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Modeling pathways of cell signalling is a challenging and important task. For example, understanding the dynamic behaviors of signaling pathways can provide clues to pathway mechanisms. In cancer cells, excessive phosphorylation and activation of the Akt pathway is responsible for cell survival advantages. The more complex these models are, the greater the challenge of reliably identifying and estimating respective model parameters. We use Global sensitivity analysis (Sobol Method) and Local sensitivity analysis (Morris Method) to refine these complex models to simplified versions. Then we use the simplified version to understand these models by showing that whether they are either incompatible or compatible with the observed dynamics. (Received January 29, 2019)