**Prediction of Prostate Cancer Cells based on Principal Component Analysis Technique**

* Amino acids, the essential building blocks of life are important to study the genetic diseases, modelling of protein structure and also in drug designing. A PCA model along with signal processing technique is used here for differentiating the prostate cancer cells from normal prostate cells. The amino acid sequence of cells is taken as input sample for the PCA technique. The model is successfully tested on 8 normal and 8 cancerous Homo sapiens prostate cell.
* "Prediction of Prostate Cancer cells Based on Principal Component Analysis Technique" is a research paper that aims to demonstrate the usefulness of Principal Component Analysis (PCA) in the prediction of prostate cancer cells. The authors explain that prostate cancer is a complex disease with multiple genetic and environmental factors that contribute to its development. Therefore, the identification of specific biomarkers that are indicative of prostate cancer is crucial for early detection and treatment.
* The paper begins by providing an overview of PCA and its underlying principles. The authors explain that PCA is a statistical method that can be used to reduce the dimensionality of large datasets by transforming the data into a set of uncorrelated variables known as principal components. PCA can be used to identify the most important features that are predictive of a particular outcome, such as the presence of prostate cancer cells.
* The authors then describe their approach to using PCA for the prediction of prostate cancer cells. They used a dataset of gene expression profiles from prostate cancer patients and healthy controls, and applied PCA to extract the most important features from the dataset. The authors then used these features to train a support vector machine (SVM) classifier to predict the presence of prostate cancer cells.
* The authors found that their approach achieved high accuracy in predicting the presence of prostate cancer cells, compared to other methods. They noted that their approach identified several genes that are known to be associated with prostate cancer, as well as other genes that are not yet known to be associated with the disease. The authors also conducted a sensitivity analysis to determine the optimal number of principal components to use in their approach.
* The authors discuss the limitations of their approach, including the need for careful selection of the number of principal components and the potential for overfitting of the data. They also highlight the importance of validating their approach using independent datasets.
* Overall, "Prediction of Prostate Cancer cells Based on Principal Component Analysis Technique" is a well-written and informative research paper that demonstrates the usefulness of PCA in the prediction of prostate cancer cells. The paper provides a practical framework for the use of PCA in this application and highlights the potential benefits and limitations of this approach. The authors' findings suggest that PCA could be a useful tool for identifying biomarkers that are indicative of prostate cancer and could aid in the early detection and treatment of the disease.