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Pathway Modeling of Prostate Cancer, Breast Cancer and Tuberculosis BKBK

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Pathway modeling gives us a view of the natural systems and their interactions and helps to generate new hypothesis. The present study focuses on the analysis of pathways involvedin Breast cancer and Prostate cancer.The hypersensitivity pathway responsible for Androgen Independent Prostate Cancer showed that the enzyme 5-α-reductase is the key regulator of this pathway. Hence, if this enzyme is targeted from the drug development aspect it may help to combat prostate cancer. Similarly, by reducing the concentration of homocysteine and controlling the low levels of folate in the metabolic pathways with respect to time course would help to control the breast cancer risk in women. Here, the COPASI model is used to know the pathway modelling of particular pathway which would help in altering the malfunctioning of the pathway. As the pathway modelling completely based on the time course and concentration levels, the amount risk factors can be controlled with equal maintenance of time and concentrations.Tuberculosis, caused by Mycobacterium tuberculosis is one of the main diseases to mankind. Designing of appropriate antimicrobial agents depend upon the novel drug targets of pathogen. COPASI model has been used for the simulation and modeling of shikimate pathway. The shikimate pathway starts from condensation of 2-phosphoenolpyruvate and D-erythrose-4- phosphate to chorismate.Chorismate is the only precursor for the amino acid biosynthesis in this pathogen.The validated kinetic model can be used to determine the contribution of each enzyme to the final product formation rate, to profile intermediate concentrations, and predict responses to inhibition effects. Using the model, conditions most appropriate for high-throughput screening can be optimized.

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Network based analysis of SNPs associated with age-related disorders

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Age-Related Disorders (ARDs) are the complex disorders associated with the process of ageing. Understanding the biology of ageing and identification of genetic markers associated with ARDs is one of the most important fields of biomedical research. Genome-wide association studies (GWAS) have found several genetic markers (SNPs) associated with ageing and age-related diseases. However, the number of markers in which the evidence for association exceeds the genome-wide significance threshold is very small and markers that do not exceed this threshold are generally neglected. We hypothesize that certain combinations of genes flagged by these markers can be identified if they belong to a common biological pathway. Here, we propose an integrated network and pathway-oriented analysis approach that take into account all SNPs with nominal evidence of association ($P<0.05$) with age-related diseases with the hope of finding the markers shared in different age-related diseases and uncovering the biochemical pathways that can solve the mystery of ageing and associated diseases.

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