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Computational modeling of cellular response mechanisms for therapeutic development

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Biotechnology increasingly relies on computational approaches to understand cellular behavior under stress and design effective therapeutic strategies. This study focuses on modeling the cellular response mechanisms of HT carcinoma cells exposed to combinations of tumor necrosis factor- α (TNF), epidermal growth factor (EGF), and insulin. The experimental setup included ten treatment scenarios to simulate diverse external stimuli influencing critical intracellular signaling pathways.

Using high-resolution expression data visualized through heatmaps, the study applied Partial Least Squares (PLS) regression and multiple regression analysis to uncover predictive patterns and cross-interactions within the signaling network. Parameters such as R^2 , adjusted R^2 , F-values, and t-tests were used to validate the computational model. The

analysis revealed consistent expression trends aligned with pro-survival or apoptotic responses, offering insights into how therapeutic modulation might influence treatment outcomes.

The approach demonstrates how integrative data mining and statistical modeling can support early-stage therapeutic development in biotechnology by predicting cellular behavior with high precision. These findings offer a foundation for further in silico testing and intervention planning in the context of cancer and chronic disease treatment strategies.

Biography

Dr. Rina Voss specializes in molecular computing and quantitative biology. With over 12 years of research experience, she focuses on protein signaling, regression modeling, and cancer systems biology. She has authored numerous publications and actively collaborates on international computational biology projects.