

# A classroom activity to work with real data and diverse strategies in order to build diverse models with the help of the computer

Marta Ginovart

Department of Applied Mathematics III, Universitat Politècnica de Catalunya

Edifici D4, Esteve Terradas 8, 08860 Castelldefels (Barcelona), Spain

marta.ginovart@upc.edu

**Abstract:** Taking into account that the majority of the models with more tradition in the mathematical curriculum to represent temporal evolutions of the number of individuals are continuous models in the class of empirical models, it has an added value to deal with these models, but where the parameters involved are claimed to have a biological meaning. These types of models are not completely mechanistic or heuristics, and therefore they are called pseudo-mechanistic models. It is a challenge to link mathematical tools and concepts with biological ideas, and also a chance to use the help that computers provide in this context. The aim of this study was to design a set of rich tasks to be performed with the help of the computer and implement them in the classroom in order to investigate a real data set to deal with empirical models and pseudo-mechanistic models. One of the main purposes in the designing of this set of tasks was to configure a framework showing different strategies to deal with the data and also, how each of these approaches could generate a variety of responses to the problem in hand. The sequence and structure of these tasks, according to the students' perceptions collected, enhanced the understanding about the construction and use of these primary growth models.

**Résumé:** Étant donné que la plupart des modèles programmes de mathématiques les plus traditionnels pour représenter l'évolution temporelle du nombre de gens sont des modèles continus appartenant à la classe des modèles empiriques, a ajouté la valeur de travailler avec ces modèles, mais où les paramètres impliqués Ils ont une signification biologique. Ces types de modèles ne sont pas totalement mécaniste ou heuristiques, et sont donc appelés modèles pseudo-mécaniste. Il est un défi de relier les outils et concepts mathématiques avec des idées biologiques, et aussi une chance d'utiliser les ordinateurs d'assistance fournies dans ce contexte. Le but de cette étude était de concevoir un riche ensemble de tâches à accomplir avec l'aide de l'ordinateur et de les mettre en œuvre dans la salle de classe afin d'étudier et de décrire un ensemble de données réelles avec des modèles empiriques et les modèles de pseudo-mécaniste. L'un des principaux objectifs dans la conception de cet ensemble de tâches a été de mettre en place un cadre pour montrer différentes stratégies pour traiter les données et aussi comment chacune de ces approches pourrait générer une variété de réponses au problème à la main. La séquence et la structure de ces tâches, selon les perceptions recueillies auprès des étudiants, sont susceptibles d'améliorer la compréhension de la construction et l'utilisation de ces modèles de croissance primaires.

## Introduction

Actually, in the twenty-first century, computation is more than an assistant support of scientific activity, computation is changing the fundamental way that science is practised and also how this it is being learnt and taught (Shiflet and Shiflet, 2014).

Computation allows us to obtain and analyse big data, consider and solve problems inaccessible until now, build sophisticated models, visualize phenomena, conduct experiments difficult or impossible in laboratories, among other options. Teaching and learning mathematics in any context should promote the development of thinking and the possibility of an appropriate use of the technology available nowadays. Processes such as developing curiosity, critical thinking, reasoning, as well as developing modes of verification, refutation, and deduction should be found in the activities proposed to our students in classroom, and for some of these processes the help of a

computer can be very valuable. In this context, for instance, analysis of real data and the building of different kinds of models for this data could be good opportunities to train in those processes. In the teaching of applied mathematics, it would be desirable to design and develop profitable strategies to tackle real data and deal with models that require thinking at multiple levels of abstraction or understanding, plus to know how to use the computational resources offered by general or specific software accessible nowadays. The computer must be seen as a convenient work “companion” and an attractive resource, and never as an obstacle for the mathematics learning. The potential of the software present in the majority of the computers of our laboratories cannot remain unexplored and unexploited when activities related to quantitative modelling and numerical methods are carried out in the classroom. In this line, teachers need to have (or develop) suitable knowledge and competences in digital technologies, otherwise their teaching will not be so effective (Bennison & Goos, 2010).

It is widely accepted that mathematical thinking arises and develops in a complex interplay of languages and representations. There is a relatively new term or idea that is “Computational Thinking” (Papert, 1996; Wing, 2006), that although its definition is still under discussion, it appears to focus on computer science concepts in relation to processes of problem solving such as: pattern recognition, pattern generation, abstraction (composition, de-composition, generalization, and specialization), modelling, algorithm design (sequence, iteration, and selection), data analysis and visualization (Caspersen & Nowack, 2014). Thus, it is also accepted that “Computational Thinking” can be envisaged as a fundamental skill for everyone and in particular that it is very attractive for anyone who is involved in teaching and learning mathematics. In the context of the Millennium Mathematics Project (a maths education and outreach initiative) can be found the NRICH website (<http://nrich.maths.org/>) containing a list with some characteristics that make a task rich, highlighting the fact that it is the way in which the task is planned and used in the classroom that makes it rich. Some of those characteristics can be common to the way in which “Computational thinking” can be practised and trained.

