DNA Pre-alignment Filter using Processing Near Racetrack Memory

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Abstract—Recent DNA pre-alignment filter designs employ DRAM for storing the reference genome and its associated meta-data. However, DRAM incurs increasingly high energy consumption background and refresh energy as devices scale. To overcome this problem, this paper explores a design with racetrack memory (RTM)—an emerging non-volatile memory that promises higher storage density, faster access latency, and lower energy consumption. Multi-bit storage cells in RTM are inherently sequential and thus require data placement strategies to mitigate the performance and energy impacts of shifting during data accesses. We propose a near-memory pre-alignment filter with a novel data mapping and several shift reduction strategies designed explicitly for RTM. On a set of four input genomes from the 1000 Genome Project, our approach improves performance and energy efficiency by 68% and 52%, respectively, compared to the state of the art proposed DRAM-based architecture.

Index Terms—Genome sequencing, seed location filtering, processing-in-memory, DNA sequence alignment.

1 INTRODUCTION

Sequence alignment is a fundamental but computationally expensive step in genomic analysis, where short DNA fragments of a query genome are mapped and compared against a reference genome. High-throughput sequencing (HTS) technologies generate a massive amount of sequencing data, making the sequence alignment a performance bottleneck. In particular, solutions based on dynamic programming are extremely slow and quickly become impractical [1]. Current algorithms thus use a seed-and-extension approach that better scales with the data volume [2], [3]. However, these algorithms still spend considerable time analyzing genome locations that eventually do not align. To alleviate this problem, recent research employs pre-alignment filters [4], [5], [6]. These filters significantly reduce the number of DNA fragments that are passed on to the more computational expensive alignment phase.

Recent pre-alignment filters have been implemented on GPUs [7], FPGAs [8], ASICs [6] or on CPUs with die-stacked DRAMs [4], [9]. This work mainly concentrates on the near-memory pre-alignment filter with a novel data mapping and several shift reduction strategies designed explicitly for RTM. We demonstrate a DNA pre-alignment filter designs employing RTM, which achieves performance and energy efficiency improvements of 68% and 52%, respectively, compared to the state-of-the-art DRAM technique [9] by 63% and 48%, respectively. Our evaluations show that naively replacing DRAM with RTM leads to significant performance and energy overheads. We propose RTM optimized storage and data management approaches that leverage characteristics of the pre-alignment filtering algorithm to significantly reduce the RTM shifts and maximize access parallelism across subarrays. In particular we make the following contributions:

- We interleave accesses of different tokens across subarrays which reduces latency by pipelining memory accesses.
- We minimize shifts by ensuring that subarrays without a matching token will not shift.
- We demonstrate a preshifting technique to avoid latency overhead of shifts.
- We utilize a circular unlimited single-shift technique to allow buffers to automatically reset to their original position.

Applying interleaved accesses and minimizing shifts for tokens not in the query read decreases runtime and energy versus the state-of-the-art DRAM technique [9] by 63% and 48%, respectively. When adding preshifting and unlimited single-shiftings, these improvements grow to 68% and 52%, respectively.

2 BACKGROUND AND RELATED WORK

This section provides the background on RTM architectures and the pre-alignment filters.

2.1 Racetrack memory

A single RTM magnetic nanowire can store up to 100 data bits. We assume planar RTM tracks that are grouped to form subarrays. Each track in a subarray has one or more access ports that enable reading/writing data from/to the track. Due
to the larger area footprint of access transistors, each track can only have a limited number of access ports. Therefore, data placement to minimize shifting for data accesses is an important performance and energy optimization criterion.

### 2.2 State-of-the-art pre-alignment filters

In the state-of-the-art pre-alignment [4], [9], the reference genome \( R \) is divided into \( n \) fixed-size bins. The query genome \( Q \) is divided into \( m \) reads where each read \( q_i \) contains many nucleotides. The four nucleotides in DNA are represented by the alphabet \( \Gamma = \{A, C, G, T\} \). The matching operation is performed at the granularity of a token which is a string over \( \Gamma \) consisting of \( y \) nucleotides, i.e., in \( \Gamma^y \). We assume \( y = 5 \), the minimum token size to provide high fidelity [3]. Each nucleotide can be encoded as a 2-bit symbol where \( A = "00" \), \( C = "01" \), \( G = "10" \), and \( T = "11" \).

Mathematically, ordered set of all possible size five tokens is \( S = \{\Gamma^y_i | 0 < i < 1023 \land \Gamma^y_i \subset \text{\texttt{CAAAA}} \} \) indexed by \( f : S \rightarrow i \in \mathbb{N}^+ \cup \{0\} \).

