new environment. *ComBase Predictor* offers the user the choice to use this version of the history effect, called the initial physiological state.

The way that the initial physiological state is presented in ComBase Predictor 1.0 can be found in a project report:
Final Report, UK Food Standards Agency, Project B13003
Development of ComBase-PMP, a combined database and predictor of microbial responses to the food environment (January 2004 – March 2007) by J. Baranyi and Y. Le Marc
Institute of Food Research, April 2007

In detail: the individual growth curves were fitted by the model of Baranyi and Roberts (1994) to obtain the four parameters typically characterizing the sigmoid curves used: y_0, y_{max} (inoculum and stationary phase level), the λ (lag time) and the μ_{max} slope, where y_0, y_{max} and μ_{max} are all expressed as the natural log of the measured cell concentrations. The μ_{max} (maximum specific growth rate) was the only parameter that was modelled as a function of the environment. y_{max} (maximum population density) estimates were taken as the average of all the y_{max} estimates for the organism in question. The default value for the parameter y_0 was equivalent to 1000 cell/ml; this is typical of the experiments that provided the raw data (though not necessarily to a food scenarios). The lag was modelled via $\lambda=h_0/\mu_{max}$ as follows:

The $h_0=\lambda\cdot\mu_{max}$ transformation results in the parameter h_0 that replaces the lag with a quantification of the "work to be done" by the cells during the lag phase. This work depends

on the history of the cells, therefore on the experimenter. So, it is a "free parameter" just as y_0, (i.e., determined by the specific experimental design). Specifically, h_0 can be reduced acclimating the inoculum to be used in the experiment to the conditions to which they are to be exposed, that is to grow the first under those environmental conditions before transferring to the growth environment where growth kinetics will be measured. For a constant, the multiplicative average of the h_0 estimates over those curves that were used for the growth model of the organism was used.

The α_0 initial physiological state parameter is just a rescaling of h_0: $\alpha_0 = \exp(-h_0)$. It quantifies (by number between 0 and 1) how ready the cells are for the new environment.

The user can see different α_0 values for the different organisms, because h_0 was averaged over the data belonging to that organism. However, in ComBase Predictor 1.1, $\alpha_0=1$ will be the default in all cases. As mentioned above, it is a free parameter just as the inoculum level. **The $\alpha_0=1$ choice is a safe option and the α_0 values in ComBase Predictor 1.0 said more about the experimental procedure than the organism-food scenario**.

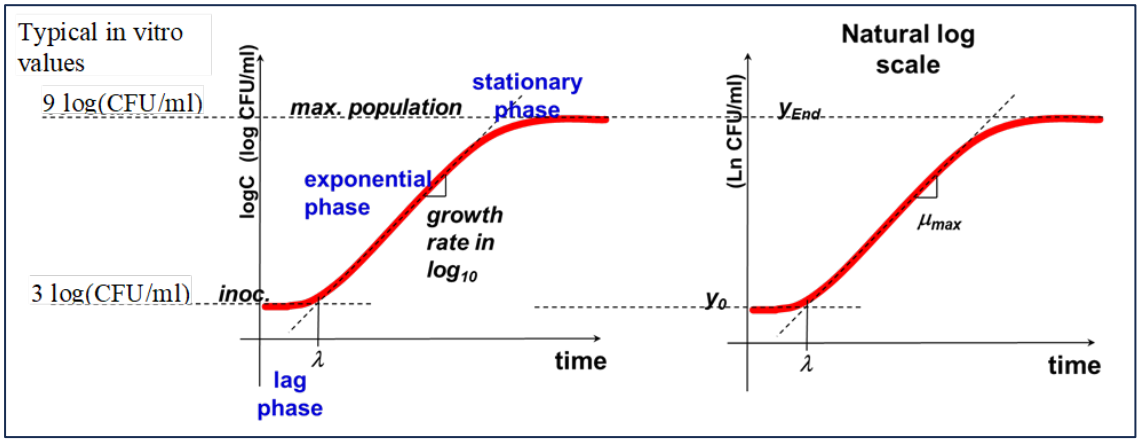
A practical example: if the hazard is that an already contaminated piece of meat touches another one then the transferred cells will not be expected to show any lag (the cells don't necessarily even notice that there was a change in their environment, so $\alpha_0=1$). However, if it touches a totally different kind of food, then there IS expected to be a lag time, and α_0 is probably even lower than in laboratory experiments, where the substrate did not change, only became "fresher" (i.e., nutrient levels restored to the original conditions with no depletion of nutrients, nor accumulation of 'waste' metabolites) when inoculating the bacteria from the stationary phase.

Appendix

Primary modelling of growth curves

In-vitro growth curves were fitted by the primary model of Baranyi and Roberts (1994). The model parameters are demonstrated by Fig.1.

Fig.1. Four parameters characterize a primary growth model. The μ_{max} , y_0 , y_{End} , parameters (measured on the natural log-scale) are ln(10)≈2.3-times bigger than their $\log_{10}$-equivalent.



