Literature Review

1. In the report [1], are used in order to detect Influenza, another great report which enhances upon the use of such methods in modern healthcare.
2. In the article [2], the estimation has been done through two methods: direct estimation method which involves study and calculation of cause-specific deaths, while the second one is a more indirect way of approximation, and enumerates all-cause mortality. They highlight that a predefined death rate was needed to identify differences arising from calculation of excess mortality.
3. In the article [3], insightful reports and useful information surrounding epidemic control for Influenza has been given.
4. In the article [4], connections of influenza virus spread with avian influenza virus have been made, citing the pandemics of 1957 and 1968. A review of the ecology and evolution of highly pathogenic avian influenza H5N1 viruses, assess the pandemic risk, and address aspects of human H5N1 disease in relation to its epidemiology, clinical presentation, pathogenesis, diagnosis, and management has been done.
5. In the article [5], information about the 2009 influenza spread has been given. This review provides an update encompassing the virology, epidemiology, clinical manifestations, diagnosis, treatment, and prevention of the 2009 H1N1 virus.
6. In the report [6], they observe the implications of the vaccines administered by the United States in lieu of the influenza season which coincides with the spread of SARS-COV2 virus, also known as Covid-19. They mention the arrangement and protocols needed to be followed by the authorities for controlled handout of the vaccines.
7. In the article [7], they have created an intricate and information-comprehensive database for the 2009 pandemic influenza A/H1N1 describing the genome-sequence data and characteristics of the virus that are potentially much use for research.
8. Subah waala
9. In the article [9], ensemble techniques have been used for classifying cancer given gene expression data. Genome RNA expression studies permit systematic approaches to understanding the correlation between gene expression profiles to disease states or different developmental stages of a cell, while the use of Microarray analysis provides quantitative information about the complete transcription profile of cells that facilitate drug and therapeutics development, disease diagnosis, and understanding in the basic cell biology, has been stated.
10. In the article [10], use of machine learning techniques to predict and diagnose various chronic diseases has been reviewed.
11. This article [11], catches the need of predictive analysis to diagnose heart diseases with learning techniques. This work is focused on developing various machine learning predictive models using support vector machine, decision tree, neural network and K-nearest neighbour for prediction of heart disease.
12. In the article [12], the need for good pre-processing of patient data collected for various purposes has been emphasised, citing that with such databases having large amounts of data, machine learning techniques could be used for automatic processing.
13. From here [13], we accumulate the data, which we used in our research and perform various technique.
14. Here [14], This review stresses on easy and reliable interpretation of the ROC curve and following certain guidelines for writing and presenting such analysis.