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A biphasic model of lifespan in nematode *Caenorhabditis elegans* worm

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Ageing research focuses on identifying lifespan modifiers and understanding and appropriately interpreting their effects. One of the most relevant quantities being studied is the shape of the survival curve that can reveal crucial information on the mechanism of action. Here, we introduce a bilogistic model to describe the shape of the lifespan curves of *Caenorhabditis elegans* populations. Using the corrected Akaike information criterion and the RMSE as goodness-of-fit tests, we show that the bilogistic model provides a better fit to the experimental data from nematode worms than other mathematical models and can identify and confirm biphasic lifespan data. Our parametric model offers a method to interpret replicate experiments data in terms of the shape parameters of the lifespan curve and enables robust statistical analysis of intra- and inter-group variance. We apply the model to novel lifespan data from *C. elegans* and *Drosophila melanogaster* and provide a rational statistical analysis of lifespan modifiers such as temperature and *daf-16/FOXO* mutation.

1. Introduction

Today, many societies face the challenge of a rapidly ageing population with associated health problems and increase in healthcare expenses. A crucial step towards our understanding of ageing is the identification and characterization of lifespan modifiers such as temperature [1], diet [2], pharmacological interventions [3]

and genetic pathways [4]. The most common approach for testing a potential lifespan modifier is to use the non-parametric Kaplan–Meier estimator [5] followed by a log-rank test, which tests the null hypothesis that there is no statistically significant difference between the control and test groups [5]. This allows a qualitative comparison between a control and a test group, but not between replicates. Crucially, as it is only a significance test comparing two curves, it is unable to identify where differences occur or to provide an interpretation of them. One alternative is to perform parametric modelling of the data by fitting a mathematical function to the survival curve. Common distributions for lifespan data comprise simple exponential and sigmoidal distributions [6]. Two-parameter sigmoidal functions such as the Logistic [7], Weibull [8] or Gompertz [9] models use a death rate and a temporal quantification (e.g. median time lag, age-dependent mortality) as parameters to account for the shape and scale of the lifespan curve. Sigmoidal functions fit data points to a typical curve shape with a shoulder, a rapid decrease and a tail [6,10]. However, these models do not always adequately fit experimental data, leading to over-smoothing of the curves and unintentional discarding of features of the lifespan curve. For example, it has recently been shown for *Caenorhabditis elegans* that there are short-lived and long-lived worms resulting in survival curves which are different from a standard, monophasic decrease and that can be described as biphasic [11,12].

Here, we introduce a novel bilogistic model that describes and distinguishes two phases within the survival curve of a population, each with its own median survival. We apply this model to new experimental lifespan data for *C. elegans* obtained for different temperatures (worm lifespan depends on temperature [1,13]). The bilogistic model has four parameters, two median time constants, one death rate and the fraction of the population following either phase dynamics. We show that the bilogistic model allows for a clear identification of biphasic lifespan data for which it provides a significantly better fit of experimental data compared to several other models. This is demonstrated by the corrected Akaike information criterion (AICc) [14,15] that considers the different number of parameters of models, but we also apply other goodness-of-fit tests. We discuss a five-parameter extension (two different death rates), and a four-parameter variant (two different death rates but equal proportion between the subpopulations) of the model that can be appropriate to model specific experimental conditions.

2. Material and methods

2.1. *Caenorhabditis elegans* lifespan assay

The *C. elegans* strains N2 (wild-type) and *daf-16* (*mu86*) were acquired from the Caenorhabditis Genetics Center (CGC), University of Minnesota. All strains were maintained on solid nematode growth media (NGM) plates supplemented with nystatin ($10 \mu\text{g ml}^{-1}$; Sigma) and seeded with *Escherichia coli* OP50 strain (CGC) at 20°C unless stated otherwise.

NGM plates used for lifespan assays were supplemented with 5-fluoro-2'-deoxyuridine (FUDR) ($50 \mu\text{M}$; Melford, UK) to prevent growth of unwanted offspring. Lifespan assays were conducted on a population of worms synchronized by alkaline hypochlorite treatment. Once synchronized, 50 (unless stated otherwise) L4 stage worms were transferred onto fresh NGM FUDR plates for the start of the experiment. Worms were transferred onto fresh plates weekly, but more frequently if the seeded OP50 was depleted or if in case of unwanted bacterial or fungal contamination. Day 0 is considered as the first day of adulthood and time points for events (death or censorship) were marked almost daily. Worms were classified into three categories at each time point: alive, dead or censored.

2.2. *Drosophila* lifespan assay

Control w^{Dah} was derived by backcrossing w^{1118} into the outbred wild-type *Dahomey* background. The *dfoxa1* flies were previously described [16]. Flies were raised and maintained on standard sugar/yeast medium [17]. Lifespan experiments were conducted at 25°C on a 12 : 12 h light/dark cycle at constant humidity. Flies were reared at standard density, allowed to mate for 24 h, sorted by sex and then transferred to experimental vials at a density of ten flies per vial. Approximately 100 flies were used per experimental replicate. Flies were transferred to fresh vials three times a week, and deaths were scored during transferral.

2.3. Survival curve plots

Kaplan–Meier survival curves were constructed by inputting events occurring at given time points into GraphPad Prism 9. Survival proportions at each time point were calculated and a log-rank (Mantel–Cox)

test was conducted to statistically compare differences between two curves. p -values less than 0.05 were interpreted to show statistically significant differences between groups.

