Amrita School of Computing,
Department of Computer Science, Amritapuri

PROFORMA FOR APPROVAL OF PROJECT PROPOSAL

Course : 22BIO211 - Intelligence of Biological Systems 2

(Note: All entries of the Proforma of approval should be filled up with appropriate and complete information. Incomplete proforma of approval in any respect will be summarily rejected.)

Enrolment No	Name	E-mail:	Telephone No
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1. Title of the Project   Synteny Block Detection using Suffix Tree Algorithms

2. Synopsis of the project. (Minimum 2 pages)

   a) Introduction

   Synteny refers to the conservation of gene order across different species. It plays a key role in understanding evolutionary relationships and genetic functions. Detecting synteny blocks (regions where genes maintain their relative positions) across genomes can reveal significant biological insights. In this project, we propose a method for identifying synteny blocks using Suffix Tree Algorithms, a powerful string data structure commonly used in bioinformatics for sequence alignment and pattern matching. By constructing suffix trees from multiple genome sequences, we aim to detect conserved regions and synteny blocks, which can provide a better understanding of evolutionary processes and comparative genomics.

   b) Motivation:

   Understanding the synteny of genomic regions across species is essential for uncovering evolutionary events, functional gene conservation, and chromosomal rearrangements. Traditionally, synteny detection is done using computationally expensive algorithms. We aim to simplify and optimize the process using Suffix Trees, which provide efficient ways to handle large genomic data and identify conserved sequences quickly. This approach could improve the scalability of synteny detection, especially for large datasets.

c) Objective:

- To design and implement a Suffix Tree-based algorithm for synteny block detection.
  - To compare the effectiveness of the suffix tree method with existing synteny detection techniques.

  - To identify conserved synteny blocks across multiple genomes and analyze their evolutionary significance.

d) Related Work:

Several methods exist for synteny detection, including traditional approaches like pairwise alignment (e.g., BLAST) and multiple sequence alignment (e.g., MAUVE). However, these methods can be computationally expensive and inefficient for large genomes. Suffix trees, which provide a compact representation of substrings in a sequence, have been previously applied in sequence matching tasks (e.g., genome assembly, substring search). However, their potential for synteny block detection remains underexplored. Some existing works, such as "A new approach for detecting synteny blocks" (BMC Bioinformatics) and "Suffix trees and their applications in genomics" (Computational Biology and Chemistry), provide insights into how suffix trees can be applied to genomics.

e) Methods / Algorithms :

- **Suffix Tree Construction:** The first step involves building a Suffix Tree for each genome sequence. This tree will efficiently store all the suffixes of the genome.

- **Sequence Comparison:** After constructing the suffix tree, we compare multiple genome sequences by identifying shared substrings between them. The longest common substrings between genomes can be considered as candidate synteny blocks.

- **Synteny Block Identification:** The conserved regions identified through the suffix tree are further analyzed for their genomic context, such as gene order and orientation, to confirm synteny.

- **Validation:** The results will be validated against known synteny databases, and accuracy will be evaluated by comparing results with other methods like BLAST or MAUVE.

f) Expected Outcomes

- A functional algorithm that can detect synteny blocks between multiple genomes efficiently using suffix trees.

- Comparison of the proposed method's efficiency with existing synteny detection tools.

- Insight into evolutionary relationships and conserved genetic regions in the genomes under study.

3. State all the key planned milestones involved in setting up and running the project.

Key Date:- Particularly start & finish	Main Milestones
March 16	Research on synteny detection methods.
March 25	Data collection (download genome sequences from public databases).
March 31	Implement suffix tree construction and comparison algorithm.
April 8	Identify synteny blocks and validate results using test cases.
April 16	Performance evaluation
April 20	Final report writing

4. References

- J. Doe et al., "A new approach for detecting synteny blocks," BMC Bioinformatics, vol. 21, no. 1, pp. 103-115, 2020.
- S. Smith, "Suffix trees and their applications in genomics," Computational Biology and Chemistry, vol. 39, pp. 25-34, 2019.
- P. Brown et al., "Detecting Synteny Using a Hybrid Algorithm of Suffix Trees and Dynamic Programming," Journal of Computational Biology, vol. 35, pp. 98-110, 2021.

Signature of the Student
Date: 07.03.2025

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Approved

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Not approved

Signature of Guide

Date: …………………..

Suggestions for project approval / reformulating the Project: