

1128-92-35

Jie Zhao* (jie.zhao@wsu.edu), Neill222, Washington State University, Pullman, WA 99163, and **Robert H. Dillon** (dillon@wsu.edu), Neill324, Washington State University, Pullman, WA 99163. *Mathematical Modeling of Signaling Pathways of Fibroblast in Breast Cancer*. Preliminary report.

A mathematical model has been proven as a powerfully tool in understanding, predicting, controlling a real biological system in systems biology. The most often used for dynamic biological systems is nonlinear ordinary differential equations (ODEs) or PDEs. The critical challenges is how to balance the structure of the model and parameter estimation. Usually, simplified models have simplifying assumptions and a small number of parameters; complex models allow them to provide good fits with lower residual error but have an excessively large number of parameters. How to build or choose a mathematical model for a real biological system can be very depend on what you are interested in. In this article, based on an designed experiment to investigate how cells sense the different concentrations of $TGF\beta$, we built a different mathematical models for transforming growth factor- $\beta(TGF\beta)$ signaling pathways in Fibroblast, developed a parameters estimation method based on Bayesian inference and proposed a better choice under this background. (Received January 31, 2017)