2.4. Lifespan models

In this study, we constructed a novel bilogistic model for fitting biphasic data, called Bilogistic 1kf (equation (2.1)). The f parameter splits the curve into two phases giving a weighting to each phase. There is a single death rate k and two time parameters t_1 and t_2 , representing the median survival for each phase. We also constructed two variants of this model: Bilogistic 2kf with two different death rates instead of one (k_1 and k_2 ; equation (2.2)) and Bilogistic 2k, with two different death rates k_1 and k_2 but equal weighting of the two phases (setting $f=0.5$; equation (2.3)). For each of the three models, the terms in the numerator ensure that at $t=0$, the number of living animals at the start of the experiment is equal to N_0 , the known starting number, rescaled in each experiment to be 100%. The Bilogistic 2kf model with five parameters contains the other models (Bilogistic 1kf and Bilogistic 2k) as limit cases ($k_1=k_2$ and $f=0.5$, respectively) and can itself be interpreted as a generalization of the Whiting–Buchanan model with four parameters [18], where two different time constants are applied instead of one.

Bilogistic 1kf model:

$$N(t) = N_0 \left[f \frac{1 + e^{-kt_1}}{1 + e^{k(t-t_1)}} + (1-f) \frac{1 + e^{-kt_2}}{1 + e^{k(t-t_2)}} \right]. \quad (2.1)$$

Bilogistic 2kf model:

$$N(t) = N_0 \left[f \frac{1 + e^{-k_1 t_1}}{1 + e^{k_1(t-t_1)}} + (1-f) \frac{1 + e^{-k_2 t_2}}{1 + e^{k_2(t-t_2)}} \right]. \quad (2.2)$$

Bilogistic 2k model:

$$N(t) = 0.5 N_0 \left[\frac{1 + e^{-k_1 t_1}}{1 + e^{k_1(t-t_1)}} + \frac{1 + e^{-k_2 t_2}}{1 + e^{k_2(t-t_2)}} \right]. \quad (2.3)$$

The bilogistic models were compared against six models: the Whiting–Buchanan model with four parameters (equation (2.4) [18]), the Gompertz–Makeham model with three parameters (equation (2.5) [19]), the Logistic model with two parameters (equation (2.6) [7]), the Wilson model with two parameters (equation (2.7) [20]), the Weibull model with two parameters (equation (2.8) [8]) and the Gompertz model with two parameters (equation (2.9) [9]).

Whiting–Buchanan model:

$$N(t) = N_0 \left[f \frac{1 + e^{-k_1 t_{lag}}}{1 + e^{k_1(t-t_{lag})}} + (1-f) \frac{1 + e^{-k_2 t_{lag}}}{1 + e^{k_2(t-t_{lag})}} \right]. \quad (2.4)$$

Gompertz–Makeham model:

$$N(t) = N_0 (e^{-ct - (a/b)(e^{bt} - 1)}). \quad (2.5)$$

Logistic model:

$$N(t) = \frac{N_0}{1 + e^{(t-t_{lag})/k}}. \quad (2.6)$$

Wilson model:

$$N(t) = \frac{N_0}{1 + (t/t_{lag})^k}. \quad (2.7)$$

Weibull model:

$$N(t) = N_0 (e^{-at})^b. \quad (2.8)$$

Gompertz model:

$$N(t) = N_0 (e^{-(a/b)(e^{bt} - 1)}). \quad (2.9)$$

2.5. Statistical analysis

The experimental data have been analysed using various common statistical analysis packages that allow for minimum least-squares analysis, maximum-likelihood analysis, goodness-of-fit tests (including residual analysis/RMSE and AIC/AICc) and ANOVA tests.

The MATLAB (R2016a, v.9.0.0.370719, MathWorks) curve fitting toolbox was used to fit data using a nonlinear least-squares method (Trust-Region algorithm) to estimate parameters. The root mean square error (RMSE) was used for the goodness-of-fit statistical analysis of the different models using MATLAB. It represents the model performance and lower values of RMSE indicate smaller differences between actual data and fitted curve, and hence a better fit. To account for different numbers of parameters, the adjusted (or unbiased) RMSE is used:

$$\text{RMSE} = \sqrt{\frac{\sum_{i=1}^m (y_i - \hat{y}_i)^2}{m - k}},$$

where m is the number of data points per experiment (replicate) of a lifespan curve, \hat{y}_i is the predicted value at each data point and k is the number of parameters of the model. For a number n of replicates, the mean value and standard error of the mean (s.e.m.) were used. A customized residual analysis has also been used where several data points were binned (see Results). The statistical significance between two groups was examined using two-way analysis of variance (ANOVA) followed by Tukey multiple comparison tests using GraphPad Prism 9 (www.graphpad.com). Statistical significance at $p < 0.05$, $p < 0.01$, $p < 0.001$ and $p < 0.0001$ is indicated in the figures where appropriate.

The maximum-likelihood analysis to identify the optimal fit for each experiment was performed using the statistical programming language R (<https://cran.r-project.org/index.html>; v.3.5.1). Specifically, the R function `mle2()` was used, which relies on the optimization function `optim()` that by default uses a Nelder and Mead algorithm (<https://www.rdocumentation.org/packages/bbmle/versions/1.0.20/topics/mle2>). For Gompertz and Gompertz–Makeham models, we used a limited-memory modification of the BFGS quasi-Newton method. To account for different numbers of data points in each experiment and different numbers of parameters for each parametric model, the AICc was used to compare models. It is given by the equation

$$\text{AICc} = \text{AIC} + \frac{2k^2 + 2k}{m - k - 1},$$

where m denotes the number of data points per experiment (replicate) and k denotes the number of parameters in the model and $\text{AIC} = 2k - 2\ln(L)$ denotes the value obtained from the maximum-likelihood analysis, where L is the likelihood of a model with a certain set of parameters [14,15]. Lower values of AICc indicate a more reliable prediction.

Both methods, minimum least-squares and maximum likelihood, predict the parameter values for the model equations and allow us to fit a curve to the data. We specify the curve fitting method used in each figure.

