

FiT: A software for adjusting the growth curve of animals

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ABSTRACT - This paper aims to describe and evaluate FiT, a software that streamlines the process of analysing animal growth curves. It is characterized as a web-based software, developed using the Python and R languages, that adjusts the parameters of the classical nonlinear models Brody, Von Bertalanffy, Logistic and Gompertz. These parameters are estimated using the `nlsLM` function from the `minpack.lm` package of R. For model comparison, FiT calculates the mean square of the residuals, coefficient of determination, Akaike information criterion, and Bayesian information criterion. In addition, FiT determines the weights and ages at the inflection point (IP) and asymptotic point (AP), and displays graphs of the growth curve and its derivatives, highlighting the IP and AP. It is also possible to compare growth patterns considering different types of groupings. To evaluate the tool, the models were adjusted using growth data from Santa Inês sheep, and the estimated parameters and metrics were compared to those reported in other studies that used the same dataset. The results demonstrate its efficiency in performing animal growth curve studies, with emphasis on ease of use and the information generated from the estimated parameters. The FiT software is efficient for growth curve studies, easy to use, and provides additional information about the growth patterns in a short time and without the need for programming in statistical software.

Keywords: asymptotic point, growth rate, inflection point, nonlinear models, nonlinear regression

1. Introduction

Animal growth evaluation is important to optimize management and feeding practices in livestock farming, as well as for the genetic improvement of species. In this sense, nonlinear statistical models have been adopted to describe the animal growth curve over time, which allows the evaluation of how genetic and environmental factors influence growth patterns. The shape of the growth curve can also be used in breeding programs and in individual animals, whose growth parameters are hereditary and responsive to selection procedures (Fitzhugh Jr, 1976; Wurzinger et al., 2005).

The nonlinear statistical models of Brody, Von Bertalanffy, Logistic, and Gompertz are widely used to describe animal growth curves (De Sousa et al., 2021). In these models (Table 1), parameter *A*

represents the size or asymptotic value, B is an integration constant related to the initial values of the response variable under study and has no well-defined biological interpretation, k corresponds to the growth or maturation rate, and t is time. These parameters are fundamental to understanding the growth patterns observed in different biological contexts (Lôbo et al., 2006).

Table 1 - Equations of the nonlinear models of Brody, Gompertz, Von Bertalanffy and Logistic

Model	Equation
Brody	$Y(t) = A(1 - Be^{-kt}) + \varepsilon_i$
Gompertz	$Y(t) = Ae^{-Be^{-kt}} + \varepsilon_i$
Von Bertalanffy	$Y(t) = A(1 - Be^{-kt})^3 + \varepsilon_i$
Logistic	$Y(t) = A(1 + Be^{-kt})^{-1} + \varepsilon_i$

$Y(t)$ = observed measure of response variable; A = the size or asymptotic value; B = an integration constant related to the initial values of the response variable; k = the growth or maturation rate; t = time; ε_i = fitting error.

Growth curve studies have been widely developed in beef cattle (Hartati and Putra, 2021; Arré et al., 2019), in chickens and broilers (Yadav et al., 2023; Masoudi and Azarfar, 2017) and in sheep and goats (Sharif et al., 2021; De Sousa et al., 2021), among other species. These studies are based on the use of computational methods to estimate the parameters of nonlinear models and are generally performed using statistical software such as R, SAS, and SPSS, which provide a wide variety of functions with the most diverse purpose and an environment in which users must write or select commands to carry out the study. These instructions must be entered via the command line and must follow their own syntax established by some programming language, which is a challenge for those who have no programming experience. This can lead to delays or even errors in the process of estimating the curve parameters.

In the literature consulted, few initiatives for the development of tools that make it easier to apply nonlinear models to describe animal growth were observed. Reiter and Vorholt (2024) propose a web application that allows a fast and interactive analysis of microbial growth curves. However, the resources and analyses offered by this system are not the most suitable for studying the growth curve of animals, since their proposal is to analyze microbial abundance over time. Enot et al. (2018) and Wang et al. (2017) proposed software for the study of, respectively, the growth of tumors and the child growth.

