

# Editorial

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# Some Implications of Mathematical Analyses of Epidemics

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## Introduction

Mathematical analysis is a powerful tool that facilitates conceptualization and understanding of epidemics of infectious diseases [1]. The time-course of cumulative case count in epidemics is well-described by the sigmoidal shape of discrete and continuous logistic functions. For example [2], the Pearson coefficient 'r' for correlation between the observed cumulative sequence count and the computed values of logistic-type functions varied from a minimum of 0.9495 to a maximum of 0.9991 for pandemic influenza A (H1N1) pdm09 (pH1N1) hemagglutinin (HA) sequences collected at 23 geographic locations distributed world-wide (p<2.22e-16 at each location). A normalized version of this logistic function is given below as equation 1:

$$Y = 1/(1 + e^{-at})$$
(1)

Plots of values of Y and its first 5 derivatives with respect to time (t) are shown in figure 1 with parameter (a) varying from 0 to 2.0. The results of variation of the non-linear parameter (a) in figure 1 reflect a framework for conceptualization and modeling a smooth flow of mutant subsets, probabilistically produced as quasispecies [3] and moving those quasispecie mutants through space and time in laminas of evolutionary viral trajectories. Because of their simplicity and goodness-of-fit to the observed data, logistic and other sigmoidal functions are useful components of differential and difference equations for the analysis of influenza and other infectious epidemics.

The fourth and fifth derivatives (Y<sup>\*\*\*</sup> and Y<sup>\*\*\*\*</sup>) of Y shown in figure 1 are of the type of "jerk", "jounce" and "swing" functions associated with turbulence of fluid flow, instability of electrical circuits and irregularity of pendulum motion [4,5]. Furthermore, it has been reported that chaotic regions have been detected in SIS ODE epidemic models [6]. The biological significance of these mathematical disturbances of evolutionary trajectory remains to be determined.

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