Legend:

y_0 : the natural logarithm of the initial cell concentration.

λ : a parameter to describe the lag phase; in case of the Baranyi and Roberts model, the instantaneous specific rate is half of its maximum here.

μ_{max} : the maximum specific growth rate. This parameter is practically the maximum slope of the Ln(*cell conc.*) *v. time* curve.

y_{End} : the natural logarithm of the maximum cell concentration.

Regarding the biological meaning of the parameters:

- y_0 is an initial value that is specific to the history of the cells inasmuch the moment of inoculation is considered as time zero. The inoculum level is set up by the experimenter, therefore it is not a function of the environment (a free parameter).
- λ depends on both the history of the cells and the actual (post-inoculation) environmental conditions. Cells that are damaged (for example after heat treatment or freezing) or come from an environment that is very different from the actual one, may require longer than expected time to adjust to the new environment.
- μ_{max} is the most important parameter, characterized by the actual environment only, regardless of the pre-inoculation history. It is (potentially) the steepest slope of the ***natural log*** of the bacterial concentration *v.* time curve. It can be also translated as the ca. average number of division of a cell in a unit time. Note that the formula should not be fitted directly to the $\log_{10}$- value of the cell concentrations but its natural logarithm; see Rockaya and Baranyi (2025)

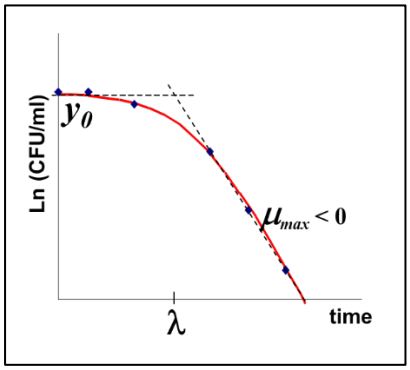
The model of Baranyi and Roberts (1994) has two extra (so-called curvature- or tuning-) parameters: *n* and *m*. These are not modelled but fixed, normally as *n*=1, *m*=1. They quantify the "suddenness" of the transition to and from the exponential phase. For large (say greater than 20) values, the transition is practically a breakpoint. Therefore, for *n*=*m*=20, the model is

equivalent to the so-called three-phase-linear model. The option n=m=0 symbolizes a straight line (no lag, no stationary phase).

Primary modelling of death curves

Death curves were fitted by the mirror image of the model of Baranyi and Roberts (1994); called Geeraerd model in predictive microbiology literature. While, for growth curves, the y_{end} parameter is the natural logarithm of the maximum cell concentration (also called the carrying capacity of the environment), here it represents the level of a surviving subpopulation characterizing the heterogeneity of the inoculum rather than the environment. If there is no such surviving subpopulation (the inoculation is homogeneous), then the m curvature parameter of the primary model of Baranyi and Roberts (1994) should be set to zero i.e. the model should have three parameters only (Fig.2). F-test can decide whether the y_{End} parameter should be fitted at all.

Fig. 2. Death curve without tail is described by a three-parameter model. Difference from growth: μ_{max} , the maximum specific death rate is negative for death curves.



Implementation of the model of Baranyi and Roberts

The model consists of two ordinary differential equations describing the where the coupled variation of two variable: $y(t)$, is the natural logarithm of the cell concentration at the time t and $q(t)$ is the temporal variation of the cells' physiological state. Explicit solution exists for $y(t)$, that can be written up in an algebraic form as:

$$y(t) = y_{\max} - \frac{1}{m}\ln\left(1 + \frac{e^{m(y_{\max}-y_0)} - 1}{e^{m\mu_{\max}A(t)}}\right) \qquad \text{(A1)}$$

or, after rearrangement:

$$y(t) = y_0 + \mu_{\max}A(t) - \frac{1}{m}\mathrm{Ln}\left(1 + \frac{e^{m\mu_{\max}A(t)} - 1}{e^{m(y_{\max}-y_0)}}\right) \qquad \text{(A2)}$$

where $A(t)$ is a gradually delayed measure of time:

$$A(t) = t - \lambda + \frac{\mathrm{Ln}\left(1 - e^{-\nu t} + e^{-\nu(t-\lambda)}\right)}{\nu} \qquad \text{(B)}$$

The (A2) rearrangement has an important consequence for the implementation of the model. Namely, it suggests that the regression should start its build from the $y_0+\mu A(t)$ bi-phasic curve (lag + exponential phase) and add the stationary phase, i.e. the last term of (A2), only if there are data indicating this. Similar line of thoughts is valid for the $A(t)$ expression described by (B).

It is convenient to introduce the $n=\nu/\mu$ ratio, so this will be a quantification of the curvature during the transition from the lag to the stationary phase. If it is big, then the transition is sudden, just as when *m* is big.

Using mechanistic reasoning, $\nu=\mu$ is assumed, i.e. $n=\nu/\mu = 1$. For the *m* curvature parameter, *m*=1 is a suitable assumption as it describes the logistic inhibition during the transition to the carrying capacity of the environment. Usually, the *n*=*m*=1 values work well for these tuning parameters. (Note that this means, if *n* and *m* are big, then we get the tri-linear model; if they are zero, then the simple linear model is obtained for *y(t)*.)

