Announcing the Final Examination of Sahar Hooshmand for the degree of Doctor of Philosophy

Time & Location: July 9, 2020 at 2:00 PM in Virtual defense https://ucf.zoom.us/j/96876099705
Title: EFFICIENT STRING ALGORITHMS WITH APPLICATIONS IN BIOINFORMATICS

In this study, we establish efficient methods for solving some algorithmic problems with applications in Bioinformatics. First, an algorithm for the genome mappability problem is presented. Genome mappability is a measure for the approximate repeat structure of the genome with respect to substrings of specific lengths and a tolerance to define the number of mismatches. The similarities between reads are measured by using the Hamming distance function. Genome mappability is computed for each position in the string and has applications in designing high-throughput short-read sequencing experiments. Next, we present an efficient algorithm to compute the Average Common Substring of two input sequences in their run-length encoded format. Besides, a method that produces a better approximation for Average Common Substring calculations is proposed, where we are allowed to have mismatches. This method is applicable to the alignment-free comparison of biological sequences at a highly competitive speed. Finally, we present two algorithms to efficiently decode the Suffix Array/Inverse Suffix Array of the reversed text, by using the FM-index of the forward text. Additionally, our experimental results are competitive when compared to the standard approach of maintaining the FM-Index for both the forward and the reverse text in approximate string-matching applications.

Major: Computer Science

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Bachelor's of Electrical Engineering, BS, 2010, University of Tabriz
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Committee in Charge:
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Gary T. Leavens, Computer Science
Sumit Kumar Jha, Computer Science
Varadraj Gurupur, Health Management and Informatics

Approved for distribution by Sharma V. Thankachan, Committee Chair, on June 16, 2020.

The public is welcome to attend.