For each bin \( r_k \in R \) a bit-vector \( \vec{r}_k \) with 1024 locations is used shown in yellow in Fig. 1. Each bit in \( \vec{r}_k \) is indexed by \( f(\Gamma^y_i) \) which is 0 to 1023 for \( \text{AAATA} \) to \( \text{TTTTT} \) as discussed above. If token \( j \) exists in \( \vec{r}_k \), its corresponding bit (referred to as presence bit) in \( \vec{r}_k \) is set, i.e., \( r_k[j] = 1 \). In GRIM [4], each read \( q_i \in Q \) is matched against \( r_k \) on a token-by-token basis. For each token in \( q_i \), the relevant presence bit \( r_k[f(\text{token})] \) is accessed and, if set, a counter \( c_k \) is incremented. Once the relevant bits from \( \vec{r}_k \) are accessed, the accumulator \( c_k \) is compared to a predefined threshold \( T \). Only the bins \( r_k \) are selected for the seed extension if \( c_k > T \) and all other bins are discarded. That is, a bin \( r_k \) is selected for read \( q_i \) if \( \sum_{\text{tokens in } r_k} r_k[f(\text{token})] > T \).

A near-memory accelerator architectures where the memory layers store the token presence bits of the bins in \( R \mid k, r_k \in R \).

Assume the set of distinct tokens in a \( q_i \) is represented by \( \Theta \), i.e., \( \Theta(q_i) = \{\text{distinct tokens in } q_i\} \). ALPHA [9] stores the count information for each \( t \in \Theta \) in a small dedicated buffer called CountBuffer. After populating the CountBuffer in the preprocessing step, \( q_i \) is compared to the reference bins to compute the matching score. For a particular bin \( r_k \in R \), the accumulated sum is computed as \( \sum_{t \in \Theta(q_i)} \text{CountBuffer}(t) + r_k[f(t)] \).

Using the CountBuffer only rows with non-zero token counts are accessed as in Fig. 2. The first access is performed on Row0 while the last access is performed on Row_{1023}. Row_{4095} and Row_{4098} are accessed only once, and \( c_{k+} = 2 \forall r_k \in R \) whose presence bits matching AACTA and/or ATATA are set. The CountBuffer improvement can reduce RTM shifting to test \( r_k \) in token index order rather than order of appearance in \( q_i \). However, the CountBuffer alone is insufficient to minimize RTM shifting, which we address in the next section.

### 3 Shift and parallellism aware data mapping

This section explains our proposed filtering in racetrack memory methodology and architecture. FIRM implements DNA pre-alignment filtering [9] (see Section 2.2), using a novel data mapping customized to optimize data access patterns for RTM to maximize parallelism and minimize shifting overhead.

FIRM defines which \( r_k[f(t)] \) is mapped to a particular subarray, track, and domain in RTM. For RTM, the logical structure of subarray, row, and column is extended into track groups shown in Fig. 1. The track group is further partitioned by track and domain as a physical address as shown in Fig. 3(a). Mapping the bins and tokens requires logically using the lower 10-bits for the token address and the upper 8-bits for the bin address as in Fig. 3(b). In GRIM and ALPHA, the data mapping is done in a SUBARRAY-COL-ROW fashion for DRAM, as shown in Fig. 3(c). While this allows a column to represent a distinct bin, it requires subsequent tokens to be mapped into the same subarray which requires shifting and other memory activities such as activate and precharge to proceed sequentially. Instead we remap the reference genome to RTM by interleaving the bit-vectors across subarrays, i.e., \( r_k[0] \) is mapped to Row0 in Subarray0, \( r_k[1] \) in Subarray1, and \( r_k[1023] \) in Subarray1023 so

![Fig. 1: ALPHA filter hardware design and data mapping of 4096 bins (i.e., \( r_0 \) to \( r_{4095} \)) in \( R \) to Subarray0. The bottom-right of the figure shows how bit-vectors are organized in RTM tracks.](image1)

![Fig. 2: ALPHA filter row access sequence for an example \( q_i \) read assuming 64 domains per track.](image2)

![Fig. 3: Logical to physical address mapping comparison for ALPHA and FIRM.](image3)
that the shifting overhead is minimized as in Fig.3(d). This provides two important improvements in RTM. First, memory accesses can be pipelined, mitigating the shift and other memory delays. Additionally, as each Subarray stores the presence bit information of unique tokens, only Subarrays matching non-zero CountBuffer entries need to be accessed.

Fig. 4 shows in detail how FIRM interleaves each token across different subarrays. Consider a query read $q_i$ which contains $AAAA$, $AAACT$, $AAAGG$, and $AACTA$ as its first four non-zero tokens. We presume that the number of bins that are compared in parallel with a particular read $q_i$ is referred to as a *binset* which is equal to the row width. An *iteration* is the processing of all bins within a binset with $q_i$. Fig. 6(a) describes the row accesses in a direct implementation of the ALPHA filter on RTM, which we note all map to the same Subarray (see Fig.1). We note that the shifting delays plus ACT, RI, and PRE times are sequential, shown in Fig. 6(c). Thus, each iteration requires 28 shifts to process the first four tokens. In contrast, FIRM accesses $Row_0$ of the required Subarrays, which can pipeline accesses as shown in Fig. 6(d) requiring only one shift per access as in Fig. 6(b). In fact, shifting is not required until the ninth iteration when the Subarrays, starting with Subarray_2, are revisited. We use *preshifting* to overlap the shift latency with the computation to reduce the impact of shift latency on the runtime of pre-alignment filtering. As soon as a row is accessed, the port positions in the active Subarray are shifted and aligned to the following row. Note, preshifting does not interfere with row accesses performed on independent subarrays and hides the shift latency because the row request is guaranteed to be serviced later.