In this context, this research aims to create and evaluate FiT, a software that facilitates the analysis of animal growth curves, allowing farmers, researchers, and professionals, including animal scientists, veterinarians, extension agents, and related specialists, to quickly visualize and analyze growth curves without the requirement for coding knowledge.

2. Material and methods

The data used to validate the FiT system were originally proposed in Sarmiento et al. (2006), a study that aimed to verify, among the Brody, Von Bertalanffy, Logistic, Gompertz, and Richards models, which one best fits the growth data of Santa Inês sheep. The database used consists of 7271 records of birth weight and weight at 28, 56, 84, 112, 140, 168 and 196 days of age from an experimental herd provided by the Empresa Estadual de Pesquisa Agropecuária da Paraíba (EMEPA-PB), controlled from 1983 to 2000, today called Empresa Paraibana de Pesquisa, Extensão Rural e Regularização Fundiária – EMPAER.

The FiT tool is characterized as a web-based software application developed using Python and R languages in conjunction with the Flask framework. The Python programming language was chosen

because of its simplicity, clarity, and wide range of available libraries. Flask, known for its ease of use and flexibility, was adopted to efficiently build the web application structure. R, which is widely recognized as a powerful and established tool in the field of data analysis and statistics, was used to estimate the parameters of nonlinear models through the use of the *nlsLM function* of the *minpack.lm package* (Mullen, 2022). The *D function* of R was also used to calculate the numerical derivatives of the models and to estimate functions of the fitted models. To incorporate these R functions, the project uses the *rpy2* package which allows R scripts to be called directly within the Python environment, facilitating advanced statistical analyses and the use of specialized packages available in R, ensuring a robust and adaptable solution to complex data analysis needs.

The FiT software performs the adjustment of classical nonlinear models, such as Brody, Von Bertalanffy, Logistic and Gompertz, whose parameters to be estimated during the adjustment are $\hat{A}$, $\hat{B}$ and $\hat{K}$. The convergence and quality of the results obtained are directly affected by the definition of initial values for these parameters, which is a critical and challenging activity. Considering that the explanatory variables (e.g., age or time measurements) and response (e.g., weight or other characteristic of interest) are, respectively, x and y , in FiT, the definition of the initial values of these parameters follows the following logic: A (asymptotic value): it is defined as the mean value of all y that corresponds to the highest x found in the database; B (initial value): the ratio of the mean value of all y corresponding to the lowest x found in the database by the lowest value of x itself; K (growth constant): 0.01, which was the value that presented the best results during the experiments, regardless of the model to be adjusted.

To evaluate the fit of the models, FiT calculates the metrics SSR – sum of squared residuals, SST – total sum of squares, MSE – mean squared error, R² – coefficient of determination, AIC – Akaike information criterion, and BIC – Bayesian information criterion, in addition to the weights and ages at the inflection point (IP) and asymptotic point (AP). IP corresponds to the point at which the function changes from increasing to decreasing, indicating a deceleration in the growth rate of the variable under study (Sarmiento et al., 2006). The moment at which this pace of growth stabilizes is represented by AP (Mischán et al., 2011).

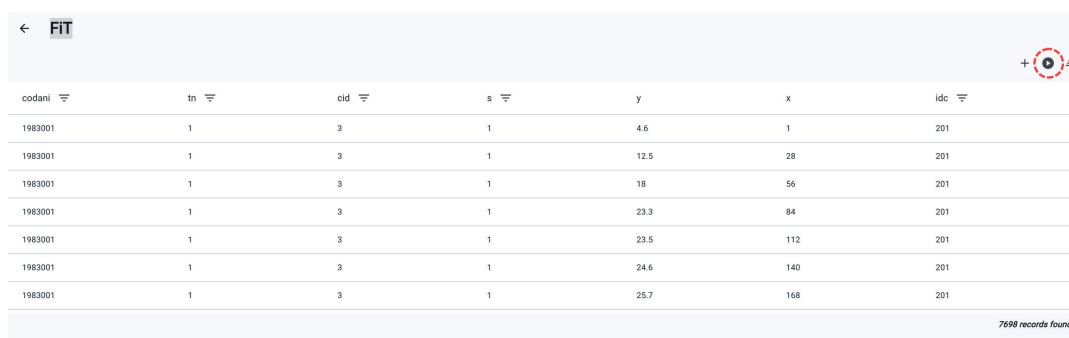
According to Mischán et al. (2011), to determine the values of IP and AP in a growth curve, it is necessary to calculate the successive derivatives of the time-adjusted nonlinear model. The IP represents the value at which the second derivative of the function with respect to time is equal to zero, i.e., $Y''(t) = 0$, starting from the value zero on the abscissa axis. The AP represents the value at which the fourth derivative of the function with respect to time cancels out, that is, also starting from the value zero on the axis of the abscissas. $Y^{IV}(t) = 0$. The searches for the roots of the derivatives in question were carried out using the numerical method of bisection (Burden and Faires, 1985).

