

MGPA: A Memristor-based Genome Processing Accelerator for Single-cell RNA Sequencing

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Abstract—With the rapid development of bioinformatics, genome processing tasks, including sequence alignment and classifications, face a serious conflict between their high computational density and the limited bandwidth of von Neumann architectures. Although in-memory computing (IMC) alleviates the contradiction, existing IMC-based genome processing architectures often incur excessive hardware overhead for nucleotide encoding. This work proposes a low-latency and energy-efficient Memristor-based Genome Processing Accelerator (MGPA), which utilizes a compact nucleotide representation scheme that reduces device count by 50%~75%. In simulations of single-cell RNA sequencing tasks, MGPA achieves a 394.6× improvement in energy efficiency and a 51.7× speedup over state-of-the-art memristor-based genome processing solutions.

Index Terms—Memristor, In-Memory Computing, Single-cell RNA Sequencing, Barcode, Compact Nucleotide Encoding

I. INTRODUCTION

Single-cell RNA sequencing (scRNA-seq) has revolutionized biological research by enabling the precise characterization of gene expression at single-cell resolution, offering a level of detail unattainable with traditional bulk RNA sequencing [1]–[4]. However, the challenges of scRNA-seq arise from the computational demands of massive data processing. As shown in Fig. 1, cDNAs from different cells must be sorted by their barcodes, which is computationally intensive.

Memristor-based in-memory computing (IMC) has emerged as an attractive approach by enabling computation directly within the memory array [5]–[8], thereby delivering exceptional speed and energy efficiency. In this work, we introduce a Memristor-based Genome Processing Accelerator (MGPA) featuring a compact encoding strategy in which a single memristor represents one nucleotide (nt), reducing device count by 50–75% compared to existing memristor-based encoding schemes, and alleviating the trade-off between computational parallelism and hardware overhead. Experimental results on real scRNA-seq datasets demonstrate that MGPA significantly surpasses state-of-the-art memristor-based solutions in both speed and energy consumption.

[#]These authors contributed equally to this work.

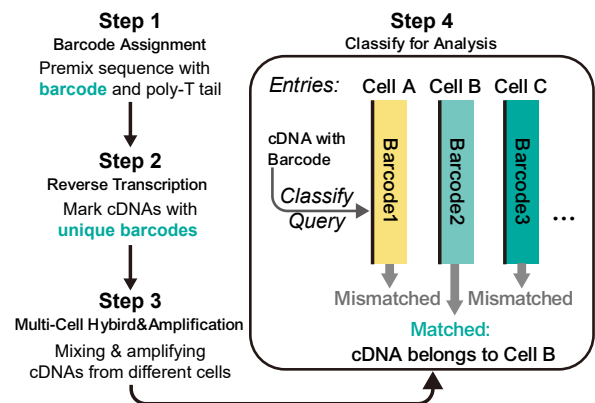


Fig. 1. The basic process of the scRNA-seq.

II. PROPOSED MGPA DESIGN

A. Device Characteristic and Conventional Encoding Scheme

Memristors are highly compatible with in-memory computing. In this study, we employ the 1T1R architecture in Fig. 2(a) and construct a device model based on experimental measurements. The conductance-switching characteristics of 100 devices are shown in Fig. 2(b). Prior work has shown that memristors can support thousands of distinct conductance states under precise electrical control [9], making them attractive for multilevel implementations.

Traditional nucleotide encoding strategies usually rely on multiple devices to represent a single nt. As illustrated in Fig. 2(c), the 1-hot encoding method [10] uses four binary memristors to encode each nucleotide, with one device in the low-resistance state (LRS) and the remaining three in the high-resistance state (HRS). Each nt is driven by a 4-bit input from the SLs, which multiplies the applied voltages by the four conductance values, sums the resulting currents, and delivers the output to the BL to indicate whether the input is matched.

B. Proposed Compact Encoding Scheme

To overcome the large device footprint of existing nucleotide encoding approaches, we develop a highly compact encoding method that minimizes the number of required

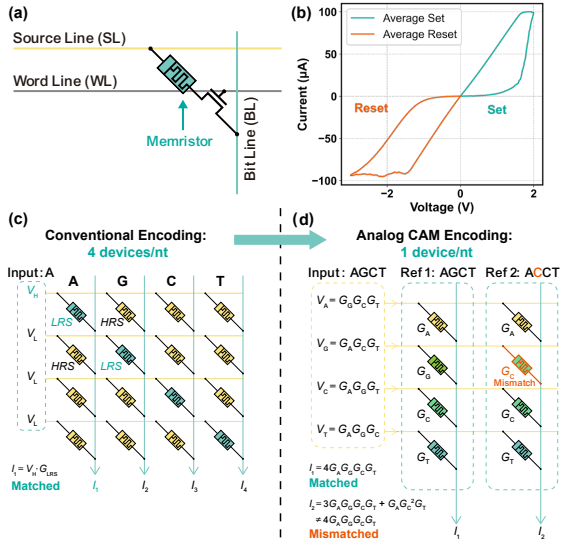


Fig. 2. (a) 1T1R cell structure. (b) conductance switching characteristics of adopted memristors. (c) Conventional 1-hot encoding and matching scheme. (d) Proposed Compact Encoding scheme.

