QUETZAL: Vector Acceleration Framework for Modern Genome Sequence Analysis Algorithms

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Accelerating the Genome Analysis Pipeline

CPU/GPU

- Flexible.
- Low entry-cost.
- Generality and flexibility limits their performance.

Custom Accelerator

- High performance and Energy efficiency.
- They are tight to a single algorithm or a single sequence length.
- High design and entry-cost.

Answer:
We proposed QUETZAL, a hardware-software co-designed vector acceleration framework.
QUETZAL supports bit-encoded operations without extra instructions.

QBUFFERs reduce the access latency from 22 cycles to only 2 cycles.

QUETZAL features custom hardware to calculate the maximum number of exact matches.
• QUETZAL significantly outperforms all the evaluated algorithms.
• **Speedup**: 5.7x better performance compared to other vectorized algorithms.
• QUETZAL is capable of accelerating both modern and classical genome sequence analysis algorithms.
Evaluation

• When processing long reads, QUETZAL outperforms by 2.7x and 1.1x for WFA and Smith-Waterman (Classical algorithm), respectively.