Once $q_i$ is compared to the entire reference genome, the track groups in the shifted subarrays must be reset to the first row to prepare for $q_{i+1}$. Note that, unlike the conventional mapping, in the proposed mapping, only those subarrays are accessed whose tokens have non-zero values in the CountBuffer (for a particular read). These subarrays are preshifted to the first row after accessing the last row in the track group to avoid any latency penalty.

Although preshifting can effectively hide the track group reset delay, they still contribute to the RTM energy consumption. To overcome this, we can add a second access port to allow a circular, unlimited single shift buffer. As shown in Fig. 7, this allows each track group to avoid resetting shifts similar to prior work using RTM to store looped instructions [16]. In the reset position (Fig. 6) the track group starts with the data shifted down with local $Row_0$ aligned with access port as shown in green. The first half of the data is read by shifting up by one for each subsequent read until the track reaches the bottom position (Fig. 8b). The second half of the data is stored in reverse order so it can be accessed by the second access point shifting up between accesses. Once the last element is read, now the track group is back in the reset position. As a result, no additional reset shifts are required to prepare for $q_{i+1}$ cutting the required shifts in half. The additional port per track increases the energy consumption, but the energy savings due to shift reduction outweighs this overhead.

4 Evaluation

For evaluation, we use four pair-end short read genomes from the 1000 Genome Project [17]. We assume a 100-nucleotide query and reference bins, with a token size of 5. Memory (DRAM and RTM) and accelerator architecture parameters including latency, and energy/power parameters are listed in Table 3 using DRAMSpec [18] for DRAM, DESTINY [19] for RTM, and Cadence RTL-Compiler Synthesis. RTM is evaluated for 64 domains per track. For system-level shifts, latency and energy estimation we use RTSim [20], an RTM simulator extended from NVMain [21]. We compare the following systems in our evaluation:

- **GRIM**: The DRAM based GRIM filter [4], shown in Fig. 1
- **ALPHA**: The recently proposed DRAM based ALPHA filter design with preprocessing [9], cf. Section 2.2
- **ALPHA-RTM**: The ALPHA filter design applied to RTM.
- **FIRM**: The FIRM filter, cf. Section 3
- **FIRMPR**: FIRM extended with the preshifting.
- **FIRMSUS**: FIRMSUS with circular unlimited single-shifts.
TABLE 2: Energy and latency values of DRAM [18] RTM [19] and CMOS accelerator using 32 nm technology and 1 GHz clock.

| General Memory Parameters | DRAM Parameters | RTM Parameters – Track Length 64 domains |
|---------------------------|----------------|-----------------------------------------|
| Memory size               | 1 GB           | 1964                                    |
| Subarrays                 | 8192           | 1.25                                    |
| Rows per Subarray         | 1024           | 0.40                                    |
| Cols per Subarray         | 4096           | 410                                     |
| Tracks per DBS            | 512            | 20-8-8-8-8-8-8-8-8-8                   |
|                           |                | 193-208-64-64-64-64-64-64-64           |

Reference Genome

CMOS Accelerator – Accumulates 1 Row (4096 bins) per cycle

| Bins in R                              | Dynamic Energy [pJ/bit] | Leakage Power [mW] |
|----------------------------------------|-------------------------|--------------------|
| 33,554,032                              | 1785                    | 16.40              |

**Fig. 7:** Normalized runtime and energy breakdown.

Fig. 7 compares the energy and runtime of different prefiltering solutions normalized to GRIM. Just replacing ALPHA's DRAM with RTM increases runtime and energy dominated by shift cost. FIRM's exploiting subarray parallelism [22] replaces a single shift for frequent long shifts when successive RTM rows are accessed, reducing shifts by 84% over ALPHA-RTM, reducing average runtime over ALPHA-RTM by 75% and over ALPHA by 63%. This helps FIRM provide an energy savings of 43% over ALPHA when combined with intrinsically reduced RTM background power.

Applying preshifting (FIRMPR) further improves the average runtime by 5.3% compared to FIRM. Applying the unlimited single-shift technique (FIRMUS) achieves the same runtime while reducing overall energy by 2.8% over FIRMPR. FIRMUS energy savings are attenuated by adding a second access port.

5 CONCLUSIONS

In this paper, we explore a die-stacked RTM design for implementing a pre-alignment seed location filtering algorithm. We motivate our design through an example that shows why existing optimizations for DRAM-based systems are not directly applicable to RTM-based designs. We propose a novel filtering in Racetrack memory scheme that provides novel data layout, preshifting, and circular buffers to significantly reduce shift operations in RTM. Our experimental evaluations show that our proposal improves performance by more than 3X while reducing energy to less than half of the state of the art approach.

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