

- **Area :** Biology

- **Group Members :**

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- **Background :**

- Our topic revolves around the discovering of disease genes in a particular individual. The first step to this, is Multipoint linkage analysis of data collected on related individuals, which detects and localizes the chromosomal regions, called as the trait loci, containing disease genes. Over time though, this process has proven to be intractable.
- Therefore, we will be presenting a new approach to the same problem, through the Markov Chain Monte Carlo process wherein it greatly extends the range of models and data sets for which analysis is practical.
- Here, several processes namely the joint updates of latent variables across loci or meiosis, integrated proposals, and many more, are included into a sampling scheme so as to minimize the error rate, and maximize accurate results in real time.

- **Importance of Topic :**

- Through the help of this project, we will be finding the uncertainty of the disease gene present into the chromosome of the DNA, of the related individual.
- With this, we can provide the respective precautions for the given disease (Alzheimer's disease), at an early stage.
- And thus, we will be able to compute the probability, of the given disease (Alzheimer's disease), which in turn will be useful for modeling the uncertainty present into the related individual from his/her inherent parents.

- **Inference :**

- To find the uncertainty in genetic diseases, we will be using the Markov Chain Monte Carlo process. The above process helps in obtaining the samples of the desired distribution by observing the chain after a number of steps.
- Here, we use this process because there are many chromosomes in DNA and furthermore, there are many genes in the chromosomes. Hence, there is a huge hierarchical model as well as unknown parameters for the integration part and this is where the MCMC algorithm will be useful.

- **Reference :**

- <https://towardsdatascience.com/a-zero-math-introduction-to-markov-chain-monte-carlo-methods-dcba889e0c50>
- <https://www.ncbi.nlm.nih.gov/pubmed/10436380>
- https://www.researchgate.net/publication/38326981_Discovering_Disease_Genes_Multipoint_Linkage_Analysis_via_N