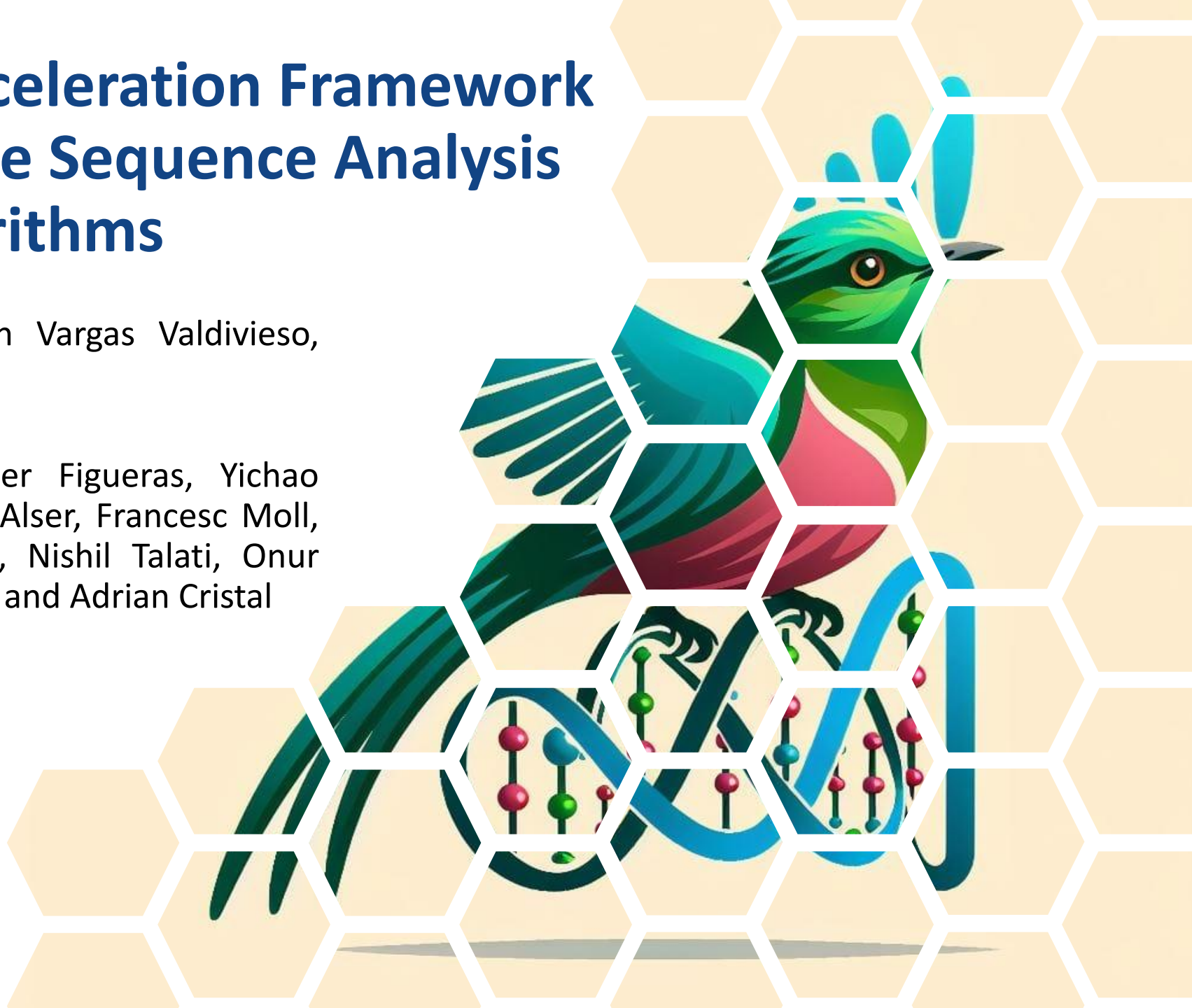
# QUETZAL: Vector Acceleration Framework for Modern Genome Sequence Analysis Algorithms

**Lead authors: Julian Pavon**, Ivan Vargas Valdivieso, Carlos Rojas, Cesar Hernandez

**Co-authors:** Mehmet Aslan, Roger Figueras, Yichao Yuan, Joel Lindegger, Mohammed Alser, Francesc Moll, Santiago Marco Sola, Oguz Ergin, Nishil Talati, Onur Mutlu, Osman Unsal, Mateo Valero and Adrian Cristal



ETH zürich

TOBB ETÜ
Ekonomi ve Teknoloji Üniversitesi

BSC Barcelona Supercomputing Center
Centro Nacional de Supercomputación

University of Michigan

# Fun facts

**QUETZAL Team:**




In the initial QUETZAL team we were all Mexicans.

