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### **Epigenetic switches and network transitions**

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We investigate dynamics of gene networks which are regulated by both the fast binding/unbinding of transcription factors to/from DNA and the slow processes of chromatin structural change or histone modification. This heterogeneous dynamics consisting of different time scales is analyzed by the mean-field approximation and the stochastic simulation to show that the network exhibits multiple metastable states and is characterized by transitions among them. We discuss distribution and fluctuation of states of the core gene network of embryonic stem cells as an example of such heterogeneous dynamics and the simulated transitions are compared with the experimental data on the distribution of stem cell states.