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## Computer aided classification of marker proteins for cell survival death

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## **Abstract**

The signaling system underlying cell death allows the cell to process input signals capturing information coming from the environment of the cell to lead to one of two possible outputs: cell survival or cell death. This work examines signaling networks that control the survival decision treated with combinations of the pro-death cytokine, tumor necrosis factor- $\alpha$  (TNF), and the prosurvival growth factors, epidermal growth factor (EGF) and insulin. There are ten different combinations of TNF, EGF and insulin whose values are in ng/ml. We have considered the heat map image which is showing 11 different proteins: MK2, JNK, FKHR, MEK, ERK, IRS, AkT, IKK, pAkT, ptAkT and EGFR for the HT carcinoma cells which helps in cell survival/ death. The average of all outputs were taken which were normalized to maximum. Data mining methods have the potential to identify groups at high risk. There are different steps for processing the data so as to extract their results: data collection, data pre-processing, feature extraction, feature selection, data partitioning, and data classification. In this paper different regression analysis methods were discussed on marker proteins. There are different types of regression analysis. Out of which simple regression and multiple regressions was considered. For calculation purpose we have used PLS analysis which calculates squared r values. We have validated our results by calculating adjusted regression coefficient, predicted regression coefficient regression coefficient cross validation, rm2, F-test values, Coefficient of determination, ANOVA, t-value, Durban Watson statistics for the different proteins. Later multiple regressions were used as we have different independent variables (proteins). To validate the results we have calculated the coefficient, standard error, standard coefficient, tolerance, t value and p value, variation explanation of predictors and estimators which gives cumulative percentage.

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## **Biography**

S. Jain has received PhD degree from Jaypee University of Information Technology, Waknaghat, Solan. She has a teaching experience of around 14 years. She has specialization in Biomedical Signal Processing, Computer- Aided design of FPGA and VLSI circuits, combinatorial optimization. She has published more than 50 papers in reputed journals and 30 papers in International conferences. She is a senior member of IEEE, life member of Biomedical Engineering Society of India and member of IAENG. She has completed one externally funded projectfunded by DRDO entitled

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