Individual-based models (IBMs) have been used in biology for over 40 years. As demographic and spatial data became more standard, the utilization of IBMs increased as a preferred tool in modeling populations. In this talk, I will present an historical overview on how advances in data acquisition increased the utility of IBMs, discuss some recent work on feral hog management, and use recent articles to suggest how advances in data science will increase the power of IBMs in understanding the complexity of populations. (Received September 15, 2020)