In the field of mathematical biology, the capability of designing classroom activities that encompass quantitative modelling with mathematical concepts and tools to deal with biosystems is much appreciated (de Vries, Hillen, Lewis, Müller & Schönfish, 2006). In addition, these activities can justify and give room for the introduction and workout of complementary computational methods (Ginovart, 2014). Mechanistic or heuristic models are those whose development comes from the understanding of the underlying biochemical or biological processes governing populational phenomenon and their parameters have biological meaning, while empirical models are mathematical functions simply describing observations of the phenomenon. Taking into account that the majority of the models with more tradition in the mathematical curriculum to represent temporal evolutions of the number of individuals that configure the populations in certain environments reported in periods of time are continues models in the class of empirical models, it has and added value to deal with these models but in which the parameters involved are claimed to have a biological meaning. These types of models are not completely mechanistic o heuristics, and therefore they are called pseudo-mechanistic models (Perez-Rodriguez, 2014), and it is a challenge to link mathematical tools and concepts with biological ideas, and also a chance to use the help that the computers can provide.

The aim of this study was to design a set of rich tasks to be performed with the help of the computer and implement them in the classroom in order to investigate a real data set (a temporal evolution of a microbial population grown in a specific environment) to deal with empirical models and pseudo-mechanistic models. One of the main purposes in the designing of this set of tasks was to configure a framework showing different strategies to deal with the data and also, how each of these approaches could generate a variety of responses to the problem in hand. The students’ perceptions about if the sequence and structure of these tasks have enhanced their understanding about the construction and use of these primary growth models were collected and analysed.

## Material and methods

The participants in this study were a group of 50, third-year students of a Bachelor's degree in the field of Biosystems Engineering at the Universitat Politècnica de Catalunya (Barcelona, Spain). The prior coursework for these students was related with the following compulsory subjects: Mathematics I and II, Physics I and II, Chemistry I and II, General Biology, Microbiology, Statistics, among others. This previous preparation guarantees a good knowledge of some biological systems (microbial systems in particular) and basic mathematical concepts and tools.

Students' responses regarding analyses and modelling of the growth population data and the distinct methodologies applied sequentially for the study of the different phases observed in the pattern of this temporal evolution, were collected via commented spreadsheets, outputs of statistical software, open-ended questionnaires, and face-to face dialogues during the development of the sessions in the computer lab. The students' perceptions about the set of tasks conducted were explicitly questioned and collected at the end.

A set of 17 observations corresponding to the size of a population (numbers of microbes) grown in a liquid medium of 1 mL with an initial quantity of sugar and no further addition of nutrient during a period of 48 hours is the data to be analysed (Table 1), and used to build empirical models and pseudo-mechanistic models. Each student had a computer with access to spreadsheet (Excel), mathematical software (Maple) and statistical software (Minitab and R) utilized in previous subjects, and with a free connexion to Internet when looking for specific information. The activities were designed to be carried out individually, however, with lab sessions and small groups of students, comments, suggestions, and interactions with the teacher were always held whenever required or considered appropriate.

Time (h)	Number of microbes
0	145349
3	146217
6	139333
9	143620
12	168557
15	287768
18	972270
21	2996236
24	4444266
27	5953756
30	7245644
33	7614686
36	8187928
39	10214427
42	11842517
45	13650985
48	12837014

Table 1. The experimental data to be analysed.

Some preliminary questions were answered without reading the guide to the activity, as a first task, so that the students had the possibility to reflect on what they have studied and learned up to now, as well as what was convenient to apply to solve this kind of problem. These preliminary questions were: *Taking into account that the set of data in Table 1,*

- Which strategies or resources that already know can be used to analyse this data?
- Which type of function or model can be adjusted?
- Which programs can be utilised for that purpose?

### **The outline of the set of tasks to be performed with the help of the computer**

**Part A.** To perform an exploratory analyse of the data and decide the best way to represent it, performing or not some nonlinear transformations of this data. It is important to point out that the context application of this data is microbiology and we are dealing with the growth of huge number of microbes.

