Fibration Symmetries and Computational Dynamics in Gene Regulatory Networks

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In this presentation, we explore how the structure and dynamics of gene regulatory networks (GRNs) are influenced by their underlying fibration symmetries. We begin by analyzing six key circuits found in both natural and synthetic GRNs, demonstrating how these symmetries identify synchronous steady states and characterize local bifurcations, thereby providing insights into their functional roles within cellular processes [1]. Building on this, we present a fast and memory-efficient algorithm that we developed to identify these symmetries in large networks [2], which optimally detects the symmetrical flow of information in complex biological systems. Finally, we show how fibration symmetry gives rise to logic computational circuits in GRNs [3], establishing similarities between these biological circuits and classical solid-state electronic components.

References

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ORAL