1. The (A2) rearrangement has a useful practical use to find good initial values for fitting (the tri-linear is not recommended, for several reasons). Omit those measured points which are, according to our best knowledge, do not belong to the linear phase (like (log cell conc.) > 6). Fit the three-parameter model, without the y_{max} i.e. omit the last term in (A2). This bi-phasic model has monotone-increasing derivative, so it will always produce a robust fit (apart from numerical stability, which would require another arrangement of (B), but that is a different issue). For the three-parameter fit, use for example the middle of the time interval and the slope of a simple linear regression as initial values for the lag and the $\mu_{max.}$
2. Another use of (A2) is when not enough data indicate the stationary phase. As the above three-parameter version is nested in the 4-parameter (A2) model, use F-test to decide whether it is worth introducing the upper asymptote at all. This is equivalent to the question whether the *m* parameter is significant or it (i.e. the upper asymptote) can be omitted.

Secondary model for y_0 and y_{End}

If the inoculum level is not specified by the user, then *ComBase Predictor* assigns a default value for it that corresponds to 3 logCount/ml for growth and 6 logCount/ml for survival and death models (remember, the primary model's y_0 parameter is ca 2.3-times bigger than this). The y_{End} parameter is modelled by a species-specific constant, independently of the environment. Its value varies between 17 and 21 Ln(CFU/ml). This was estimated by taking an average of its fitted values when regressing the primary model on the original logCount curves.

DEMO

The screenshot below shows the prediction of *B. cereus* growth, according to the old *ComBase Predictor 1.0*, at temperature 20 C, pH 5 and NaCl% = 8. The rate is claimed to be by some 50% higher in the presence of 60% CO_2, though there is no evidence for such an effect of the CO_2 (there is no data in *ComBase* at this extreme pH and NaCl).

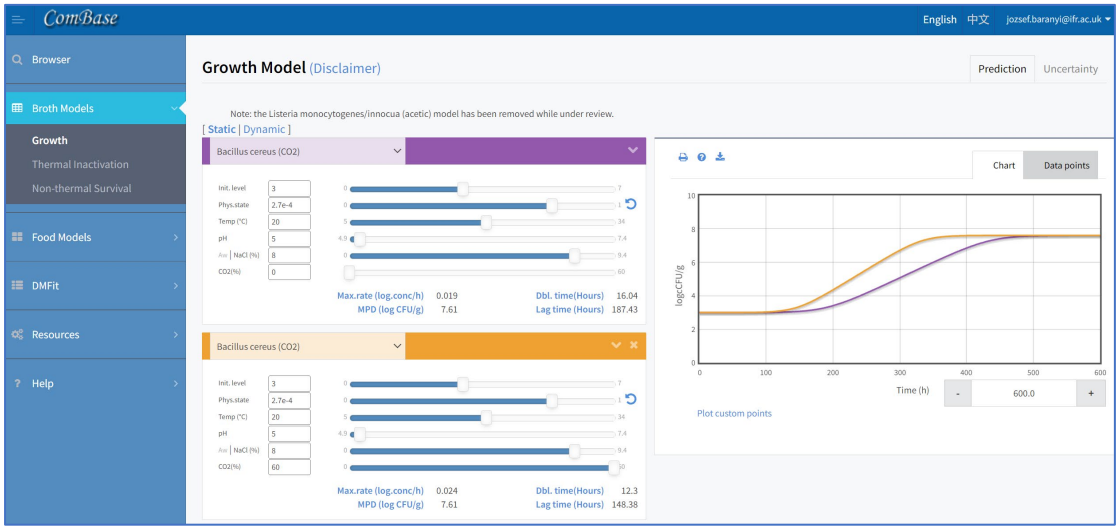


Fig. 3a. Effect of CO_2 on the growth of *B. cereus* at temperature 20 C, low pH (pH=5) and low Aw (NaCl=8%), according to the old ComBase Predictor. Adding 60% CO_2 to the medium **increased** the maximum specific growth rate by ca 25% (note that here the rate is meant in log10-sense, which is 2.3-times smaller than the specific rate in Ln-sense). In fact, there is no data in ComBase at low pH, low Aw and high CO_2; it is unlikely that adding CO_2 would increase the bacterial growth rate.

The wrong effect of CO_2 at the same conditions is demonstrated on the heatmap of the Ln(μ_{max}) response below. According to the old ComBase Predictor v1.0 , at pH=5 and NaCl=8%, the specific growth rate increases with CO_2.