**Part B.** To deal with the use of polynomial functions to describe or fit the data and highlighting some advantages and disadvantages of this type of approach.

**Part C.** To identify the three different phases in the temporal evolution and use straight lines to describe each of these phases. The succession of phases may be conveniently distinguished because they are characterized by variations of the growth rate: first, the lag phase with growth rate null, second, the exponential phase with a constant rate, and third, the stationary phase with no clear growth. The reading of the paper of Buchannan and coauthors (Buchanan, Whiting & Damert, 1997), where the so-called three-phase linear model is presented, completes this part where the students can recognize their own work.

**Part D.** To build, step by step, a discrete logistic model by means of set of calculations and linear approximations of the transformed data. After this, the comparison of the built model with the observed data is carried out with a simulation in a simple way in a spreadsheet assessing the agreement between them.

**Part E.** To introduce the family of mathematical models known as sigmoid functions and their relation to the growth models, being the continuous logistic model one of them. The use of the mathematical software to manipulate their mathematical expressions and graphical representations with the purpose of identifying the role of the set of parameters involved in their definitions. The identification of the meaning of these parameters is followed by a convenient reparameterization of them, allowing us to have parameters with a clearer biological meaning and models utilized in the prediction of microbial growth in real applications.

**Part F.** To explore the options that R, a free statistical software, and the packages developed to manage growth curves have to deal with this data (<http://www.inside-r.org/packages/cran/nlstools/docs/growthmodels>).

At the end of the activity, and after the work was carried out through the six parts describe above, the questions posed at the start were presented again to the students in a new context: *If you have to analyse another set of microbial growth data, what would your answers be to those preliminary questions?*, and one more: *What would your priority be in the set of tasks to be carried out in order to model the new data set?*

### **Results and discussion**

Students' responses regarding the analyses of the data and the various microbial growth models were prepared individually and collected by means of file texts, giving answers to the questions posed, spread sheets with comments, and outputs of mathematical and statistical programs inserted in an explicative text. In addition, interviews and personal communication during the sessions in the computer lab made it possible to collect further information on the development of the activity.

This activity has been divided into a set of tasks which have been grouped in six different parts (A, B,..., F) facilitating the organization of the work to be performed by the students. The various parts were carried out in three lab sessions of two hours each, so the extension and diversity of the results

obtained by the students were remarkable.

The answers to the preliminary questions before beginning the tasks of the activity (“*Which strategies or resources already known can be used to analyse this data?*”, “*Which type of function or model can be adjusted?*”, and “*Which programs can be utilised for that purpose?*”) were rather disappointing and poor. The majority of these responses were about the use of a spreadsheet to achieve a graphical representation, but no references to the use of mathematical programs like Maple or statistical programs like Minitab or R, programs that had been used in the previous mathematical and statistical subjects. Undoubtedly, it was also evident that no relationships or links between the previous knowledge of microbiology and different phases of the growth of the population were made or identified, in spite of these phases being linked with the numerical derivatives of the data by means of growth rates. The possibility of connecting the two disciplines involved in the modelling process, microbiology and mathematics, did not appear in those first answers. Only the 10% approximately of the students mentioned the fact that the transformation of the data by means of the logarithm function could be helpful in this microbial context, due to the magnitude of the numbers and the rate in the population growth. It was really a discouragement to see the lack of association with other subjects in these students’ answers. Maybe, this is something not really surprising in the teaching in general, taking into account that subjects and teachers have their own specific areas, and on very few occasions do they allow interference or collaboration in sharing activities that involve simultaneously diverse areas of knowledge, and it that moment the students were in a mathematical-computing context.

The set of results that the students obtained, analysed and discussed in connection with their knowledge of biology were graphic representations of the temporal evolutions of the number of individuals in the population and the transformations performed with the data, definitions and manipulations of mathematical functions to construct and formulate different models, together with the calculation of the corresponding parameters involved in those models, plus the assignment of biological meaning to them in the case of pseudo-mechanistic models. Only some aspects or parts of the processes involved in the tasks designed will be presented in this section, accompanied by some computer screenshots to illustrate them.

