Abstract Submitted
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Level architecture in genetic regulatory networks and the role of microRNAs J. M. SCHWARZ, Physics Department, Syracuse University — It is well known that genes that code for proteins regulate the expression of each other through protein-mediated interactions. With the discovery of microRNAs[1] (miRNAs), it has been conjectured that there are many such regulatory miRNAs in the cell that are never transcribed into proteins but are important for regulation and, hence, could explain the nature of the non-coding (or junk) DNA.[2] Furthermore, miRNAs are highly conserved molecules. So, just as genes that code for proteins form regulatory networks, we conjecture that miRNAs form a higher-level regulatory network amongst themselves as mediated by the genes-coding-for-proteins regulatory network to form a complex organism. We investigate this conjecture within the framework of random Boolean networks where the two-level architecture is modelled via two coupled random Boolean networks with one network taking precedence over the other for various input/output values. Aspects of the evolution of the lower-level network will also be addressed. [1] D. P. Bartel, Cell **116**, 281 (2004). [2] J. S. Mattick, Sci. Amer. **291**, 60 (2004).

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