CO_2(%)

NaCl(%)	0	8	16	24	32	40	48	60
0	-0.971	-1.043	-1.115	-1.187	-1.259	-1.331	-1.403	-1.51
0.5	-0.943	-0.99	-1.037	-1.084	-1.132	-1.179	-1.226	-1.297
1	-1.026	-1.063	-1.099	-1.136	-1.173	-1.21	-1.246	-1.302
1.5	-1.13	-1.158	-1.187	-1.216	-1.244	-1.273	-1.301	-1.344
2	-1.246	-1.268	-1.29	-1.311	-1.333	-1.354	-1.376	-1.408
2.5	-1.372	-1.387	-1.403	-1.418	-1.433	-1.449	-1.464	-1.487
3	-1.505	-1.515	-1.524	-1.534	-1.543	-1.553	-1.563	-1.577
3.5	-1.644	-1.649	-1.653	-1.657	-1.662	-1.666	-1.67	-1.677
4	-1.79	-1.789	-1.788	-1.788	-1.787	-1.786	-1.785	-1.784
4.5	-1.941	-1.935	-1.93	-1.924	-1.918	-1.913	-1.907	-1.899
5	-2.097	-2.087	-2.076	-2.066	-2.056	-2.046	-2.035	-2.02
5.5	-2.258	-2.243	-2.228	-2.214	-2.199	-2.184	-2.17	-2.148
6	-2.423	-2.404	-2.385	-2.366	-2.347	-2.328	-2.309	-2.281
6.5	-2.593	-2.57	-2.547	-2.524	-2.501	-2.477	-2.454	-2.42
7	-2.768	-2.741	-2.713	-2.686	-2.659	-2.632	-2.604	-2.563
7.5	-2.947	-2.916	-2.884	-2.853	-2.822	-2.791	-2.759	-2.712
8	**-3.13**	**-3.095**	**-3.06**	**-3.024**	**-2.989**	**-2.954**	**-2.919**	**-2.866**

Lower growth with higher CO_2

Higher growth with higher CO_2

Wrong trend for the effect of ef_4 *per se* cannot happen if the coefficients are all negative or zero. If they are not, such heatmaps can demonstrate (see below an example on **Listeria with ef_4=Nitrite**) that their trend is reasonable with the new ComBase Predictor v1.1, even at the edges of their nominal interpolation region. However, the lower limit of NaCl is 0.5% and the upper limit of pH is 7.1 in the updated version.

Nitrite(ppm)

NaCl(%)

	0	16	32	48	64	80	96	112	128	144	160	176	192	200
0	-4.186	-4.196	-4.206	-4.216	-4.226	-4.235	-4.245	-4.255	-4.265	-4.275	-4.285	-4.295	-4.304	-4.309
0.5	-3.973	-3.982	-3.992	-4.002	-4.012	-4.022	-4.032	-4.042	-4.051	-4.061	-4.071	-4.081	-4.091	-4.096
1	-3.951	-3.961	-3.971	-3.981	-3.991	-4	-4.01	-4.02	-4.03	-4.04	-4.05	-4.059	-4.069	-4.074
1.5	-3.963	-3.973	-3.982	-3.992	-4.002	-4.012	-4.022	-4.032	-4.042	-4.051	-4.061	-4.071	-4.081	-4.086
2	-3.992	-4.002	-4.012	-4.022	-4.032	-4.042	-4.052	-4.061	-4.071	-4.081	-4.091	-4.101	-4.111	-4.116
2.5	-4.034	-4.044	-4.054	-4.064	-4.074	-4.084	-4.094	-4.103	-4.113	-4.123	-4.133	-4.143	-4.153	-4.158
3	-4.086	-4.096	-4.106	-4.116	-4.125	-4.135	-4.145	-4.155	-4.165	-4.175	-4.184	-4.194	-4.204	-4.209
3.5	-4.145	-4.155	-4.165	-4.175	-4.185						44	-4.253	-4.263	-4.268
4	-4.211	-4.221	-4.231	-4.24	-4.25						09	-4.319	-4.329	-4.334
4.5	-4.282	-4.292	-4.302	-4.312	-4.322						81	-4.391	-4.401	-4.406
5	-4.359	-4.369	-4.379	-4.389	-4.399						58	-4.468	-4.477	-4.482
5.5	-4.441	-4.451	-4.461	-4.47	-4.48						39	-4.549	-4.559	-4.564
6	-4.527	-4.537	-4.547	-4.557	-4.566						26	-4.635	-4.645	-4.65
6.5	-4.617	-4.627	-4.637	-4.647	-4.657						16	-4.726	-4.736	-4.741
7	-4.712	-4.722	-4.732	-4.741	-4.751						81	-4.82	-4.83	-4.835
7.5	-4.81	-4.82	-4.83	-4.84	-4.849	-4.859	-4.869	-4.879	-4.889	-4.899	-4.909	-4.918	-4.928	-4.933
8	-4.912	-4.922	-4.932	-4.942	-4.952	-4.961	-4.971	-4.981	-4.991	-5.001	-5.011	-5.02	-5.03	-5.035
8.5	-5.018	-5.028	-5.037	-5.047	-5.057	-5.067	-5.077	-5.087	-5.097	-5.106	-5.116	-5.126	-5.136	-5.141
9	-5.127	-5.137	-5.147	-5.156	-5.166	-5.176	-5.186	-5.196	-5.206	-5.216	-5.225	-5.235	-5.245	-5.25
9.5	-5.24	-5.249	-5.259	-5.269	-5.279	-5.289	-5.299	-5.309	-5.318	-5.328	-5.338	-5.348	-5.358	-5.363
10	-5.356	-5.365	-5.375	-5.385	-5.395	-5.405	-5.415	-5.424	-5.434	-5.444	-5.454	-5.464	-5.474	-5.479
10.5	-5.475	-5.485	-5.494	-5.504	-5.514	-5.524	-5.534	-5.544	-5.554	-5.563	-5.573	-5.583	-5.593	-5.598
11	-5.597	-5.607	-5.617	-5.627	-5.637	-5.647	-5.656	-5.666	-5.676	-5.686	-5.696	-5.706	-5.715	-5.72
11.5	-5.723	-5.733	-5.743	-5.753	-5.762	-5.772	-5.782	-5.792	-5.802	-5.812	-5.821	-5.831	-5.841	-5.846