The evaluation of the tool was conducted by comparing the results produced by the FiT tool with the results achieved by Sarmiento et al. (2006), which used the same database of Santa Inês sheep.

3. Results

3.1. Key system features

In this version of FiT, the user can easily and quickly adjust the Gompertz, Brody, Von Bertalanffy, and Logistic nonlinear models, only requiring the user to have the database organized in a file in CSV format (*comma-separated values*). It is mandatory that in this file the names of the explanatory variables (age or time measure) and response (weight or other characteristic of interest) be, respectively, x and y , and the values are numerical and not null. After the database is loaded, the system displays a table with a sample of the records contained in the file (Figure 1).



The screenshot shows the FiT interface with a table of data. A red dashed circle highlights the Run icon (a circle with a play symbol) in the top right corner. The table has columns: codeni, tn, cid, s, y, x, and ldc. The data rows show values for these columns, with the last row indicating 7698 records found.

codeni	tn	cid	s	y	x	ldc
1983001	1	3	1	4.6	1	201
1983001	1	3	1	12.5	28	201
1983001	1	3	1	18	56	201
1983001	1	3	1	23.3	84	201
1983001	1	3	1	23.5	112	201
1983001	1	3	1	24.6	140	201
1983001	1	3	1	25.7	168	201

7698 records found

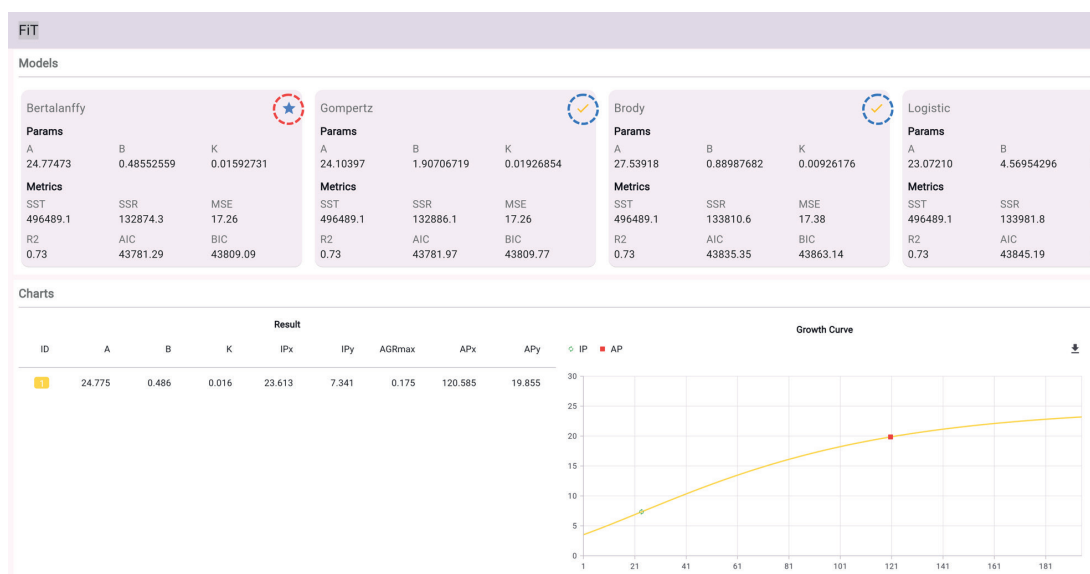
The icon inside the red dashed circle indicates the Run option.

