In the presentation, we will describe a Bayesian Boolean Network (BBN) model for simulating gene regulatory system involved in breast cancer development. Profiling expression of large number of genes is an important approach for understanding the gene regulatory relationship from a global perspective. Information contained in the high throughput data of gene expression and protein interaction has become a fundamental platform for modeling gene interactions in a cellular process. Data obtained from microarray gene expression contain a large amount of uncertainty as a result of the imperfection of the technology and the stochastic nature of biological events. It is a great challenge to extract meaningful information from a large volume of the high throughput data and develop a model that can faithfully describe the underlying biological process, and make reliable predictions. We will introduce the basic architecture of Bayesian Boolean Network model and explain how the model is able to cope with the uncertainty in the data of various sources. We will also explore the possibility of using the model to integrate information from heterogeneous datasets, and explain how the model can be updated with new information in consistence with the advances of relevant lab research. The computational issues related to learning the model will be addressed. We will introduce a stochastic simulation method to learn the model structure and the model parameters.