AnySeq/GPU: A Novel Approach for Faster Sequence Alignment on GPUs

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Overview

The paper introduces **AnySeq/GPU**, a fast sequence alignment library optimized for GPUs. It improves performance by reducing memory accesses using **warp shuffles** and **half precision arithmetic**, and it uses the **AnyDSL compiler** for efficient GPU code generation. The library achieves up to **3.8 TCUPS**, outperforming previous GPU-based aligners like GASAL2 and NVBIO by up to **19.2x**. It runs efficiently on both NVIDIA and AMD GPUs and is open-source.

Motivation

Sequence alignment is essential in bioinformatics, especially with the rapid growth of **Next-Generation Sequencing (NGS)** data. Traditional alignment algorithms like **Needleman-Wunsch** and **Smith-Waterman** use dynamic programming (DP) and have high time complexity, making them slow for large-scale NGS data (both short and long reads). While many alignment tools have been developed for **CPUs, GPUs, and FPGAs**, current GPU-based tools often suffer from: Inefficient memory access patterns, Lack of performance portability across different sequence lengths and alignment types, Limited optimization to only specific CUDA-enabled GPUs. To overcome these limitations, the authors propose AnySeq/GPU, an optimized GPU-based extension of the AnySeq library.

Methodology and Key Contributions

1. **Unique Parallelization Strategy:** Introduces a new fine grained GPU Parallelization technique using **warp intrinsics** and a novel **DP Matrix Partitioning** scheme that handles batches with varying sequence lengths efficiently.

2. **Hardware Independent Implementation:** It leverages **AnyDSL**, a domain specific language framework which is used to generate optimized kernels for both **NVIDIA** and **AMD** GPUs.