Figure 1 - Screenshot of the FiT that displays the columns available in the database (including the mandatory x and y), some rows of the CSV file uploaded by the user and the icons for actions.

3.2. Adjusting the models

To adjust the models, the user must click on the option Run, as illustrated in Figure 1. At the end of the processing, the system displays, in the Models section, the estimated values for the parameters $\hat{A}$, $\hat{B}$, and $\hat{K}$ and the SST, SSR, MSE, R2, AIC, and BIC metrics for each of the adjusted models (Figure 2). By default, the first model in the list is the one that presented the best fit (lowest BIC value).

In the Charts section (Figure 2), the system presents the coordinates on the x and y axes of the IP, respectively, IPx and IPy; the maximum absolute growth rate (AGRmax); the coordinates on the x and y axes of the AP, respectively, APx and APy; the growth curve graph, indicating IP and AP; and the graphs of the first four derivatives of the model, which were omitted in Figure 2, but can be seen in the results section.



The icon inside the red dashed circle indicates the model that achieved the best fit, while the icons inside the blue dashed circles indicate the Change Model option. Clicking in this option the user can choose one of the other models to view the detailed results.

Figure 2 - A screenshot of the FiT system that includes the Models and Graphs sections and that displays the results of the model adjustments.

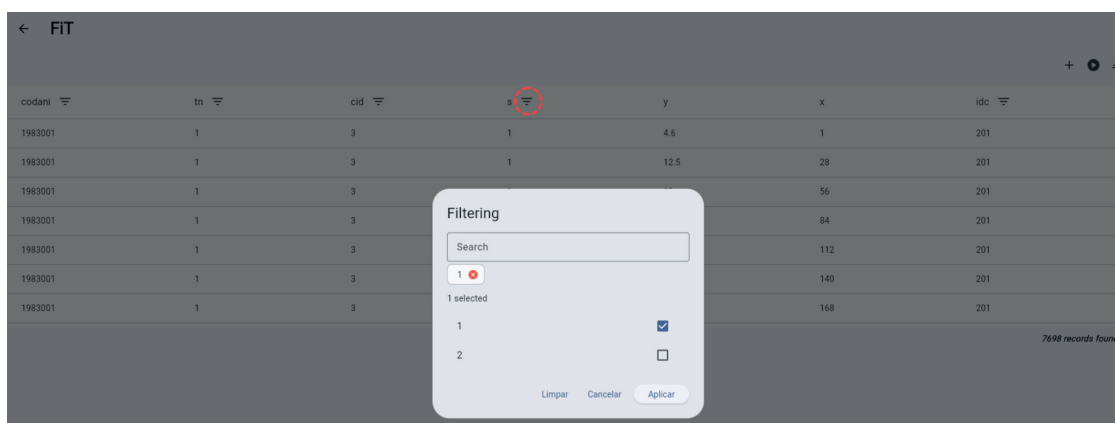
3.3. Model change

The results presented in the Charts section (Figure 2) so far consider the Von Bertalanffy model, which was the one that presented the best fit. However, the system allows the user to choose one of the other models to also view the results. To do so, the user just needs to click on the option Change Model of the desired model, as illustrated in Figure 2.

3.4. Filter a subset of the data

The results presented in the Charts section (Figure 2) were calculated from the complete database. The FiT system, however, allows the user to calculate the same information for a subset of the data by applying filters. The objective is to allow the comparison of the growth patterns of animals considering different types of groupings, such as males and females, single and multiple births, management groups, among other comparison possibilities.

To perform the filtering, the user must click on the option Filter corresponding to the attribute of interest, as illustrated in Figure 3. The system will display a list with the different values, allowing the user to select multiple options as desired. Filtering can be applied to more than one attribute at the same time. After applying the Filter, the user must click again on the option Run to adjust the models and produce all the estimates considering the filtered subset of data. As a result, a new row of parameters will be added to the Charts section, as well as a new row to each chart.