devices without sacrificing reliability, as depicted in Fig. 2(d). This method takes advantage of the memristor’s ability to store analog conductance values, allowing one device to stand for a single nucleotide. In the reference array, nucleotides A, G, C, and T are mapped to four distinct conductance states (G_A , G_G , G_C , G_T). For sequences input via voltage signals, each nucleotide is represented by the product of three conductance values corresponding to the other three nucleotides. Under this formulation, a matching input–reference pair yields a BL current equal to the product of the four conductance levels, whereas any mismatch results in a different current magnitude. By monitoring the BL current, the system can reliably discriminate whether the input nucleotide matches the stored one. When moving from the matching of a single nucleotide to an entire sequence, an additional requirement arises: the total current produced by multiple mismatched nucleotides must not coincide with the current generated by a fully matched sequence of the same length. This requirement can be expressed mathematically as the following proposition:

$$B = \left\{ \frac{G_i}{G_j} \mid i, j = A, G, C, T \right\}, \forall b_k \in B (1 \leq k \leq len),$$

$$\overline{b_1 = b_2 = \dots = b_{len} = 1} \rightarrow \sum_{k=1}^{len} b_k \neq len.$$

Here, len represents the sequence length. Should this condition remain unmet, certain currents from “mismatched” nucleotides could become identical to those from a fully “matched” sequence, rendering the two scenarios indistinguishable.

C. Experimental Evaluations

Building on the proposed encoding strategy, we introduce a memristor-based genome processing accelerator (MGPA) and assess its performance through simulations of cDNA classification on a scRNA-seq dataset from 10x Genomics [11]. Fig. 3(a) presents a performance comparison of MGPA with state-of-the-art memristor-based genome processing solutions

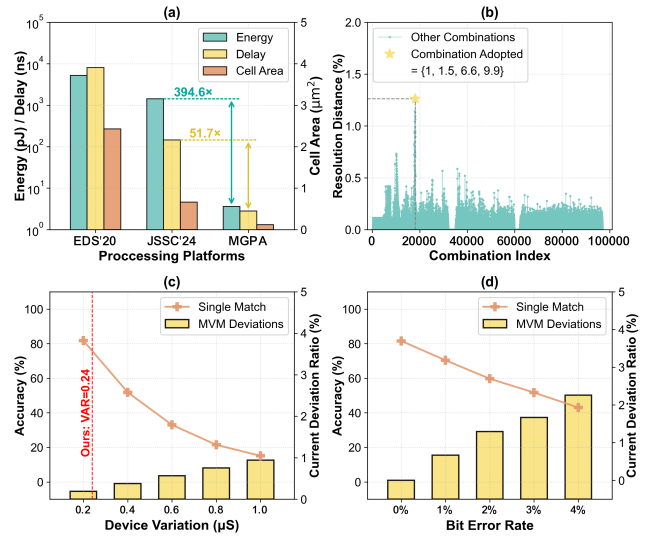


Fig. 3. Performance evaluation and Robustness discussion of the proposed architecture.

during a single match task. Thanks to its co-optimized algorithm and hardware architecture, MGPA achieves a $394.6\times$ improvement in energy efficiency and a $51.7\times$ speedup relative to the benchmark with an ultra-low area overhead, while maintaining classification accuracy above 99.99%, fully satisfying the requirements for practical deployment.

Reliability is also a critical attribute of circuits. Fig. 3(b) shows the effect of the conductance setting, and we chose the one that maximizes discrimination between matched and mismatched cases. Fig. 3(c)-(d) illustrate the performance degradation caused by increasing read noise and process variation, whereas our approach demonstrates strong reliability.

III. CONCLUSIONS

In this study, we introduce a Memristor-based Genome Processing Accelerator (MGPA) tailored for single-cell RNA sequencing applications. Employing a novel nucleotide encoding strategy, MGPA reduces device requirements while delivering low-latency, high-accuracy, and energy-efficient cDNA classification, effectively addressing the trade-off between input-level parallelism and hardware overhead present in previous approaches. Evaluations show that MGPA achieves remarkable improvements, with a $394.6\times$ increase in energy efficiency and a $51.7\times$ acceleration over SOTA memristor-based solutions. This advancement paves the way for real-time, large-scale transcriptomic analysis.

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