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Autore	Schmitz Ulf
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Sommario/riassunto	Long description: This work is a showcase for the integration of systems biology and bioinformatics tools, algorithms and models for deciphering biological phenomena. More specifically, it integrates (i) prediction algorithms for identifying and characterizing molecular interactions, (ii) structural modelling of molecule complexes, (iii) network analysis approaches, and (iv) mathematical modelling and simulation. Two comprehensive workflows are implemented for the analysis of collective target gene regulation by microRNAs and for the prediction of cooperating microRNA pairs and their mutual target genes. In two case studies mechanisms of fine-tuned target gene regulation are revealed for different cellular processes and the phenomenon of cooperative target regulation is identified as frequent mechanism of gene regulation in humans.