The icon inside the red dashed circle indicates the Filter option corresponding to the selected column.

Figure 3 - Demonstration of how to adjust the curves by groups of animals from the filtering of the column *s*, which represents 1 for males and 2 for females.

4. Discussion

The evaluation of the system was conducted by comparing the results produced by FiT with the results in Sarmento et al. (2006) using the same database of Santa Inês sheep. The results achieved are quite similar (Table 2). Although the values of the parameters and evaluation metrics are slightly different, the order of the models is the same as that found in the reference work when both the MSE and R2 are considered as comparison factors. It was not possible to evaluate the convergence of the results of the Richard model, since it has not yet been implemented in the system.

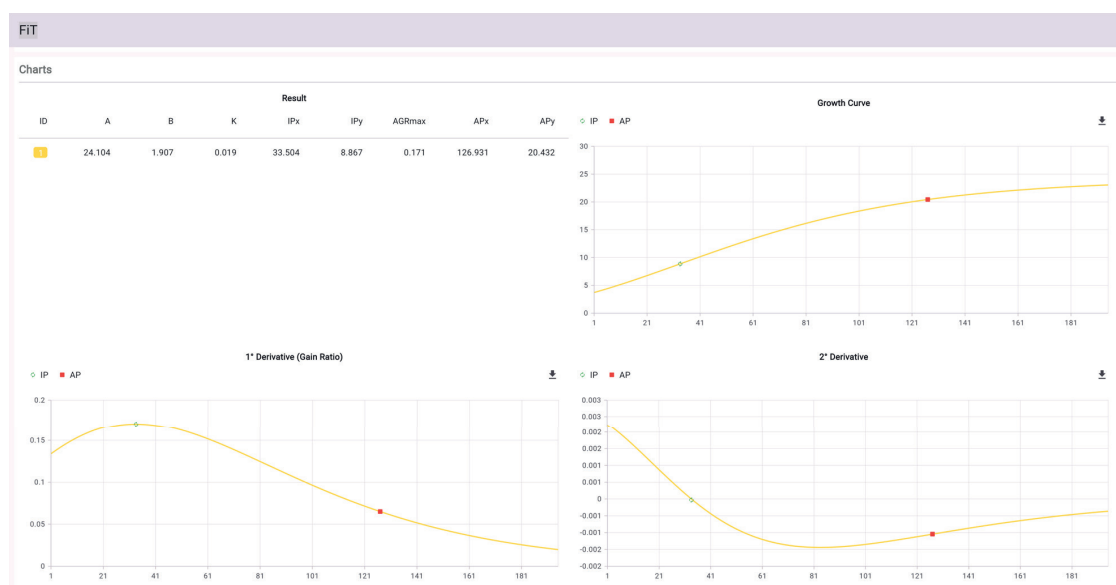
Table 2 - Comparison of model's estimated parameters and evaluation criterion found in Sarmento et al. (2006) and calculated via FiT

Model	Parameters estimated						MSE_r	MSE_f	$R2_r$	$R2_f$
	$\hat{A}_r$	$\hat{A}_f$	$\hat{B}_r$	$\hat{B}_f$	$\hat{K}_r$	$\hat{K}_f$				
Bertalanffy	24.8055	24.7747	0.4799	0.4855	0.0159	0.0159	17.2646	17.2624	0.7202	0.7323
Brody	27.4134	27.5391	0.8865	0.8898	0.0094	0.0092	17.3723	17.3825	0.7185	0.7304
Gompertz	24.1653	24.1039	1.8731	1.9070	0.0191	0.0192	17.2688	17.2624	0.7205	0.7323
Logistic	23.1683	23.0721	4.3772	4.5695	0.0287	0.0292	17.4055	17.4047	0.7180	0.7301

The values $\hat{A}_r$, $\hat{B}_r$, $\hat{K}_r$, MSE_r and $R2_r$ refer to the results found in Sarmento et al. (2006) and $\hat{A}_f$, $\hat{B}_f$, $\hat{K}_f$, MSE_f and $R2_f$ correspond to the results obtained by the FiT.

