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***User-Friendly Numerical Integration of Dynamical Systems: An HIV  
Pathogenesis Model***  
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Models used to study the dynamics of diseases often take the form of nonlinear dynamical systems, whose integration requires considerable expertise. However, such models are increasingly used in applications by non-numerical specialists, and simple methods for their integration are thus desirable. In this note, a model for the cellular interaction dynamics of the human immunodeficiency virus (HIV) is considered as an example. The model consists of a first order nonlinear dynamical system of five equations, with class variables for native CD4 T-lymphocytes, infected CD4 T-lymphocytes, native CD8 T-lymphocytes, activated T-lymphocytes, and HIV virions. A model created using the dynamic programming software Stella to integrate the considered system is discussed. While the software is user-friendly and easy to use for non-specialists, incorrect results can easily be obtained due to nonlinear integration limitations of the numerical methods on which Stella is built. The model may consequently be incorrectly interpreted by the numerically inexperienced user, leading to errors in biomedical conclusions derived from it. A nonstandard finite difference scheme and its simple implementation is given and discussed as an alternative to overcome these limitations.