Regarding the tasks in Part A which were in some way conducted with questions like:

- *Is it better to work with the original data or can you imagine a linear or nonlinear transformation of this data?*
- *Are the magnitudes of the observed values (and their changes) at the beginning of growth very different from those obtained at the end of the experiment?*
- *What mathematical function can be used to modify or modulate this behaviour?*

the students completed an exploratory analysis of the data by deciding which was the best way to represent it, considering the nature of the experimental observations that they handled and remembering the way to present data in a microbiology field. The graphical representation of the original data at different scales and through some nonlinear transformations were options examined by the students. At the beginning of the temporal evolution the original data had values of about  $10^5$  and values of around  $10^7$  were reached at the end of the evolution, so the magnitude of the range to be represented was considerable. The increases (in absolute values) of one time to another time showed very different magnitudes depending on the time sampled. At this point, the students appreciated why in the context of microbial communities, the populations are usually expressed in logarithmic units (base 10). Logarithm transformations with different bases were one of the strategies tested by students in the spreadsheet (Figure 1).

In Part B, and after verifying that neither linear nor exponential growth were detected with this data, the fittings with polynomials of diverse degrees to describe the original data were examined and discussed by students, focusing this discussion on some advantages of this empirical modelling and emphasis on some of its disadvantages. In particular, the concept of the model or what a model

should be, together with its purpose was debated, and the conclusion in this part was that this type of model (polynomial functions) did not exemplify it very well. They discussed what it was like to work with empirical models (fittings of functions) and what the limitations were, and applauded the possibility of providing a pseudo-mechanistic model in this context. The coefficients of the fitted polynomials showed no opportunity to incorporate any of the ideas behind the microbial growth phenomenon. The purpose would be to try the description of this phenomenon: a population located in a space, in a new environment with nutrient, using the energy resources found in it, thus enabling the reproduction of individuals in the population, increasing its size; nevertheless, with this utilization of nutrient from the environment without its replacement, leads to an unfavourable situation, which is no longer possible for the population to continue to grow. The inability of these empirical models to explain the biological phenomenon, added to the fact that some of the fitted polynomials reached negative values, made it evident that they are not appropriate and these mathematical expressions had lost all meaning to represent this data.

In Part C of the activity, the use of the logarithm transformation of the number of microbes observed over time, along with the increases observed in each of the sample time (Figure 2), allowed the identification of various growth phases that occurred during the temporal evolution of the population size. A first approach for the construction of a simple model with the capability to pick up the features or major trends in this type of growth goes through consideration or recognition of the three main phases of the growth, lag phase, exponential phase and stationary phase, and it uses piecewise linear functions for its formulation. The students studied this option with the spreadsheet using linear regressions to describe each of these phases which are characterized by significant variations in growth: first, the lag phase with a zero growth rate, after the exponential phase with a constant growth rate, and finally no growth for the stationary phase (Figure 3). Reading the companion document of Buchannan and others [2] to which the students could access, entitled "When good enough is simple: a comparison of the Gompertz, Baranyi, and three-phase linear fitting models for bacterial growth curves", illustrated and revealed that the piecewise linear model built by the students was in tune with one of the possible solutions that researchers presented and accepted in the environment of predictive microbiology. The three-phase linear model was the first pseudo-mechanistic model obtained, as in its formulation parameters with biological significance were recognized, such as the logarithm of the initial population and the final population, duration of the lag phase (intersection of the two first straight lines) and the maximum growth rate (slope of the second line), start of the stationary phase (intersection of the second and third lines). Students were able to recognize their own work in a spreadsheet as a simple modelling choice but well placed in a broader context of interest in biotechnology and predictive microbiology.

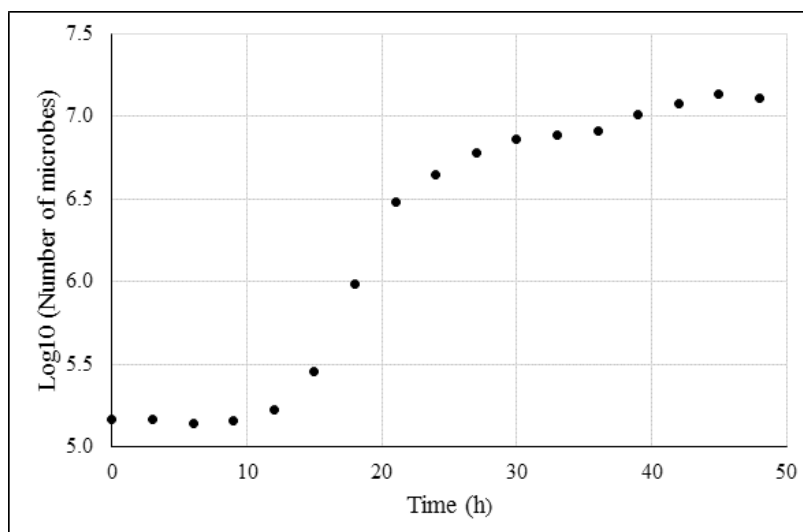


Figure 1. Temporal evolution of the logarithm of the number of microbes.