The perceived difference is slight and can be justified by the adoption of different strategies for parameter estimation and model fitting. In FiT, which uses the `nlsLM()` package of R, the estimation of the parameters is based on the Levenberg-Marquardt algorithm. This algorithm is a refinement of the Gauss-Newton procedure, adopted in the reference work, which increases the chances of local convergence and avoids the occurrence of divergence (Moré, 1978). Regarding fitting strategy, in Sarmento et al. (2006), the adjustment of the models occurred for each animal, and the values of $\hat{A}$, $\hat{B}$, and $\hat{K}$ reflect the mean of these values. In FiT, the fit of the models reflects the average curve for all animals at once.

In the Charts section (Figure 4), FiT exhibits the values of the inflection and asymptotic points considering the Gompertz model, which was chosen by Sarmento et al. (2006) as the best-fit model. The weight of the animal at the inflection point (IPy) and the weight gain at the inflection point (AGRmax) also coincide with the values found in the reference study. The 1st derivative graph shows the absolute growth rates (AGR), which represent the daily weight gain over time. Furthermore, FiT calculates the AP, which is a very important additional information in the study of the growth patterns, but which is rarely presented in studies in the literature. This point represents the moment when the animal's weight gain stabilizes and can be interpreted as an indication of the moment when the increase in

**Figure 4** - Estimates of the parameters ($\hat{A}$, $\hat{B}$ and $\hat{K}$), inflection point (IP), asymptotic point (AP) and growth curve of the Gompertz model using the FiT tool.

weight tends to stability (Mischan et al., 2011), which can serve as a reference to indicate the moment of commercialization, slaughter, or even adjustments in the feeding strategy, since the animal can deposit more fat from this moment on.

It is noteworthy that the AP is not easily obtained with statistical software, as it requires additional knowledge and programming skills. Therefore, most publications in the animal growth analysis field do not present this estimate, such as Sarmiento et al. (2006), even though it is very important to understand growth patterns. On the other hand, IP is a point widely addressed in the literature; however, its identification is usually based on model-specific equations. In FiT, the calculation of IP and AP is based on the identification of important points of the derivatives of the equation, as mentioned above, so it can be applied to all growth models with sigmoidal behavior, provided that there are weight samples from birth to adulthood of the animal.

In addition to the confidence in the results generated by the FiT tool, it should be noted that the user only needs a database in CSV format to carry out the study easily and quickly. Between uploading the database and completing the adjustment of the models, it took approximately 15 seconds. This saves users time and effort, as it avoids the need to invest time in learning how to use tools like R to perform a growth analysis, whether academic or not. However, it is still extremely important that the user has the necessary knowledge to interpret the results of the estimated parameters.

4.1. Additional tool features

To evaluate the application of filters to compare different subsets of the database, five filters were applied to analyze the growth curve of different groups (Figure 5), respectively: 1 (in yellow) - database with all animals; 2 (in red) - males only; 3 (in blue) - females only; 4 (in green) - males of single birth; 5 (in purple) - males of double births.



Figure 5 - Estimates of the parameters ($\hat{A}$, $\hat{B}$ and $\hat{K}$), inflection point in days (IPx) and weight (IPy), maximum daily weight gain at the inflection point (AGRmax), asymptotic point in day (APx) and weight (APy) and the representation of the growth curves based on the Gompertz model for different subsets of the selected data.

FiT also shows the graphs of the 1st, 2nd, 3rd, and 4th derivatives corresponding to all groups (Figure 6). By means of the graph of the 1st derivative, single-birth males (line in green) reach the inflection point earlier and with a higher growth rate than males of double births (line in purple).

The results found in this study demonstrate, therefore, that FiT allows the easy and fast study of the growth curve of animals of different species, contributing to the democratization of data-driven agricultural analysis, emphasizing accessibility for farmers, researchers, and professionals, including animal scientists, veterinarians, and extension agents, even without programming backgrounds. However, new experiments with other databases should be carried out to ensure the robustness of the results. It is worth mentioning that the FiT, in version 1.0, is not appropriate for studies in which one seeks to evaluate the effect of different environmental factors on the parameters of the growth curve by means of analysis of variance or related techniques.