3. Results

3.1. Variability in lifespan curves in *Caenorhabditis elegans*

The nematode worm *C. elegans* is a commonly used organism for studying lifespan. As previously described, lower temperatures generally result in longer lifespan in the worm [1]. Here, we use three experimental replicates to illustrate the variability in the lifespan curves for the same temperature, and the variability between three temperatures (15°C, 20°C and 25°C; figure 1a–c). Any single lifespan curve for 15°C, 20°C and 25°C is significantly different from any other lifespan curve at a different temperature when tested with the non-parametric Kaplan–Meier estimator followed by a log-rank test. For N2 worms, we have $n = 20$ replicates for 15°C, $n = 15$ replicates for 20°C and $n = 14$ replicates for 25°C. Therefore, the question arises of how to analyse quantitatively a set of replicates for identical experimental conditions and between different experimental conditions. For this, we use a parametric modelling approach.

3.2. Biphasic lifespan curves in *Caenorhabditis elegans*

To address the questions raised above and using the observation that *C. elegans* populations can show a biphasic lifespan behaviour [11,12], we propose a bilogistic model (see Methods, equation (2.1)), named

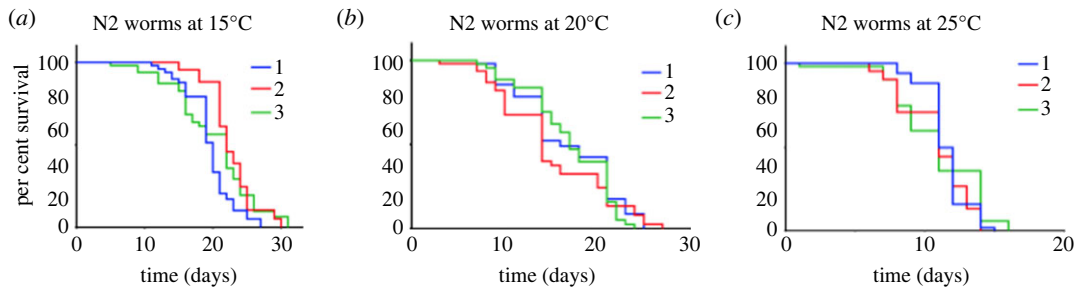


Figure 1. Experimental replicates of *C. elegans* lifespan. Representative experimental triplicate (coloured segments) of lifespan curves of N2 worms maintained at different temperatures ((a) 15°C, (b) 20°C, (c) 25°C) illustrates intra-group variability. Each experiment contained 100 worms.

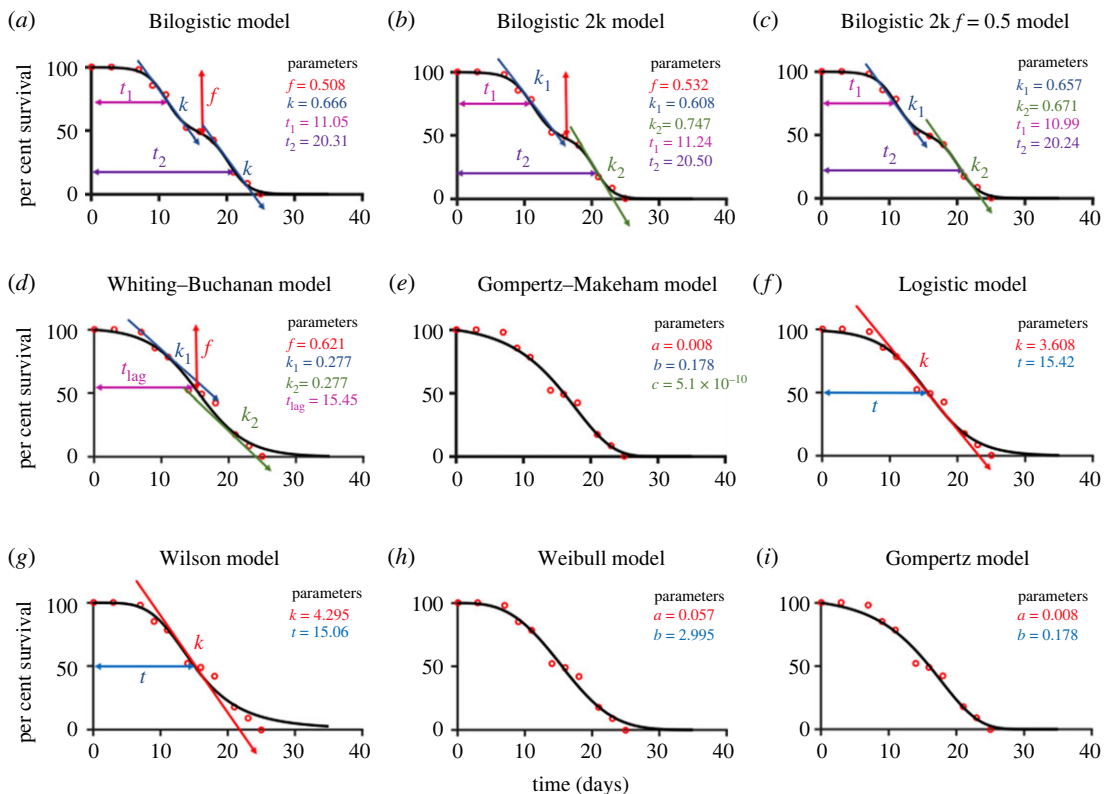


Figure 2. Curve fitting and parameter estimation of *C. elegans* lifespan. The Bilogistic 1kf model (a) and variants (b,c), together with common lifespan models (Whiting–Buchanan (d), Gompertz–Makeham (e), Logistic (f), Wilson (g), Weibull (h) and Gompertz (i)) were used to fit the same lifespan data of a single experiment (100 N2 worms maintained at 20°C). Data are represented by red circles and model fits (minimum least squares) by black curves. The parameters for each model are also given. An illustration of the meaning of the parameters is given for the Bilogistic models.