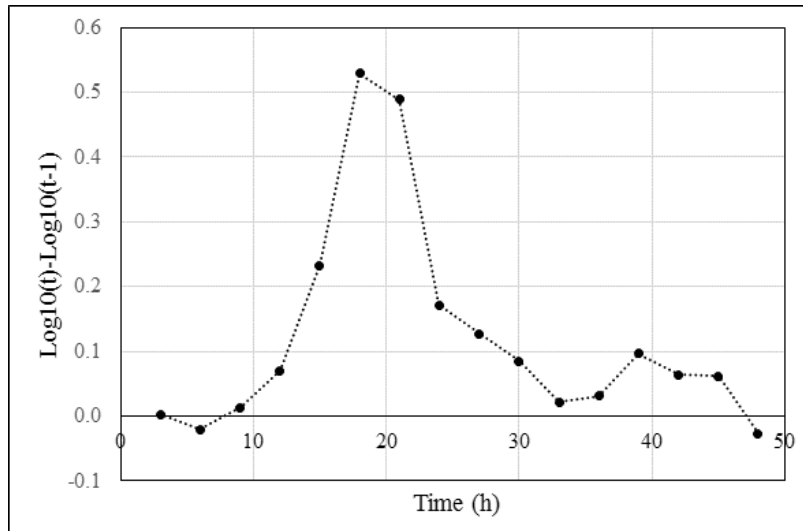


Figure 2. Variations in the logarithm of the number of microbes during the temporal evolution.

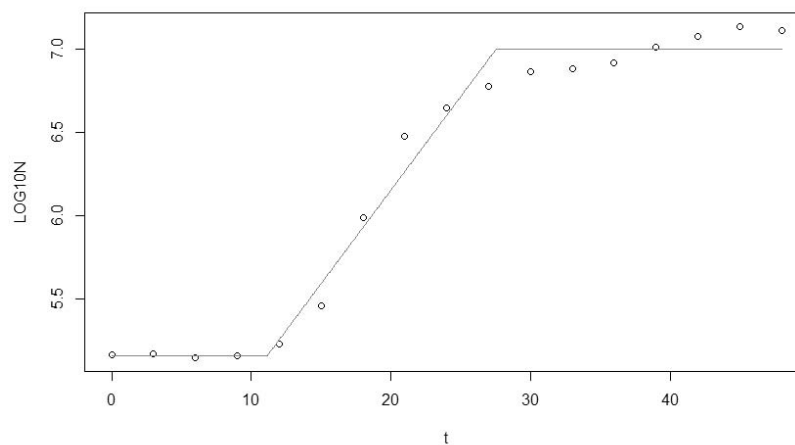


Figure 3: The three-phase linear fitting model for microbial growth, a simple pseudo-mechanistic model.

In relation to the possible use of the logistic function and other functions of the sigmoid family (corresponding to the Parts D and E), only some results will be presented and discussed here, those connected with the process of assigning biological meaning to the parameters involved in the definitions of those functions. Figure 4 shows some parameters illustrating or denoting important features of the microbial population growth. The logistic function is one of the most frequently studied, but in this study we focus on the use of Gompertz function, another sigmoidal function also widely used for certain temporal evolutions, and defined as follows:

$$y(t) = A \cdot \exp\left(-\exp(B - C \cdot t)\right) + A e^{-B-C}$$

where A, B and C are the parameters involved. The process allowing reassignment of these parameters to others with biological meaning makes it possible to connect and use previous mathematical knowledge. As we know that microorganisms can grow exponentially over a period of time, it is useful to apply the logarithmic transformation on population size ( $N = N(t)$ ) as has been mention before. Thus, working with the natural logarithm (or logarithm) in this case, the relative size of the population can be considered a new variable as follows:

$$y(t) = \text{Ln} \left( \frac{N(t)}{N_0} \right)$$

The three main phases of the microbial growth curve can be described by three parameters (Figure 4):

- 1) The maximum specific growth rate,  $\mu_m$ , which is defined as the tangent at the inflection point of the curve.
- 2) The latency or lag time,  $\lambda$ , which is defined as the value of the intersection of this tangent with the abscissa.
- 3) The asymptote determined by the maximum value that the population can reach, Max.

