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عنوان پایاننامه	ارائه یک روش موازی و آگاه از حافظه برای تسریع اجرای الگوریتم های بیوانفورماتیک

Sequence alignment is the most widely used operation in bioinformatics. With the exponential growth of the biological sequence databases, searching a database to find the optimal alignment for a query sequence (that can be at the order of hundreds of millions of characters long) would require excessive processing power and memory bandwidth. Sequence alignment algorithms can potentially benefit from the processing power of massive parallel processors due their simple arithmetic operations, coupled with the inherent fine-grained and coarse-grained parallelism that they exhibit. However, the limited memory bandwidth in conventional computing systems prevents exploiting the maximum achievable speedup. In this paper, we propose a processing-in-memory architecture as a viable solution for the excessive memory bandwidth demand of bioinformatics applications. The design is composed of a set of simple and light-weight processing elements, customized to the sequence alignment algorithm, integrated at the logic layer of an emerging ۳D DRAM architecture. Experimental results show that the proposed architecture results in up to ۲.٤x speedup and ٤١٪ reduction in power consumption, compared to a processor-side parallel implementation.

چکیده پایان نامه

کلمات کلیدی	تطابق توالی پروتئین، شتاب دهنده سخت افزاری، پردازش در حافظه، تطابق ژن
کلمات کلیدی انگلیسی	Sequence Alignment, Accelerator, Processing-in-memory