Bilogistic 1kf, for fitting the experimental data (least-squares fit or maximum likelihood, see Methods) and comparison against other models. In figure 2, we show the procedure for a single experiment (for 100 N2 worms at 20°C), where we performed a least-squares fit against Bilogistic 1kf and the other parametric models. The parameters of Bilogistic 1kf are as follows: the f value (which denotes the weighting or proportion of the two phases), the median survival times t_1 and t_2 and the death rate k for both phases (figure 2a). The phases represent a short-lived (1st phase) and a long-lived subpopulation (2nd phase). The Bilogistic 1kf model uses the same k value for both phases although we have also tested variants with two different k values (Bilogistic 2kf, equation (2.2); figure 2b) or with two different k values but equal phase distribution (Bilogistic 2k, equation (2.3); figure 2c). The Bilogistic 1kf model and its variants were used to fit the lifespan data points (figure 2a–c) and show a good visual agreement between data and curves. We fit the same data against a range of common lifespan models (see Methods, equations (2.4)–(2.9); figure 2d–i) and observe a systematic deviation for

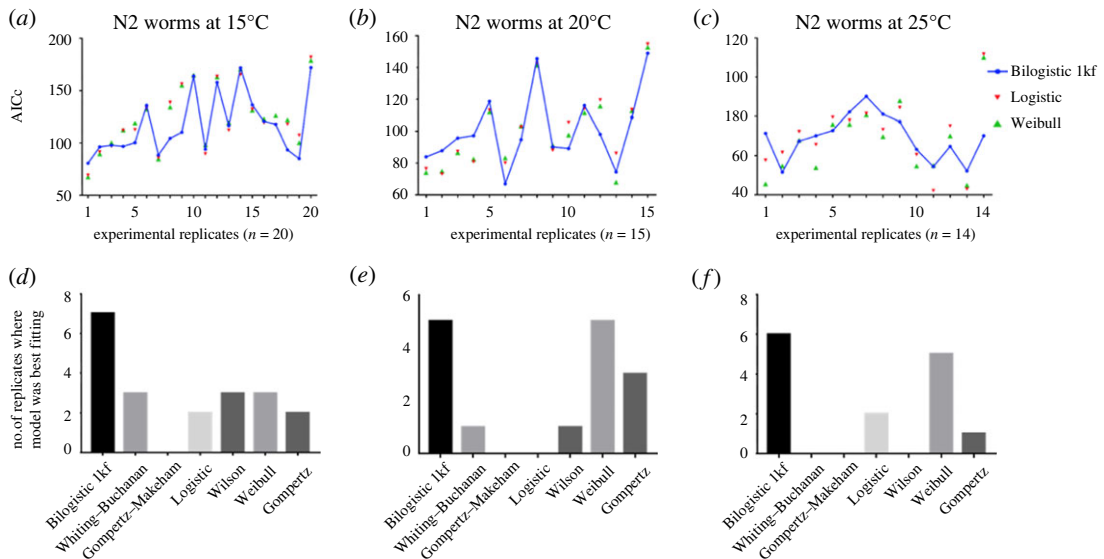


Figure 3. Analysis of lifespan models with the Akaike information criterion with small sample correction (AICc). The Bilogistic 1kf model and a panel of lifespan models were used to fit the lifespan data from N2 worms maintained at 15°C, 20°C and 25°C using the maximum-likelihood method. The AICc was calculated for each fit (a–c). The blue curve highlights the AICc values obtained from the Bilogistic 1kf model. Smaller values indicate better fits and the Bilogistic 1kf model was a best fit more often than the other models (d–f). The Weibull model was equally good for the 20°C data.

intermediate time moments (roughly, between Days 14 and 20) for all six models, and additionally for Days 3 and 7 for the Gompertz, Gompertz–Makeham and Logistic models. We quantify the goodness of fit systematically below, but already observe that the bilogistic models can fit the data well, clearly suggesting the existence of two phases, while there are systematic deviations for the other models which do not capture the biphasic nature of the survival curve.

3.3. Comparison of lifespan models using AICc and RMSE

To confirm or reject this observation and to compare the goodness of fit of the parametric models, we considered two independent measures to test for model selection: the AICc for the maximum-likelihood analysis and the RMSE for the minimum least-squares analysis.

Since we are comparing models with different numbers of parameters, the AICc was used to account for the number of parameters in the model. A lower AICc score indicates best fit. From a set of experimental replicates of *C. elegans* maintained at 15°C ($n = 20$; figure 3a,d), 20°C ($n = 15$; figure 3b,e) and 25°C ($n = 14$; figure 3c,f), the Bilogistic 1kf model consistently scored a lower AICc than other models for all three temperatures. Only the Weibull model with two parameters was as good as our model for the 20°C dataset (figure 3e).

