certain subsets of elements (see Fig. 5). Our example concerning the cell state stops at the second order regulatory structure, but one can think further. For instance, as the chromatin strand folds within the nucleus, certain regions of DNA can become inaccessible to both epigenetic state modifiers and transcription factors Grewal and Moazed (2003). This process does not affect the epigenetic state of the folded regions. However, the procedure does cause silencing of the genes within the folded regions. In our model, this would mean that the folding process has locally eliminated epigenetic influence on transcription. In other words, it has turned off the epigenetic switch between silent and accessible regimes. The epigenetic states are still there, but whatever they are, the transcription regime is silent. Thus the switching mechanism has been exchanged for a constantly silent one by a master-switch which depends on the folding structure.

7. Discussion

The study of Boolean networks allows us to understand the characteristic features of the cell dynamics despite the great complexity of cell regulatory networks. A fundamental pre-requisite to achieve this goal is the use of ensembles of Boolean networks whose average properties are representative of the cell behavior. It is clear that a multi-level system such as the one described above can as well be encoded as an ordinary Boolean network. However, such a network will be a very rare realization within the entire set of Boolean networks with no pre-defined level organization. In other words, the average properties derived from the study of ordinary Boolean networks are not representative of a cellular system with its natural hierarchical struc-