Amrita School of Computing
Department of Computer Science and Engineering

Minor Project: 19CSE495
(2020-2024 B.Tech CSE)

GROUP B2

A STUDY OF GENOME VARIATIONS OF HUMAN PATHOGENS USING PANGENOME GRAPH

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ABSTARCT:

The problem addressed in this project is the study of genome variations of human pathogens using a pangenome graph. The pangenome graph is a representation that combines multiple genomes of a species into a single graph structure, capturing the genetic diversity within a population. The project aims to analyze the genome variations of human pathogens, such as bacteria or viruses, to understand their genetic diversity, evolutionary patterns, and potential implications for disease transmission, virulence, and drug resistance. By studying the genome variations using a pangenome graph approach, researchers can gain insights into the adaptive strategies of pathogens, improve diagnostics, and develop targeted interventions to combat infectious diseases. This research is relevant as it contributes to a better understanding of pathogen dynamics, aiding in the development of effective strategies for disease control and prevention.

MOTIVATION:

The motivation for undertaking the project of studying genome variations of human pathogens using a pangenome graph arises from the imperative to comprehend the diverse genetic makeup and evolutionary dynamics of pathogens. This knowledge holds immense significance in the realm of disease control and prevention. By delving into genome variations, researchers can unravel critical insights into pathogen behavior, modes of transmission, virulence attributes, and drug resistance mechanisms. This information serves as a foundation for developing targeted interventions, refining diagnostic techniques, and formulating effective treatments and vaccines. For instance, in the context of the COVID-19 pandemic, examining the genome variations of SARS-CoV-2 enabled the identification of novel concerning variants, evaluation of their impact on disease severity and vaccine efficacy, and facilitated informed decision-making to alleviate the suffering experienced by communities.

REFERENCES:

1. Lee H, Kingsford C. 2018. Kourami: graph-guided assembly for novel human leukocyte antigen allele discovery. Genome Biol. 19:16
2. Ding W, Baumdicker F, Neher RA. panX: pan-genome analysis and exploration. Nucleic Acids Res 2018; 46(1): e5.
3. Corman VM, Landt O, Kaiser M, et al. Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR. Euro Surveill 2020; 25(3).
4. Huang C, Wang Y, Li X, et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. Lancet 2020.
5. pangenomeDB This database contains a pan genome of all complete viruses from BetaCoronaVir

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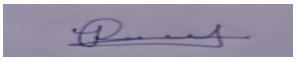
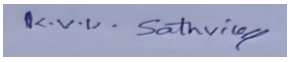
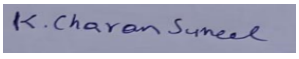
RUSHIKESH REDDY



SATHVIK KESAVA



CHARAN SUNEEL



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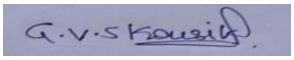

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