The adjusted RMSE is a measure of the residual differences between actual experimental lifespan data points and fitted model curve if models have a different number of parameters (see Methods). The residual differences are first calculated for each replicate of each dataset before undergoing a data binning procedure along the temporal axis to smooth the data. Residuals were grouped into bins of 2, 3 or 4 days and plotted (electronic supplementary material, figure S1). Plots which show the smallest residual error without systematic deviations throughout the lifespan indicate the best fit. The Bilogistic 1kf model shows the smallest residual error in all bins with a minimum of systematic deviations when compared to the other models (electronic supplementary material, figure S1), indicating that it is the most appropriate model for the data (we will comment on the use of the Bilogistic 2kf and Bilogistic 1k models in the Discussion). The results are relatively independent of the bin size, although bin size 2 performs slightly worse for the Bilogistic models. Following on, the adjusted RMSE was calculated for each curve. This type of analysis considers the varying number of parameters present in each model by giving a penalty for a model with more parameters. Using the data of the lifespan of *C. elegans* maintained at 20°C, we observed consistently smaller residuals using the Bilogistic 1kf model compared to other models (figure 4a–h). Consequently, we found significantly lower RMSE values for the Bilogistic 1kf when averaged over all replicates (figure 4i). We find similar results for

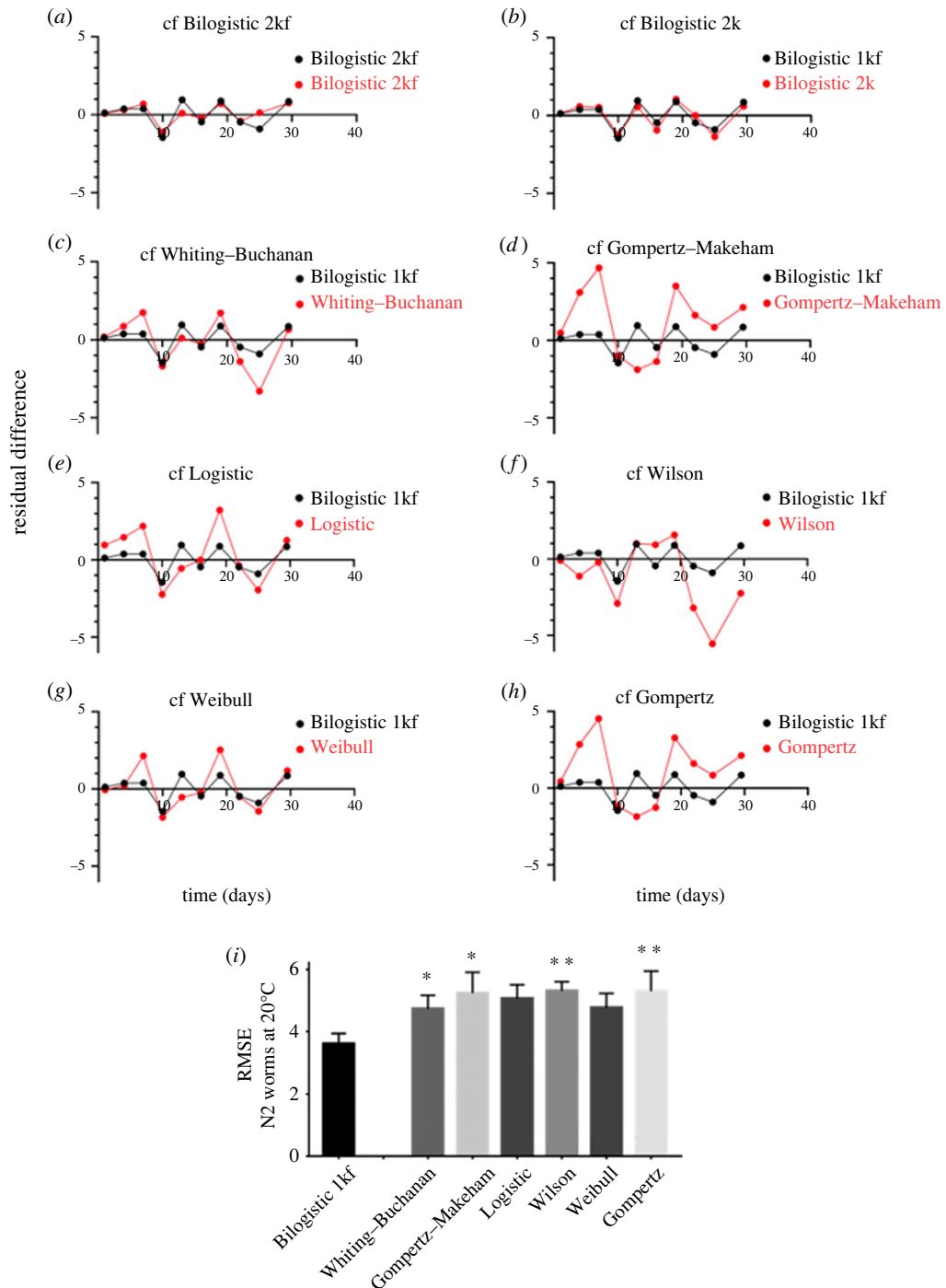


Figure 4. Analysis of lifespan models by residual difference analysis. (a–h) Comparison of residual differences from minimum least-square fits against the Bilogistic 1kf model (black) and against a panel of lifespan models (red) onto experimental replicate of N2 worms maintained at 20°C ($n = 15$). Binning was set to 3 days. The smaller the residual differences, the better the fit. (i) Analysis of the adjusted root mean square error (RMSE) for the panel of models ($n = 15$). Data are shown as mean \pm s.e.m. * $p < 0.05$, ** $p < 0.01$.

worms maintained at 15°C and 25°C (electronic supplementary material, figures S2 and S3). Thus, the unbiased RMSE shows that the Bilogistic 1kf model is significantly better at fitting lifespan curves of *C. elegans* across different temperatures.