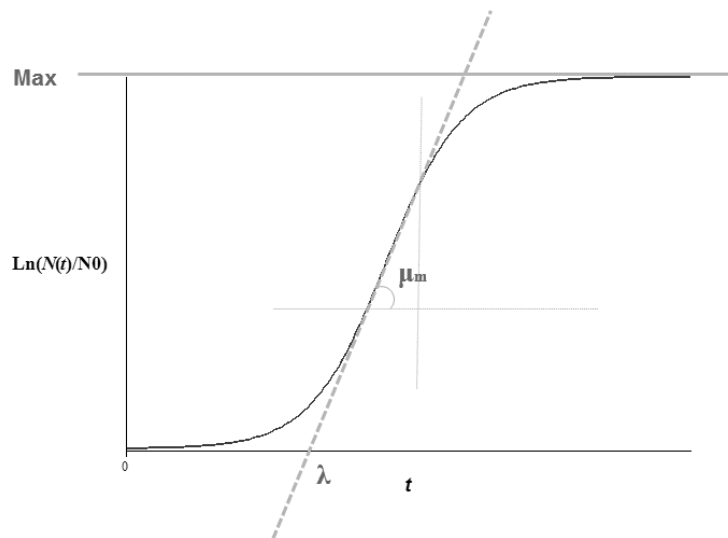


Figure 4. Generic microbial growth curve parameters: maximum growth rate ( $\mu_m$ ), lag time ( $\lambda$ ), and the maximum possible value that can be achieved (Max).

A study of the first derivative and second derivative of the function allows us to identify the role played by the parameters involved in the definitions. Identifying the meaning of the parameters of these Gompertz functions, followed by a suitable reassignment, enables us to have a function with meaningful biological parameters in the context of microbial growth, and consequently obtaining a new pseudo-mechanistic model for this context [12].

The purpose of this task is to rewrite the Gompertz function using the Maple program, a new expression replacing the parameters A, B, and C given in the above expression (with no biological significance) by the parameters  $\mu$ ,  $\lambda$ , and Max (with biological significance) as Figure 4 illustrates. Whereas this could be solved by hand (with pencil and paper), and because one of the purposes is the use of the computer, the calculations involved in this process were carried out with Maple, avoiding errors in transcription or errors in simplification, and making these calculations faster. The students' responses to this part of parameters' reassignment to obtain the pseudo-mechanistic model were surprisingly interesting. It allowed students to use the incessantly repeated knowledge during their previous stages in Mathematics: first derivative, second derivative, inflection point, slope of the tangent line at a point, asymptote ..., but this time in a context that gave meaning to everything they had learned in both mathematics and microbiology.

A screenshot of the sequence of steps performed with Maple to get this pseudo-mechanistic model with  $\mu$ ,  $\lambda$ , and Max is as follows:

$$> y(t) := A \cdot e^{-e^{(B-C \cdot t)}}$$



$$y := t \rightarrow A e^{-e^{B-Ct}}$$

$$> \frac{d}{dt} y(t)$$

$$A C e^{-Ct+B} e^{-e^{-Ct+B}}$$

$$> \frac{d}{dt} \frac{d}{dt} y(t)$$

$$-A C^2 e^{-Ct+B} e^{-e^{-Ct+B}} + A C^2 (e^{-Ct+B})^2 e^{-e^{-Ct+B}}$$

$$> \text{solve}\left(\frac{d}{dt} \frac{d}{dt} y(t) = 0, t\right)$$

$$\frac{B}{C}$$

$$> \text{eval}\left(\frac{d}{dt} y(t), t = \frac{B}{C}\right)$$

$$A C e^{-1}$$

$$> \text{mumax} = A C e^{-1}$$

$$\text{mumax} = A C e^{-1}$$

$$> \text{solve}(\text{mumax} = A C e^{-1}, C)$$

$$\frac{\text{mumax}}{A e^{-1}}$$

$$> C := \frac{\text{mumax}}{e^{-1} A}$$

$$C := \frac{\text{mumax}}{A e^{-1}}$$

$$> 0 = y\left(\frac{B}{C}\right) + \text{mumax} \cdot \left(t - \frac{B}{C}\right)$$

$$0 = A e^{-1} + \text{mumax} \left(t - \frac{B A e^{-1}}{\text{mumax}}\right)$$

$$> \text{solve}\left(0 = y\left(\frac{B}{C}\right) + \text{mumax} \cdot \left(t - \frac{B}{C}\right), t\right)$$

$$\frac{A e^{-1} (B - 1)}{\text{mumax}}$$

$$> \text{lag} = \frac{e^{-1} A (B - 1)}{\text{mumax}}$$

$$\text{lag} = \frac{A e^{-1} (B - 1)}{\text{mumax}}$$

$$> \text{solve}\left(\text{lag} = \frac{e^{-1} A (B - 1)}{\text{mumax}}, B\right)$$