temp(C) = 1
pH=7.1

Nitrite(ppm)

	0	16	32	48	64	80	96	112	128	144	160	176	192	200
0	-5.93	-6.068	-6.206	-6.343	-6.481	-6.618	-6.756	-6.894	-7.031	-7.169	-7.307	-7.444	-7.582	-7.651
0.5	-5.717	-5.854	-5.992	-6.13	-6.267	-6.405	-6.542	-6.68	-6.818	-6.955	-7.093	-7.231	-7.368	-7.437
1	-5.695	-5.833	-5.971	-6.108	-6.246	-6.383	-6.521	-6.659	-6.796	-6.934	-7.071	-7.209	-7.347	-7.416
1.5	-5.707	-5.845	-5.982	-6.12	-6.257	-6.395	-6.533	-6.67	-6.808	-6.945	-7.083	-7.221	-7.358	-7.427
2	-5.737	-5.874	-6.012	-6.149	-6.287	-6.425	-6.562	-6.7	-6.838	-6.975	-7.113	-7.25	-7.388	-7.457
2.5	-5.779	-5.916	-6.054	-6.192	-6.329	-6.467	-6.604	-6.742	-6.88	-7.017	-7.155	-7.292	-7.43	-7.499
3	-5.83	-5.968	-6.105	-6.243	-6.381	-6.518	-6.656	-6.793	-6.931	-7.069	-7.206	-7.344	-7.482	-7.55
3.5	-5.889	-6.027	-6.165	-6.302						128	-7.266	-7.403	-7.541	-7.61
4	-5.955	-6.093	-6.23	-6.368						194	-7.331	-7.469	-7.607	-7.675
4.5	-6.027	-6.164	-6.302	-6.439						265	-7.403	-7.54	-7.678	-7.747
5	-6.103	-6.241	-6.379	-6.516						342	-7.48	-7.617	-7.755	-7.824
5.5	-6.185	-6.323	-6.46	-6.598						424	-7.561	-7.699	-7.836	-7.905
6	-6.271	-6.409	-6.546	-6.684						7.51	-7.647	-7.785	-7.923	-7.991
6.5	-6.362	-6.499	-6.637	-6.774						-7.6	-7.738	-7.875	-8.013	-8.082
7	-6.456	-6.594	-6.731	-6.869						695	-7.832	-7.97	-8.107	-8.176
7.5	-6.554	-6.692	-6.83	-6.967	-7.105	-7.242	-7.38	-7.518	-7.655	-7.793	-7.93	-8.068	-8.206	-8.275
8	-6.656	-6.794	-6.932	-7.069	-7.207	-7.344	-7.482	-7.62	-7.757	-7.895	-8.032	-8.17	-8.308	-8.377
8.5	-6.762	-6.9	-7.037	-7.175	-7.312	-7.45	-7.588	-7.725	-7.863	-8.001	-8.138	-8.276	-8.413	-8.482
9	-6.871	-7.009	-7.146	-7.284	-7.422	-7.559	-7.697	-7.834	-7.972	-8.11	-8.247	-8.385	-8.523	-8.591
9.5	-6.984	-7.121	-7.259	-7.397	-7.534	-7.672	-7.809	-7.947	-8.085	-8.222	-8.36	-8.498	-8.635	-8.704
10	-7.1	-7.237	-7.375	-7.513	-7.65	-7.788	-7.925	-8.063	-8.201	-8.338	-8.476	-8.614	-8.751	-8.82
10.5	-7.219	-7.357	-7.494	-7.632	-7.769	-7.907	-8.045	-8.182	-8.32	-8.458	-8.595	-8.733	-8.87	-8.939
11	-7.341	-7.479	-7.617	-7.754	-7.892	-8.03	-8.167	-8.305	-8.442	-8.58	-8.718	-8.855	-8.993	-9.062
11.5	-7.467	-7.605	-7.742	-7.88	-8.018	-8.155	-8.293	-8.431	-8.568	-8.706	-8.843	-8.981	-9.119	-9.187