3.4. Analysis of the effect of temperature on nematode lifespan using the Bilogistic 1kf model

The lifespan curves for worms maintained at 15°C ($n = 20$ replicates), 20°C ($n = 15$ replicates) and 25°C ($n = 14$ replicates) were fitted against the Bilogistic 1kf model using the maximum-likelihood method

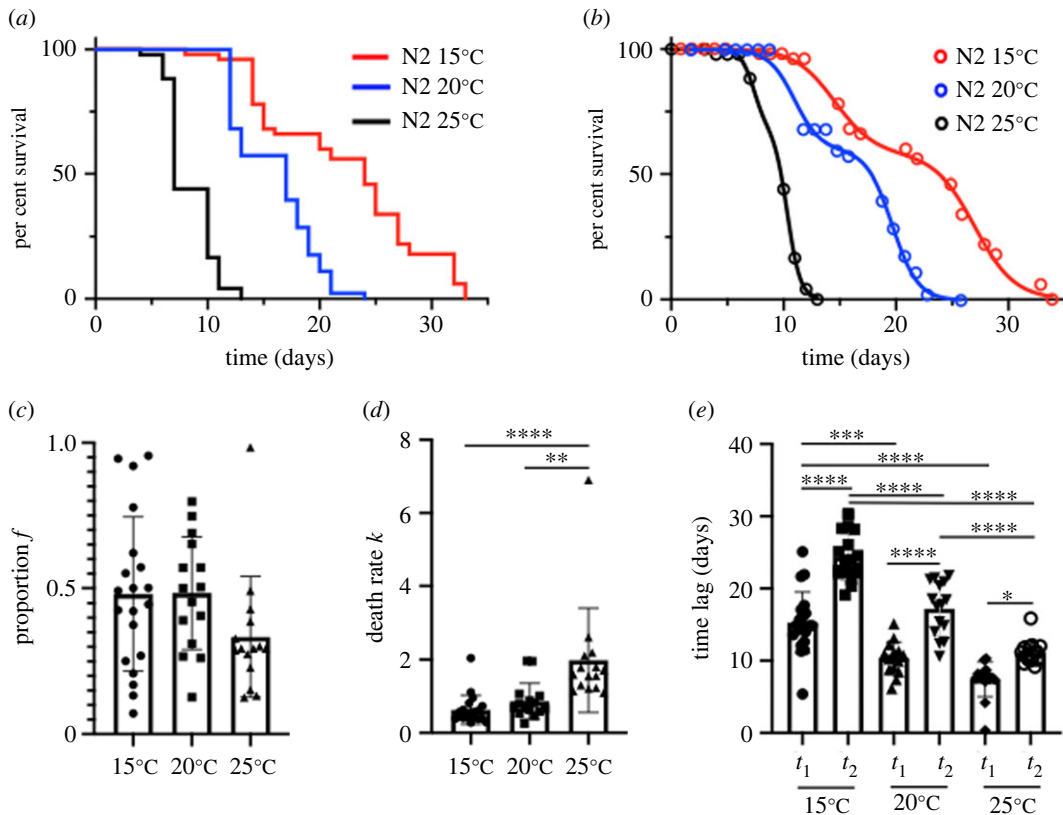


Figure 5. Effect of temperature on *C. elegans* lifespan. (a) Representative lifespan data for N2 worms maintained at 15°C, 20°C and 25°C and (b) fitted against the Bilogistic 1kf model with the maximum-likelihood method. (c–e) Analysis of the model parameters (f , k , t_1 and t_2) for lifespan curves of N2 worms maintained at 15°C ($n = 20$), 20°C ($n = 15$), 25°C ($n = 14$). Data are shown as mean \pm s.e.m. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ and **** $p < 0.0001$.

(representative data in figure 5a,b) and the model parameters for each temperature condition were analysed. While at 25°C the f parameter is lower in many replicates compared to the parameters at 15°C and 20°C, this turned out not to be statistically significant since the overall spread is large (figure 5c). However, the death rate k is significantly increased as the temperature is increased from 15°C to 25°C or from 20°C to 25°C (figure 5d). The time parameters t_1 and t_2 were significantly different from each other, indicating the presence of two phases, although the difference becomes smaller and less significant for 25°C. Furthermore, both t_1 and t_2 were significantly decreasing as the temperature was increasing (figure 5e). Thus, the temperature has significant effects not only on the timing of the two phases, but also on the death rate.

3.5. Conserved effects of *daf-16*/FOXO deletion on lifespan

We then asked whether the model could be applied to measure the effects of genetic manipulations on lifespan. We considered the Forkhead Box O (FOXO) nematode orthologue *daf-16*, known to play a critical role in regulating lifespan [4]. *daf-16* (*mu86*) worms lack *daf-16*, resulting in a significantly shorter lifespan (figure 6a), which could be fitted with our model (figure 6b). The loss of *daf-16* did not affect the presence of the two phases and significantly increased the death rate k (figure 6d), with no effects on the other parameters.

We hypothesized that these effects of FOXO loss-of-function on lifespan are conserved in other organisms. To test this, we analysed the lifespans of *Drosophila melanogaster* lacking FOXO (*dfoxo* Δ), which also have a shorter lifespan than their control [16] (figure 6f) and which again could be better described by our model (figure 6g–j). The *Drosophila* lifespan curve has two phases as demonstrated by the two significantly different time parameters t_1 and t_2 . However, the effects of *dfoxo* deletion in *Drosophila* did not exactly mirror our findings from the *daf-16*(*mu86*) worms. Thus, we observed a higher death rate in the mutant *dfoxo* Δ fly ($p = 0.058$) and statistically significantly decreased time parameters t_1 and t_2 .

