Boolean networks (BN) have been proposed as an appropriate framework for modeling the state of cells due to their simplicity and the variety of tools available for model analysis. However, some complex gene interactions cannot be represented in the Boolean setting and several generalizations of the Boolean approach have been developed. Multistate models, a generalization of the BN framework, where the genes can attain more than two states have been proposed as appropriate models for capturing complex gene expression patterns, such as consideration of three states (low, medium, and high). This talk will present two results for the analysis and control of multistate networks. The first result will provide a partition of the inputs of any discrete function into canalizing and non-canalizing variables and, within the canalizing ones, we can categorize the input variables into layers of canalization. The second result will be a formula for counting the maximum number of transitions that will change in the state space upon an edge deletion in the wiring diagram. This formula relies on the stratification of the inputs of the target function where the number of changed transitions depends on the layer of canalization that includes the input to be deleted. (Received January 14, 2019)