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STUDY ON MUTATION MECHANISMS OF HUMAN BREAST CANCER IN SRI LANKA

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Breast cancer is a genetic disease that has become a major health problem in developing countries like Sri Lanka. The incidence rate of breast cancer in Sri Lanka continues to rise. Therefore, this study was conducted to analyze the breast cancer data descriptively, compare age-specific incidence rate patterns for gender, and investigate the mutation mechanisms to determine how many mutations are needed for breast cancer. The breast cancer data was obtained from the National Cancer Control Programme in Sri Lanka. Preliminary data analysis was done to identify the age, gender, district, and province wise prevalence of breast cancer, and the age-specific incidence rate of breast cancer was calculated. The multistage stochastic model was built and parameters were estimated. Then the system of differential equations in the model was numerically solved to obtain the value of the hazard function. The chi-square goodness of fit test was used to examine the optimal fitting stage model. The results show that a high number of breast cancer incidence was evident among women in Sri Lanka. The incidence of female breast cancer was high in postmenopausal women. The results further indicated that the incidence of breast cancer depends on the morphology types of breast carcinoma (Infiltrating duct carcinoma 79.04%, Neoplasm malignant 10.64%, etc.). When considering the percentage of women having breast cancer to the districts' population, an increased rate of incidences of female breast cancer was observed in highly populated urban districts in Sri Lanka. According to the result of the model, there should be at least two to three mutations in the genome of breast stem cells for them to become a malignant cell. It is evident from the result that three gene mutations ($p = 0.06$) with estimated parameters fit very well in Sri Lankas' data on female breast cancer.

Keywords: Breast cancer, Gene mutation, Stochastic model