FiT can be accessed through the link <https://fit-web-78abd.web.app/>. However, it is still in beta version, which means it may experience performance issues or unhandled errors during use. We are continually working to enhance the user experience and address any potential bugs.

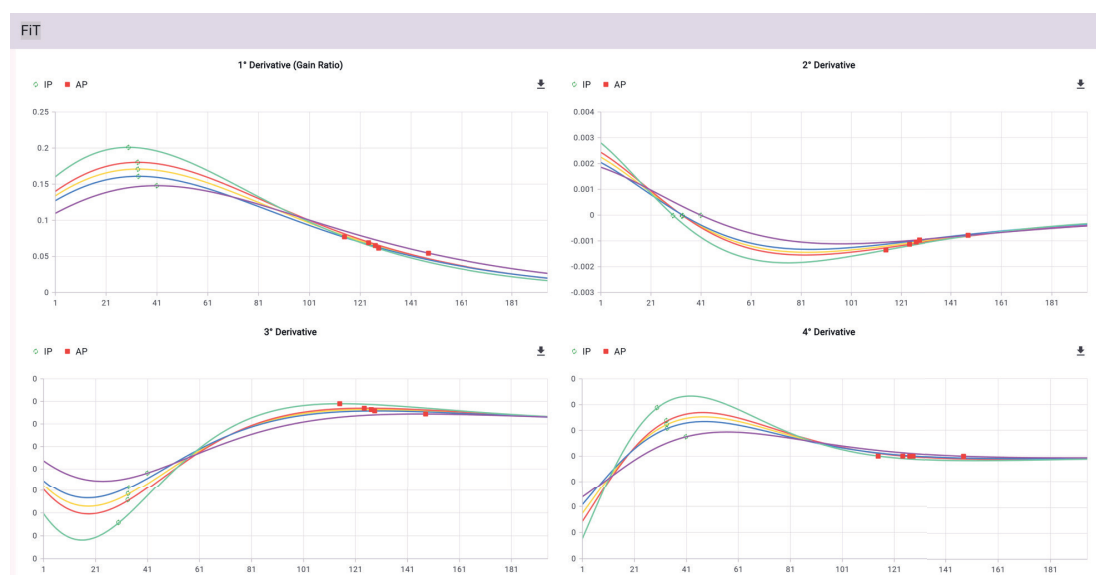


Figure 6 - Graph of the 1st, 2nd, 3rd, and 4th derivatives obtained from the Gompertz model estimated for the selected subsets.

5. Conclusions

Built on top of modern, powerful, and established technologies like Python and R, FiT is an easy-to-use web application that streamlines the process of animal growth analysis. By adopting FiT, researchers and professionals can reduce the time required to adjust nonlinear statistical models to analyze growth curves from hours to minutes without the requirement for coding knowledge.

Data availability

The data used to support the conclusions of this article is not public and will not be made available by the corresponding author; however, users will be able to download a demonstration dataset directly within the tool.

Author contributions

Conceptualization: Sousa, E. C.; Silva, L. A. S.; Costa, J. L. and Sarmento, J. L. R. **Data curation:** Sousa, E. C. **Formal analysis:** Sousa, E. C. and Costa, J. L. **Investigation:** Sousa, E. C. **Methodology:** Sousa, E. C.; Silva, L. A. S.; Costa, J. L. and Sarmento, J. L. R. **Project administration:** Sousa, E. C. **Resources:** Sousa, E. C. **Software:** Sousa, E. C. **Supervision:** Sarmento, J. L. R. **Validation:** Sousa, E. C.; Silva, L. A. S.; Costa, J. L. and Sarmento, J. L. R. **Visualization:** Sousa, E. C. **Writing – original draft:** Sousa, E. C.; Silva, L. A. S.; Costa, J. L.; Laurent, L. and Sarmento, J. L. R. **Writing – review & editing:** Sousa, E. C.; Silva, L. A. S.; Costa, J. L.; Laurent, L. and Sarmento, J. L. R.

Conflict of interest

The authors declare no conflict of interest.

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