temp(C) = 1
pH=7.1

	0	16	32	48	64	80	96	112	128	144	160	176	192	200
0	-1.815	-1.953	-2.091	-2.228	-2.366	-2.503	-2.641	-2.779	-2.916	-3.054	-3.191	-3.329	-3.467	-3.536
0.5	-1.602	-1.739	-1.877	-2.015	-2.152	-2.29	-2.427	-2.565	-2.703	-2.84	-2.978	-3.115	-3.253	-3.322
1	-1.58	-1.718	-1.855	-1.993	-2.131	-2.268	-2.406	-2.544	-2.681	-2.819	-2.956	-3.094	-3.232	-3.3
1.5	-1.592	-1.729	-1.867	-2.005	-2.142	-2.28	-2.418	-2.555	-2.693	-2.83	-2.968	-3.106	-3.243	-3.312
2	-1.621	-1.759	-1.897	-2.034	-2.172	-2.31	-2.447	-2.585	-2.722	-2.86	-2.998	-3.135	-3.273	-3.342
2.5	-1.664	-1.801	-1.939	-2.076	-2.214	-2.352	-2.489	-2.627	-2.765	-2.902	-3.04	-3.177	-3.315	-3.384
3	-1.715	-1.853	-1.99	-2.128	-2.266	-2.4						-3.229	-3.366	-3.435
3.5	-1.774	-1.912	-2.049	-2.187	-2.325	-2.4						-3.288	-3.426	-3.494
4	-1.84	-1.978	-2.115	-2.253	-2.39	-2.5						-3.354	-3.491	-3.56
4.5	-1.912	-2.049	-2.187	-2.324	-2.462							-3.425	-3.563	-3.632
5	-1.988	-2.126	-2.264	-2.401	-2.539	-2.6						-3.502	-3.64	-3.709
5.5	-2.07	-2.208	-2.345	-2.483	-2.62	-2.7						-3.584	-3.721	-3.79
6	-2.156	-2.294	-2.431	-2.569	-2.707	-2.8						-3.67	-3.808	-3.876
6.5	-2.246	-2.384	-2.522	-2.659	-2.797	-2.9						-3.76	-3.898	-3.967
7	-2.341	-2.478	-2.616	-2.754	-2.891	-3.029	-3.167	-3.304	-3.442	-3.579	-3.717	-3.855	-3.992	-4.061
7.5	-2.439	-2.577	-2.714	-2.852	-2.99	-3.127	-3.265	-3.403	-3.54	-3.678	-3.815	-3.953	-4.091	-4.159
8	-2.541	-2.679	-2.816	-2.954	-3.092	-3.229	-3.367	-3.505	-3.642	-3.78	-3.917	-4.055	-4.193	-4.261
8.5	-2.647	-2.784	-2.922	-3.06	-3.197	-3.335	-3.473	-3.61	-3.748	-3.885	-4.023	-4.161	-4.298	-4.367
9	-2.756	-2.894	-3.031	-3.169	-3.307	-3.444	-3.582	-3.719	-3.857	-3.995	-4.132	-4.27	-4.407	-4.476
9.5	-2.869	-3.006	-3.144	-3.281	-3.419	-3.557	-3.694	-3.832	-3.97	-4.107	-4.245	-4.382	-4.52	-4.589
10	-2.985	-3.122	-3.26	-3.397	-3.535	-3.673	-3.81	-3.948	-4.086	-4.223	-4.361	-4.498	-4.636	-4.705
10.5	-3.104	-3.241	-3.379	-3.517	-3.654	-3.792	-3.93	-4.067	-4.205	-4.342	-4.48	-4.618	-4.755	-4.824
11	-3.226	-3.364	-3.502	-3.639	-3.777	-3.914	-4.052	-4.19	-4.327	-4.465	-4.603	-4.74	-4.878	-4.947
11.5	-3.352	-3.49	-3.627	-3.765	-3.903	-4.04	-4.178	-4.315	-4.453	-4.591	-4.728	-4.866	-5.004	-5.072

