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Title:	Detailed Study of the Class of Chain Functions in Context of Boolean Gene Regulatory Networks
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Keywords:	Gene Regulatory Networks Chain Functions Theoretical Properties Random Boolean Networks
Issue Date:	May-2024
Publisher:	IISER Mohali
Abstract:	Gene regulatory networks (GRNs) have been modelled extensively using boolean net- works (BNs). The network design and the regulatory logic rules (also known as Boolean functions, or BFs) corresponding to individual nodes determine how BNs behave. It has been demonstrated in the large-scale investigations of reconstructed Boolean models that nested canalyzing functions (NCFs) are enriched among the BFs. We delve into a new class of functions known as the chain functions (or chain-0 functions) proposed by Gat-Viks and Shamir. From this class, we obtained the new class of chain-1 functions which is the dual of the chain-0 class, and altogether called their union as the generalized chain functions class. Next, we discover that as the number of inputs increases, the fraction of NCFs that are chain-0 (and chain-1) func- tions falls exponentially. We look at some analytical results of the generalized chain functions class within the NCFs and also derive the count of the chain functions for a given number of inputs. Then, by analyzing three different datasets of reconstructed Boolean models we find that generalized chain functions are significantly enriched within the NCFs. . We also look at the effects of utilizing generalized chain functions in Random Boolean Networks(RBNs) on the network dynamics.
Description:	Under Embargo Period
URI:	http://hdl.handle.net/123456789/5689
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