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Modeling bacteria or cell growth in oncology and microbiology, carrying out the curve fitting from the large data can be a difficult task when the pattern is complicated. It is not easy for researchers to extract the coefficients from the curve fitting process in order to characterize cell growth in oncology. A general form of the exponential function is employed, and error minimization steps to identify its coefficients is used when the curve fitting with higher-order polynomial does not describe the data well. In this paper, several functions were compared to describe a statistical bacterial growth curve. The curves were compared statistically by using a few models to figure out the characteristics of the model and their outcomes. Quantifying error in a curve fit, the fitting curve that provides a minimum error is considered as the best curve. Thus, the following assumptions were made: 1) positive or negative errors have the same value 2) weight greater errors more heavily. In the cases tested, the modified equation was checked using the Matlab programming, to see if it is statistically sufficient to describe the growth of a sample data. This technology can be further used in designing new biological experiments. (Received February 02, 2016)