



Computer aided classification of marker proteins for cell survival /cell 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- α (TNF), and the pro-survival 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 averages 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. 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 cross validation, rm^2 , 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. After analysis we get 7 proteins (AkT, Epidermal growth factor receptor (EGFR), Extracellular-regulated kinase (ERK), c-jun N-terminal kinases(JNK), Mitogen-activated protein kinase-activated protein kinase 2 (MK2), Insulin receptor substrate (IRS), and Forkhead transcription factor (FKHR))as the marker (best) proteins which were used for classification. A CAD system for the classification of MAPK proteins (ERK, JNK and p38/MK2), receptor proteins (EGFR and IRS) and AkT for HT-29 human colon adenocarcinoma cells



using different wavelet transform (discrete wavelet filter and gabor wavelet filter) for different classification techniques which gives decision on apoptosis-survival.

Biography:

S. Jain has received PhD degree from Jaypee University of Information Technology, Wahnaghat, 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.

Publication of speakers:

- 1. Jain S. (2012) Communication of signals and responses leading to cell survival / cell death using Engineered Regulatory Networks. PhD Dissertation, Jaypee University of Information Technology, Solan, Himachal Pradesh, India.
- 2. Weiss R (2001) Cellular computation and communications using engineered genetic regulatory networks. PhD Dissertation, MIT.
- 3. Gaudet S, Kevin JA, John AG, Emily PA, Douglas LA, and Peter SK. (2005) A compendium of signals and responses triggered by prodeath and prosurvival cytokines. Manuscript M500158-MCP200.

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