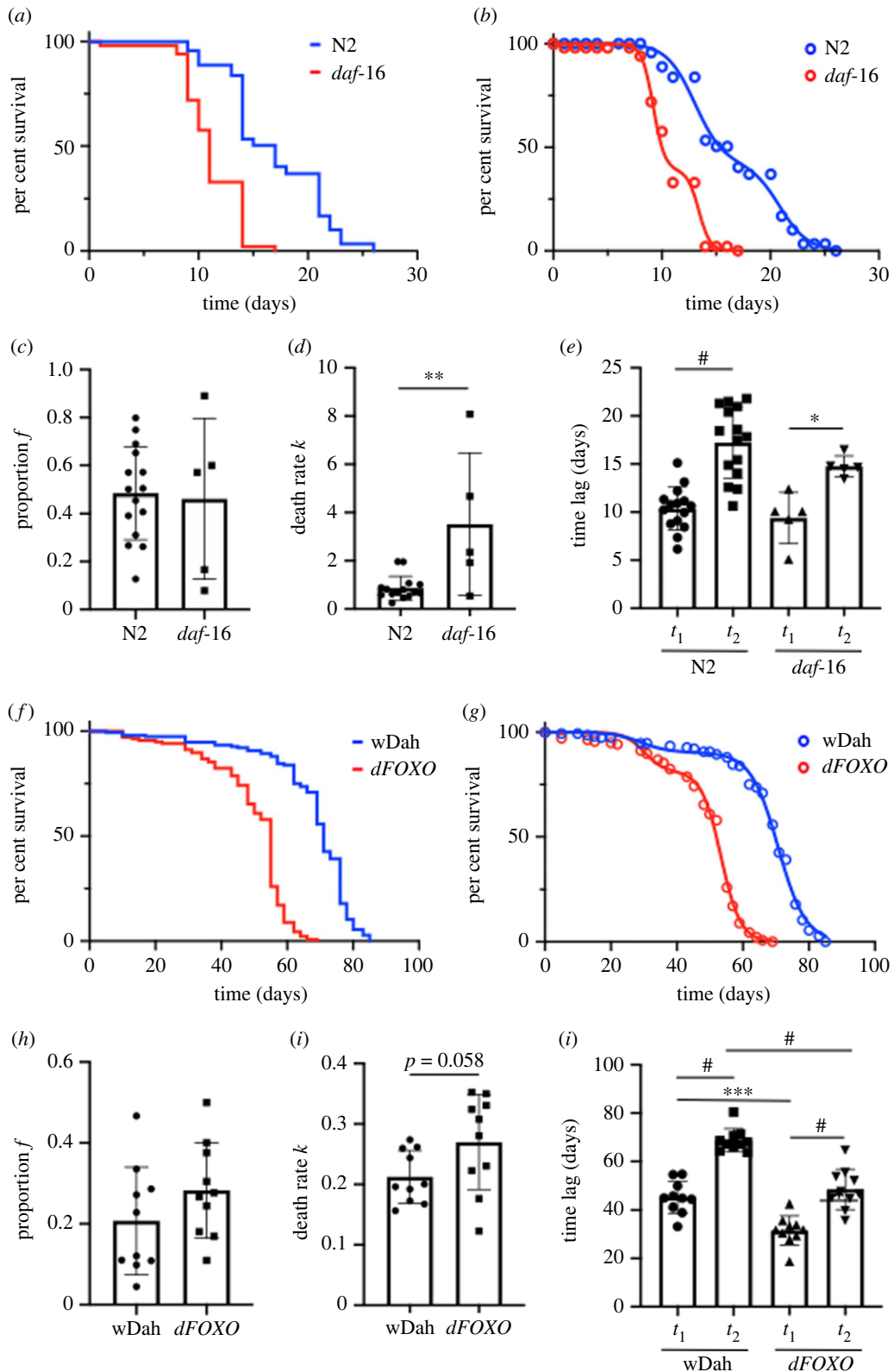


Figure 6. Effect of *daf16*/*dFOXO* mutation on lifespan. (a) Representative lifespan curves of *N2* and *daf-16* worms maintained at 20°C and (b) fitted against the Bilogistic 1kf model with the maximum-likelihood method. (c–e) Analysis of the model parameters (f , k , t_1 and t_2) for lifespan curves of *N2* ($n = 9$) and *daf-16* ($n = 5$) worms maintained at 20°C. (f) Representative lifespan curves of wild-type *wDah* and *dFOXO* mutant *Drosophila* flies and (g) fitted against the Bilogistic 1kf model with the maximum-likelihood method. (h–j) Analysis of the model parameters (f , k , t_1 and t_2) for lifespan curves of *wDah* ($n = 9$) and *dFOXO* ($n = 5$) flies. Data are shown as mean \pm s.e.m. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ and **** $p < 0.0001$.

4. Discussion

Lifespan and survival are the results of a wide range of complex interactions within and among individual organisms and discerning the effects of lifespan modifiers is a challenging task. The log-rank test from the Kaplan–Meier estimator works as a basic statistical test [21], comparing two curves and assigning whether they are statistically significantly different. However, it does not provide any insights into the mechanisms of action of the lifespan modifier and, crucially, it cannot be used to test experimental replicates. Since the variability of lifespan experiments is high even for control groups, the problem lies in how to obtain a representative lifespan curve from multiple replicates.

Parametric analysis using e.g. Gompertz and Weibull models can address such questions [6]. By using only two parameters, these models propose that lifespan modifiers simply affect the monophasic gradient [22] or shift the lifespan curves along the time axis [23]. However, this assumes a monophasic lifespan with a uniform parametric distribution, which is not the case in many instances, and biphasic dynamics can be more pronounced depending on experimental conditions or animal strains [11,24]. Note that the asymmetric shape of the Gompertz and Gompertz–Makeham curves can be referred to as biphasic, but this does not capture the dynamics described here as we do not have an explicit exponential age-dependent component.