temp(C) = 34
pH=4.4

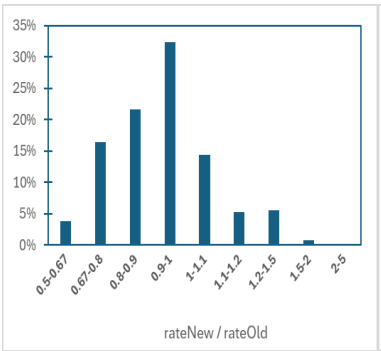
	0	16	32	48	64	80	96	112	128	144	160	176	192	200
0	-0.071	-0.081	-0.091	-0.101	-0.111	-0.12	-0.13	-0.14	-0.15	-0.16	-0.17	-0.179	-0.189	-0.194
0.5	0.1425	0.1327	0.1228	0.113	0.1031	0.0933	0.0834	0.0736	0.0637	0.0539	0.044	0.0342	0.0243	0.0194
1	0.164	0.1541	0.1443	0.1344	0.1246	0.1147	0.1049	0.095	0.0852	0.0753	0.0655	0.0556	0.0458	0.0409
1.5	0.1524	0.1425	0.1327	0.1228	0.113	0.1031	0.0933	0.0834	0.0736	0.0637	0.0539	0.044	0.0342	0.0293
2	0.1227	0.1128	0.103	0.0931	0.0833	0.0734	0.0636	0.0537	0.0439	0.034	0.0242	0.0143	0.0045	-4E-04
2.5	0.0806	0.0708	0.0609	0.0511	0.0412	0.0314	0.0215	0.0117	0.0018	-0.008	-0.018	-0.028	-0.038	-0.043
3	0.0291	0.0193	0.0094	-4E-04	-0.01	-0.02	-0.03	-0.04	-0.05	-0.06	-0.069	-0.079	-0.089	-0.094
3.5	-0.03	-0.04	-0.05	-0.06	-0.							-0.129	-0.138	-0.148	-0.153
4	-0.096	-0.106	-0.115	-0.125	-0.							-0.194	-0.204	-0.214	-0.219
4.5	-0.167	-0.177	-0.187	-0.197	-0.							-0.266	-0.276	-0.286	-0.29
5	-0.244	-0.254	-0.264	-0.274	-0.							-0.343	-0.353	-0.362	-0.367
5.5	-0.326	-0.336	-0.345	-0.355	-0.							-0.424	-0.434	-0.444	-0.449
6	-0.412	-0.422	-0.432	-0.441	-0.							-0.51	-0.52	-0.53	-0.535
6.5	-0.502	-0.512	-0.522	-0.532	-0.							-0.601	-0.611	-0.62	-0.625
7	-0.597	-0.607	-0.616	-0.626	-0.							-0.695	-0.705	-0.715	-0.72
7.5	-0.695	-0.705	-0.715	-0.725	-0.734	-0.744	-0.754	-0.764	-0.774	-0.784	-0.793	-0.803	-0.813	-0.818
8	-0.797	-0.807	-0.817	-0.827	-0.836	-0.846	-0.856	-0.866	-0.876	-0.886	-0.896	-0.905	-0.915	-0.92
8.5	-0.903	-0.913	-0.922	-0.932	-0.942	-0.952	-0.962	-0.972	-0.981	-0.991	-1.001	-1.011	-1.021	-1.026
9	-1.012	-1.022	-1.032	-1.041	-1.051	-1.061	-1.071	-1.081	-1.091	-1.1	-1.11	-1.12	-1.13	-1.135
9.5	-1.124	-1.134	-1.144	-1.154	-1.164	-1.174	-1.184	-1.193	-1.203	-1.213	-1.223	-1.233	-1.243	-1.248
10	-1.24	-1.25	-1.26	-1.27	-1.28	-1.29	-1.3	-1.309	-1.319	-1.329	-1.339	-1.349	-1.359	-1.364
10.5	-1.36	-1.37	-1.379	-1.389	-1.399	-1.409	-1.419	-1.429	-1.438	-1.448	-1.458	-1.468	-1.478	-1.483
11	-1.482	-1.492	-1.502	-1.512	-1.522	-1.531	-1.541	-1.551	-1.561	-1.571	-1.581	-1.591	-1.6	-1.605
11.5	-1.608	-1.618	-1.628	-1.637	-1.647	-1.657	-1.667	-1.677	-1.687	-1.697	-1.706	-1.716	-1.726	-1.731

temp(C) = 34
pH=7.1

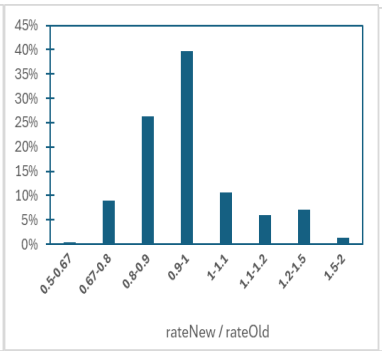
Comparing the new predictions with the old ones

Introduce q_r=*reteNew/rateOld.* The ratio quantifies the discrepancy between the two predictions. The frequency diagrams show below the distribution of the factor by which the new model deviates from the old one.

