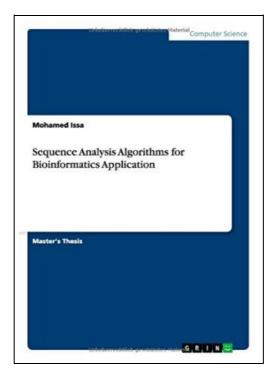
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SEQUENCE ANALYSIS ALGORITHMS FOR BIOINFORMATICS APPLICATION



GRIN Verlag Gmbh Okt 2014, 2014. Taschenbuch. Condition: Neu. Neuware - Master's Thesis from the year 2014 in the subject Computer Science Bioinformatics, grade: N, , language: English, abstract: The data from next generation sequencing technologies has led to an explosion in genome sequence data available in public databases. This data provides unique opportunities to study the molecular mechanisms of gene evolution: how new genes and proteins originate and how they diversify. A major challenge is retracing origin of extant genes or proteins, by searching existing databases for related sequences and identifying evolutionary similarities. Therefore, enhanced and faster search algorithms are being developed, e.g. on accelerators such as GPU, in order to cope with the huge size of today s DNA or protein sequence databases. Gene-Tracer is a tool was developed to localize the common sub-sequences between two ancestors and its offspring. Besides, compute percentages of ancestors contributions in offspring. Gene-Tracer was developed to find the origin of unknown shuffling/offspring sequence. A database is scanned and the similarity between offspring sequence and each one in the database is computed using pairwise local sequence alignment algorithm. Based on similarity score, 100 sequences that have the highest score is re-aligned with shuffling sequence to determine length of common sub-sequences between them using local alignment algorithm. The two sequences that have longest sub-sequences with shuffling are the nearest origin to offspring. Swiss-port database contains around 400,000 proteins is used in the test. The execution time around hours. So, GPU is to accelerate the tool. Speedup is 84x using single-GPU Tesla C2075 versus Intel Core i3 multiprocessor. Finally, the main contribution of work is developing fast tool that re-trace origins of unknown gene/protein sequences. 92 pp. Englisch.



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