Biphasicness is a subtle effect and sometimes genetic, environmental or experimental parameters can mask or amplify it (e.g. see [25,26]). Our experimental data clearly displays more pronounced biphasic dynamics in certain conditions (e.g. *C. elegans* wild-type (N2 strain) at 20°C, *daf-16* (*mu86*)). When Vaupel [27] reviewed the different rates of mortality during the lifespans of insects and worms, a two-stage Gompertz model was normally found to be better at fitting the data. The question remains about what these two phases mean biologically. Vaupel [27] mused on the heterogeneity of the population where, although the individuals are genetically identical, they would differ from each other in terms of size, weight, robustness and frailty. More recently, analysis of the pharynx of *C. elegans* corpses revealed two distinct death types which could be separated as occurring at an early and late phase [12]. Similarly, use of the Smurf Assay, where gut permeability is assessed by a blue phenotype, in *Drosophila* flies, nematode worms and zebrafish also showed two phases of lifespan [28]. One recent paper uses the term ‘bimodal survival’ to describe the short-lived and long-lived cohorts of worm which could be adopting alternative physiological states due to unknown mechanisms [29].

Thus, the proposed bilogistic model attempts to capture the two phases, accounting for a proportion of the individuals dying earlier and the remainder dying significantly later as two distinct groups. The model can be interpreted as either an extension of a simple Logistic model (similar to the bilogistic model discussed by Meyer in a different context [30]) or as an extension of the Whiting–Buchanan model [18] with two lag phases instead of one.

Analysis of two goodness-of-fit tests, AICc for a maximum-likelihood model and adjusted RMSE for a least-squares model (for a recent discussion on these measures, see [31]), shows that the model Bilogistic 1kf fits the lifespan data on average better than other lifespan models (figures 3 and 4). Due to the high variability between replicates, the Bilogistic 1kf model is not always the most likely model, but it performs better than all other models tested. We emphasize that this conclusion does not depend on whether we use the AICc for a maximum-likelihood model or an adjusted RMSE for a least-squares model.

Adding an additional parameter such as a second death rate k_2 or fixing the phase proportion f to 0.5 (while having two death rates k_1 and k_2) to modify the Bilogistic model to variants Bilogistic 2kf or Bilogistic 2k can significantly improve the fit or the advantage against other models, as shown in electronic supplementary material, figure S4. While we have used the Bilogistic 1kf model throughout this study, we observe that the Bilogistic 2kf model is more general and has a potentially wider applicability. It has five parameters, but simplifications can be applied in a straightforward way to obtain models with four parameters (Bilogistic 1kf, Bilogistic 2k) or three parameters (Bilogistic 1k) which may be appropriate for certain animal models or experimental conditions. We have, therefore, introduced a family of bilogistic models.

As is typical for survival models using logistic functions, the bilogistic models used here have not been derived from first principles but are justified *a posteriori* due to their predictive capacity. Our results agree with previous findings that logistic fittings provide better results than Gompertz–Makeham or Weibull fittings [32,33]. While a model with four or even five parameters has a higher risk of overfitting compared to a model with two or three parameters as for Weibull, Gompertz or Gompertz–Makeham, we emphasize that both goodness-of-fit tests have accounted for the numbers of parameters.

Comparing the parameters of the control curves to those for the test curves can reveal important clues to the action of the lifespan modifiers. In the case of high temperature, the death rate k increased while the phases shortened (t_1 and t_2). For the *daf-16* mutation, we only observed a statistically significant increase in the rate k but no differences in the other parameters. Interestingly, the equivalent mutation in *Drosophila* flies (dFOXO) instead showed a statistically insignificant increase in the rate k ($p=0.058$) while both time parameters t_1 and t_2 were significantly reduced. These observations warrant further experimental investigations in mechanistic explanations and the effects of the DAF-16/FOXO mutations would suggest different mechanisms for the DAF-16/dFOXO mutations in both animals.

Although our experimental organisms are genetically homogeneous, lifespan analysis shows that subpopulations of short- and long-lived individuals exist. The present analysis does not reveal the mechanisms behind the observed biphasic dynamics which is beyond the scope of this article.

In conclusion, our study proposes a new parametric model for analysing lifespan assays. We show it is able to fit experimental data from the worms and flies, both of which exhibit biphasic dynamics. We have carefully considered the danger of overfitting our data and our residual difference analysis (valid for comparing models with the same number of parameters) and AICc and adjusted RMSE analysis (valid even for comparing models with different number of parameters, and therefore penalizing models with more parameters) show that the Bilogistic 1kf model offers a better fit than existing models. It can be easily inserted in commonly used statistical analysis programmes, and we hope that this paper encourages fellow scientists to apply parametric modelling to their lifespan data. Finally, analysis of the parameters from curve fitting enables comparison of lifespan assays both within similar groups and among different experimental conditions. Our model is, therefore, expected to facilitate the rational analysis of lifespan modifiers, e.g. through genetic analysis of long- versus short-lived subpopulations [12,34], and improve our understanding of their mechanisms of action.

Summarizing, the bilogistic model and its variants are variable enough to identify clearly biphasic survival data if present and to model the biphasic features of lifespan curves observed in response to environmental, genetic or other, such as pharmacological interventions.

Data accessibility. The datasets generated and analysed during the current study are included in the electronic supplementary material as Excel files [35].

Authors' contributions. S.M.: conceptualization, formal analysis, investigation, methodology, writing—review and editing; A.R.L.: investigation; A.E.: formal analysis, methodology; C.S.: investigation; Z.B.: investigation; M.S.: conceptualization, formal analysis, funding acquisition, investigation, methodology, project administration, supervision, writing—original draft, writing—review and editing; A.C.: conceptualization, formal analysis, funding acquisition, investigation, methodology, project administration, supervision, writing—original draft, writing—review and editing.

All authors gave final approval for publication and agreed to be held accountable for the work performed therein.

Conflict of interest declaration. The authors declare no competing interests.

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