$$\frac{A e^{-1} + \text{lag} \text{mumax}}{A e^{-1}}$$

$$> B := \frac{e^{-1} A + \text{lag} \text{mumax}}{e^{-1} A}$$

$$B := \frac{A e^{-1} + \text{lag} \text{mumax}}{A e^{-1}}$$

$$> \text{simplify}\left(\frac{e^{-1} A + \text{lag} \text{mumax}}{e^{-1} A}\right)$$

$$\frac{\text{lag} \text{mumax} e + A}{A}$$

$$> B := \frac{\text{lag} \text{mumax} e + A}{A}$$

$$B := \frac{\text{lag} \text{ mumax} e + A}{A}$$

>  $A := \text{Max}$ ;

$$A := \text{Max}$$

>  $y(t)$

$$y := t \rightarrow \text{Max} e^{-e^{\frac{-\text{mumax}(t - \text{lag})e + \text{Max}}{\text{Max}}}}$$

Now considering that  $y(t) = \text{Ln}\left(\frac{N(t)}{N_0}\right)$ ,  $\text{Max} = \text{Ln}\left(\frac{N_{\text{Max}}}{N_0}\right)$ ,  $\text{mumax} = \mu_{\text{max}}$ ,  $\text{lag} = \lambda$ , we obtain

$$\text{Ln}\left(\frac{N(t)}{N_0}\right) = \text{Ln}\left(\frac{N_{\text{Max}}}{N_0}\right) e^{-e^{\left(\frac{-\mu_{\text{max}}(t - \lambda)e + \text{Ln}\left(\frac{N_{\text{Max}}}{N_0}\right)}{\text{Ln}\left(\frac{N_{\text{Max}}}{N_0}\right)}\right)}}$$

$$\text{Ln}(N(t)) = \text{Ln}(N_0) + (\text{Ln}(N_{\text{Max}}) - \text{Ln}(N_0)) e^{-e^{\left(\frac{\mu_{\text{max}}(\lambda - t)e}{\text{Ln}\left(\frac{N_{\text{Max}}}{N_0}\right) - \text{Ln}(N_0)}\right)}}$$

This last expression, which is the formulation of a pseudo-mechanistic model of the population growth from Gompertz function, is appropriate for microorganisms when population sizes are expressed in logarithmic units, and it is one of the models that the program R uses. This model has been carried out with our set of data (Table 1) and the results achieved are shown in Figure 5, where the punctual estimations of the parameters  $\mu_m$ ,  $\lambda$ ,  $\text{Log}_{10}(N_0)$  and  $\text{Log}_{10}(N_{\text{max}})$  were 12.6, 0.35, 5.15 and 7.03 respectively.

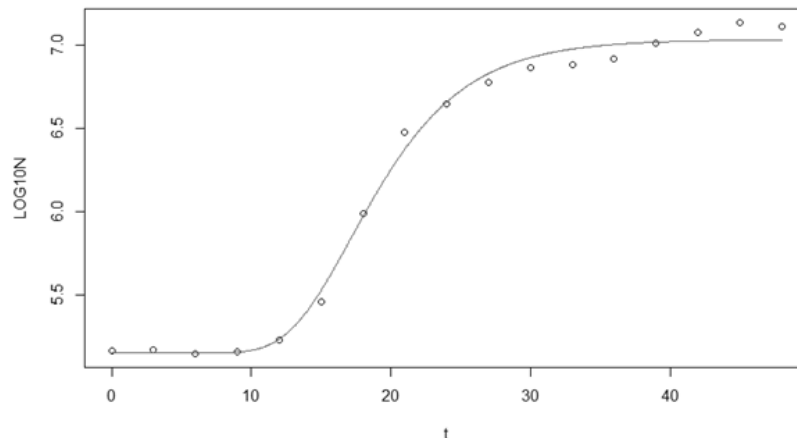


Figure 5. The Gompertz model adjusted to the data with the free statistical software R.

The perceptions of the students carrying out these tasks were collected by means of the following question: “Please, indicate any positive aspect of the activity performed”, and some of the answers were:

- ✓ Tracking the activity in parts I think it is good and helps you to get a pretty solid idea of the different ways to build a model from the same data and compare these models.
- ✓ One of the positive aspects of the activity is the use of software tools for processing data. In order to improve the development of this practice, I think it would be necessary to have prior explanations or recall programs used in previous years.
- ✓ The previous analysis of the data that has been done with spreadsheets helped me a lot. I think the section corresponding to the use of R is a higher level because you have to

understand the program and run it properly. You should also have a very clear idea of what you are analysing and what you want to achieve, because R gives you more information (graphs and tables) than what is absolutely necessary for the analysis or which for me is not completely understandable.

