School of Engineering and Applied Science (SEAS), Ahmedabad University

B.Tech (CSE Semester IV): Probability and Random Processes (MAT 202)
Special Assignment Abstract Submission

- **Group No.:** S_B1

- **Project Area:** Biology

- **Project Title:** Prediction of the Probabilities of the Transmission of Genetic Traits within Bayesian Logical Inference

- **Name of the group members :**

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Abstract

Problem Background

The theoretical probability of an event is calculated based on information about the rules and circumstances that produce the event. It reflects the number of times an event is expected to occur relative to the number of times it could possibly occur. This concept is widely used for predicting outcomes in interdisciplinary fields. Here we are applying this in the field of Genetics (Biology). Transmission of genetic information from generation to generation is what determines the traits of offspring. Traits like colour of hair, height, blood group etc. are inherited. Thus, when given the genetic details of both the parents the traits in their child can be predicted. We are particularly applying this model to investigate transmission of autosomal recessive diseases through generations.Here, autosomal refers to the autosomal chromosomes (Humans have 23 pairs of chromosomes in total out of which 22 pairs are autosomal). Recessive refers to the recessive gene (There are 2 types of genes - dominant and recessive). So, such diseases are transmitted when an infected recessive gene is crossed with another infected recessive gene.

Brief of the Article

The article [**?**] which we have referred, provides straightforward interpretation of prediction of transmission of genetic traits (Autosomal Recessive diseases as discussed above) along to generations. This paper uses special kind of stochastic process called Markov chain within Bayesian Framework. Bayesian method is used to calculate the probability of the affected offspring of given genetic cross which is obtained first by using Pedigree analysis. Here, the Bayesian Analysis plays a central role for calculating genetic risk and predicting posterior probability of transmission of genetic traits under some assumptions. The posterior probability obtained is applicable to many common scenarios generating not only a foetus but also offspring along generations for crossing with their different genotypes.

Planned Contribution

From the genetic data of prior generations, we will build a pedigree diagram which will help us to understand the crossing of the dominant and recessive genes and if the offspring are heterozygous or homozygous. Using this information, we will develop a hypothesis which will indicate effects of hereditary characteristics. With these data, information and hypothesis as element in the Bayes theorem we will get the desired posterior probability. To calculate the sum of probabilities in the Bayes theorem we use transition matrices inspired by a stochastic model called Markov chain. In order to calculate higher powers of these matrices we can either use mathematical induction or diagonalization (using eigenvalues and eigen vectors) of matrices.

References