31st Asia Pacific Biotechnology Congress

April 10-11, 2025 | Webinar

Multivariate statistical modeling of marker proteins in cell survival analysis

Eliza Thomsen
Department of Biomedical Engineering, Denmark

Introduction: The decision-making process of a cell whether to survive or undergo programmed death is heavily influenced by external signals and internal regulatory proteins. In this study, we evaluated HT carcinoma cells subjected to ten distinct combinations of TNF-α, EGF, and insulin. The expression of eleven key proteins was monitored using heatmaps to understand their roles in cell survival or apoptosis.

Methods: Protein expression data were normalized and analyzed through a structured computational pipeline involving data pre-processing, feature selection, and application of Partial Least Squares (PLS) regression. Statistical parameters such as R^2, F-test, t-values, and Durbin-Watson coefficients were used to validate model performance.

Results: The regression analysis revealed that proteins such as AKT, ERK, and EGFR showed strong predictive value in influencing cell fate. Multiple regression further clarified the combined influence of these proteins, indicating high statistical significance and low p-values for most predictors.

Conclusion: The study confirms that regression-based modeling is a powerful tool in identifying crucial proteins in cancer signaling. These models can support future diagnostic and therapeutic research by isolating biologically relevant markers from complex data sets.

Biography

Dr. Eliza Thomsen is a biomedical engineer with expertise in statistical modeling, systems oncology, and computational biology. Her research focuses on integrating data science with molecular biology to understand complex cellular behaviors, especially in cancer. With over 14 years of experience, she has developed predictive models to analyze protein signaling pathways and treatment responses in tumor cells. Dr. Thomsen has published more than 40 peer-reviewed articles in proteomics, regression analysis, and machine learning applications in biomedical research. She has contributed to several international projects aimed at translating large-scale biological data into clinically actionable insights.