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Regression-based analysis of marker proteins in cancer cell signaling

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Introduction: Cell signaling pathways govern essential processes such as proliferation, apoptosis, and survival. Disruption in these pathways can lead to uncontrolled cell growth, a hallmark of cancer. This study focuses on identifying key protein markers that influence the survival or death of HT carcinoma cells when exposed to external stimuli, namely tumor necrosis factor-α (TNF-α), epidermal growth factor (EGF), and insulin. These agents were applied in ten different ng/ml combinations, and responses from eleven critical proteins—MK2, JNK, FKHR, MEK, ERK, IRS, AKT, IKK, pAKT, ptAKT, and EGFR—were recorded through heat map analysis.

Methods: The experimental data were preprocessed by normalizing protein expression levels to account for variability and ensure consistency. Data mining techniques, including feature extraction and dimensionality reduction, were employed to identify the most informative signals. Partial Least Squares (PLS) regression was applied to evaluate the linear relationship between cytokine combinations and protein responses. Evaluation metrics such as squared correlation coefficients (R^2), adjusted R^2, ANOVA, and t-statistics were calculated to assess model strength. Cross-validation methods helped test the stability and generalizability of the results.

Results: The regression models revealed that proteins such as AKT, ERK, and EGFR consistently showed high significance, with p-values well below 0.05, indicating their strong predictive capability. The PLS model achieved R^2 values ranging from 0.78 to 0.91, suggesting a robust correlation between input signals and protein activity. Multiple regression analysis further identified cumulative contributions of each protein, revealing complex interactions among signaling pathways. High tolerance and low standard error values supported the reliability of these findings. The adjusted R^2 values indicated that over 85% of the variance in cell survival could be explained by the selected protein variables.

Conclusion: This study demonstrates the utility of regression-based modeling in decoding the cellular response to pro-survival and pro-death stimuli. The results confirm that AKT, EGFR, and ERK act as major regulators in survival signaling networks and are potential targets for therapeutic intervention. Computational models such as PLS and multiple regression offer powerful tools to interpret high-dimensional biological data and guide clinical decision-making in cancer research. The integration of statistical approaches with molecular biology provides a foundation for precision medicine and targeted treatment strategies in oncology.

Biography

Dr. Saif Khan is a computational bioinformatics researcher with a specialized focus on cancer signaling networks and statistical data modeling. With over a decade of experience, he has published more than 30 peer-reviewed papers in the fields of systems biology, machine learning in healthcare, and molecular data analysis. His research centers on building algorithmic frameworks that translate complex biological data into actionable insights for clinical research. Dr. Khan is actively involved in collaborative projects that integrate large-scale data with predictive analytics for cancer diagnosis and therapy planning. He frequently contributes as a reviewer for top-tier bioinformatics journals and mentors graduate students in biomedical computing. His ongoing work seeks to bridge the gap between theoretical modeling and translational medicine, with the aim of improving patient outcomes through computational precision tools.