This demonstration presents a module on building population models with differential equations. The goal is to begin with the most basic population models in one variable, motivate the addition of various terms to the equation or system of equations, and demonstrate the derivation of a standard model of HIV infection at the immune system level. For the mathematical biologists out there, the models here are nothing new. The point is the sequence of model-building, the pedagogical framework for the recursive structural improvements of a particular thread of models. One key is analogy: similarities serve as useful tools in building models in various contexts. Another key is technology: the graphical solution capabilities of standard mathematical software packages provide for immediate feedback on model modifications, from varying parameters to modifying the algebraic structure of terms in the equations. While many more sophisticated models of HIV infection at the immune system level have been developed and investigated over the past several years, some of the early ones are very ”reachable” in a standard introductory course in differential equations. One pedagogical path to presenting such models is presented here. (Received October 04, 2004)