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Abstract: This paper has arisen as a result of teaching Models in Biology to undergraduates of Bioengineering at the Gediminas Technical University of Vilnius. The aim is to teach the students to use a fresh approach to the problems they are familiar with, to come up with an articulate verbal model after a mental effort, to express it in rigorous mathematical terms, to solve (with the aid of computers) corresponding equations, and finally, to analyze and interpret experimental data in terms of their (mathematical) models. Investigation of microbial growth provides excellent possibilities to combine laboratory exercises, mathematical modeling, and model-based data analysis. Application of mathematics in this field proved to be very fruitful in getting deeper insight into the processes of microbial growth. The step-by-step modeling resulted in an extended model of the growth covering conventional “lag,” “exponential,” and “stationary” phases. In contrast to known models (differential equations that can be solved only numerically), the present model is expressed symbolically as a finite combination of elementary functions. The approach can be applied in other areas of modern biology, such as dynamics of various cellular processes, enzyme and receptor kinetics, and others.

Keywords: Verhulst equation, logistic equation, growth rate, generation time, lag time