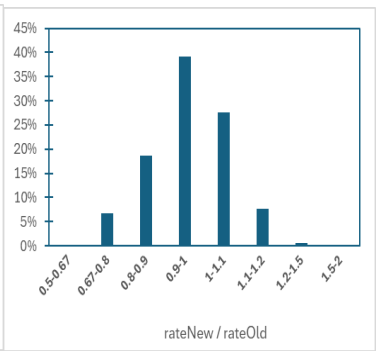
Bc_CO_2



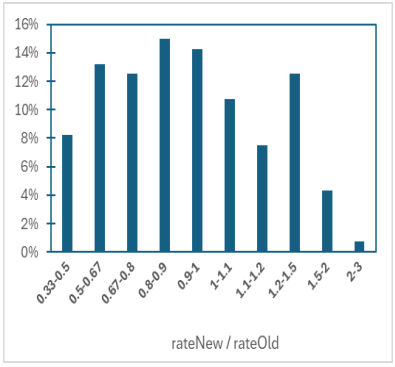
Ec_CO_2



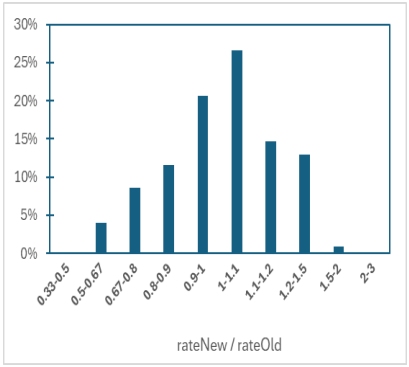
Lm_CO_2



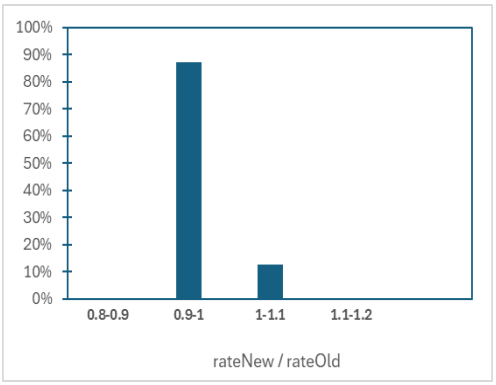
Ss_CO_2



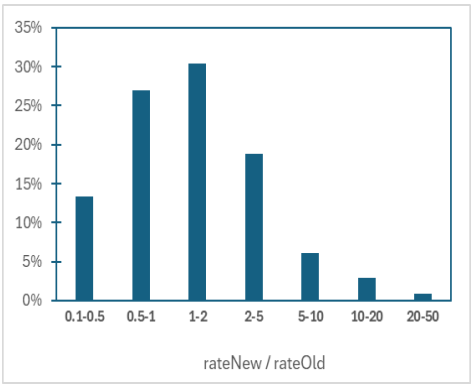
Ye_CO_2



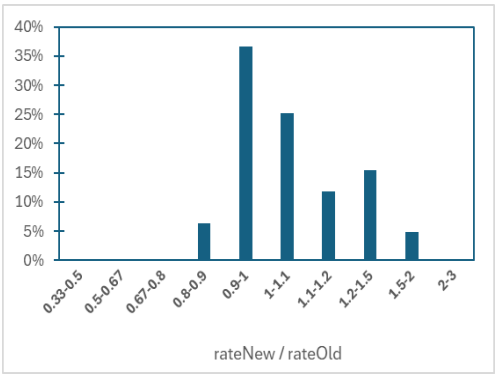
Lm_nitr (Old-New: very similar)



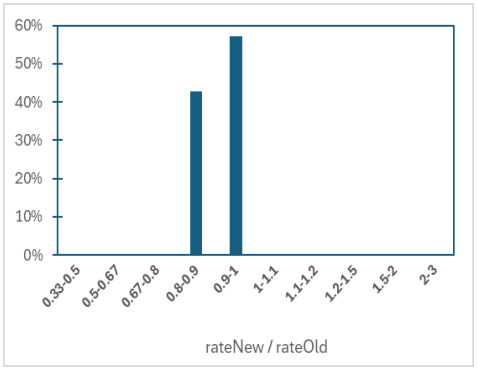
Ss_nitr (Old-New: very different)



Lm_lact



Ye_lact (rateOld: no ef_4-effect)



REFERENCES

- Baranyi and Roberts TA (1994). A dynamic approach to predicting bacterial growth in food. *Int. J. Food Microbiol.* 23. 277.
- Baranyi J, Ross T, McMeekin and Roberts TA (1996). Effects of parameterization on the performance of empirical models used in predictive microbiology. *Food Microbiol.* 13. 83.
- Baranyi J, Tamplin ML. (2004). ComBase: A common database on microbial responses to food environments. *J. Food Prot.* 67. 187
- Geeraerd AH, Herremans CH and Van Impe JF (2000). Structural model requirements to describe microbial inactivation during a mild heat treatment. *Int. J. Food Microbiol.* 59. 185.
- Masana MO, Baranyi J (2000). Adding new factors to predictive models: the effect on the risk of extrapolation. *Food Microbiol*. 17. 367
- Resnik SL and Chirife J. (1988). Proposed theoretical a_w values at various temperatures for selected solutions to be used as reference sources in the range of microbial growth. *J. Food Prot.* 51. 419.
- Rockaya M, Baranyi J (2025). Variability of growth parameter estimates - The role of rescaling and reparameterization. *Food Microbiol.* 128. 104726.
- Zwietering MH, De Wit JC, Notermans S (1996). Application-of predictive microbiology to estimate the number of *Bacillus cereus* in pasteurised milk at the point of consumption. *Int. J. Food Microbiol.* 30. 55.