- ✓ We have built and represented models which are easily understood in a particular case like the growth of microorganisms.
- ✓ It is important to learn to manage helpful data processing programs, and this practice gives us an idea of how to do this. Plot some functions using Maple and compare the differences between Excel solver and the R program has helped me to better understand the data analysis and modelling. However, I think prior oral explanation of the practice would have been helpful to refresh some mathematical concepts and programming.
- ✓ On my part, the entire process, applying different ways of analysing the same data, trying to discover which is the best fit for the data, testing what happened when increasing, or decreasing or increasing the parameters of functions, was a good idea. So, the whole process of going slowly and answering the questions has helped me learn a way to try using some experimental data, and also the fact that you can apply many models and some of them will adjust better or worse. Nevertheless, it is really important to try to understand the situation and not just end up having results or numerical values of certain parameters, for example. If you have not made the effort to think about the data, may not be able to interpret these results correctly.
- ✓ One positive aspect of this activity could be the use of mathematical programs such as Maple, because it is a very useful when solving differential equations, representing data, drawing graphs of functions, and manipulating expressions.
- ✓ It helps you understand that in order to solve the problem with the data available you can choose different methods. My opinion is that the practice has been very good. The fact that it is structured in straightforward steps makes it possible to follow without getting lost, while improving learning. At the same time it encourages an order and an explanation of the steps. It teaches us that every experiment fits a certain model and goes through a series of steps to obtain the best result.
- ✓ I have seen many different models to fit the initial data and that means that I will be able to analyse data using methods which I did not know before this activity.
- ✓ I learned various methods to address a situation that may recur in my studies such as the growth of microorganisms, and also the fact that what I did can be extrapolated to other populations.
- ✓ I found it very positive to understand the fundamentals of a solid growth model used in the R program. Testing other available options and how these can help us to solve our problems as biological engineers, using our current knowledge without advanced programming skills, have been profitable.

### **Final remarks**

A rich context for exploring mathematical ideas and developing mathematical skills is biology. In this context, the models have been used in order to analyse and understand phenomena and to design and construct instruments that make a virtual “experimentation” possible, improving in an iterative way our representation of reality. The tasks designed have encouraged some imaginative applications using previous mathematical knowledge that students already had in order to build new models, starting with initial and not complicated approximations and relatively simple models to go deeper into the mathematical understanding of more sophisticated models, where the help of the computer has been revealed as indispensable. Its use was justified and integrated efficiently, training and improving the digital literacy of the students, that is, the general ability to use computers to tackle real problems.

## REFERENCES

- Papert, S. (1996). An exploration in the space of mathematics educations. *International Journal of Computers for Mathematical Learning*, 1, 95-123.
- Bennison, A., & Goos, M. (2010). Learning to Teach Mathematics with Technology: A Survey of Professional Development Needs, Experiences and Impacts. *Mathematics Education Research Journal*, 22, 31-56.
- Buchanan, R.L., Whiting, R.C., Damert, W.C. (1997). When is simple good enough: a comparison of the Gompertz, Baranyi, and three-phase linear models for fitting bacterial growth curves. *Food Microbiology*, 14, 313-326.
- Caspersen, M.E., & Nowack, P. (2014), Model-based thinking and practice: a top-down approach to computational thinking. In: Koli Calling '14 *Proceedings of the 14th Koli Calling International Conference on Computing Education Research*. ACM New York, pp.147-15.
- de Vries, G., Hillen, T., Lewis, M., Müller, J. & Schönfisch, B. (2006). *A course in mathematical biology: quantitative modeling with mathematical & computational methods*. Philadelphia: Society for Industrial and Applied Mathematics.
- Ginovart, M. (2014). Discovering the power of individual-based modelling in teaching and learning: the study of a predator-prey system. *Journal of Science Education and Technology*, 23, 496-513.
- Perez-Rodriguez, F. (2014). Development and application of predictive microbiology models in food. In: D. Granato & G. Ares (Eds.) *Mathematical and statistical methods in food science and technology* (321-361). IFT Pess, Wiley Blackwell.
- Shiflet, A.B, & Shiflet, G.W. (2014). *Introduction to computational science: Modelling and simulation for the science*. Princenton: Princenton University Press.
- Wing, J.M. (2006). Computational thinking. *Communications of the ACM*, 49, 33-35.