In ancient cultures in Mexico, QUETZAL was a holy bird.

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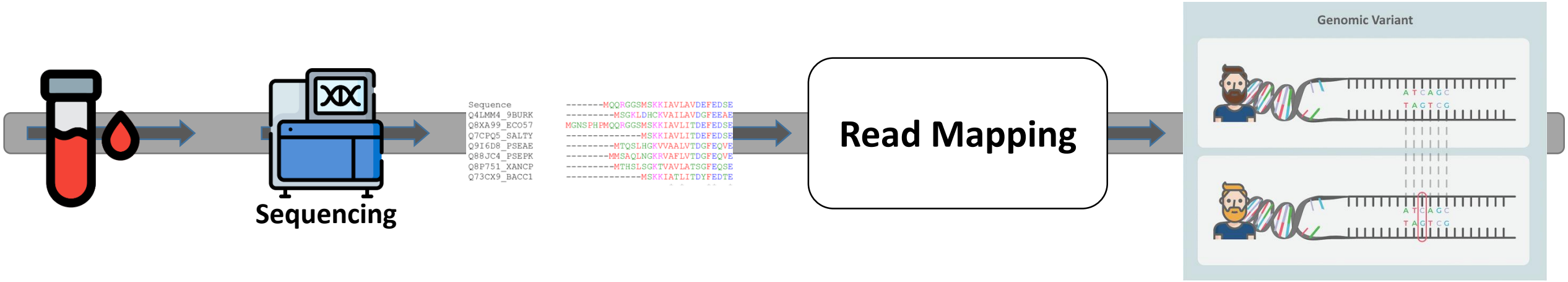
# Genome Analysis Pipeline



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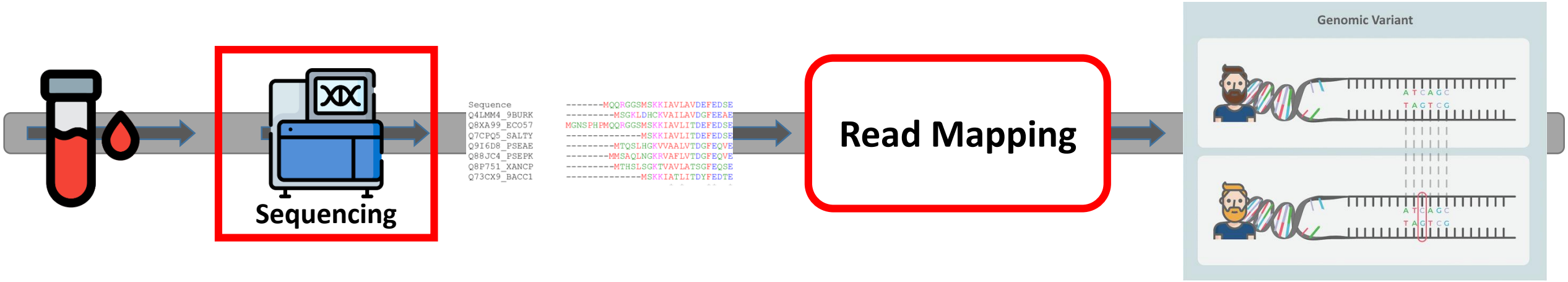

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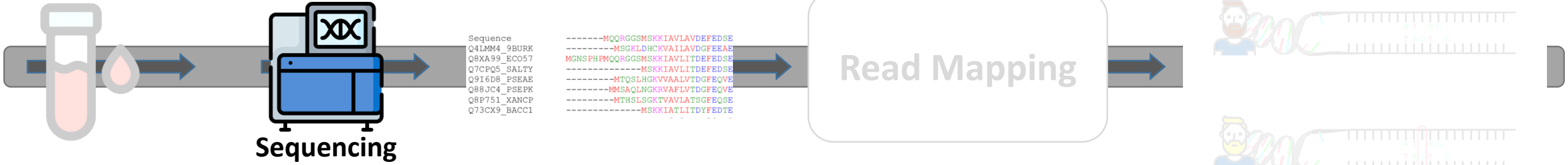


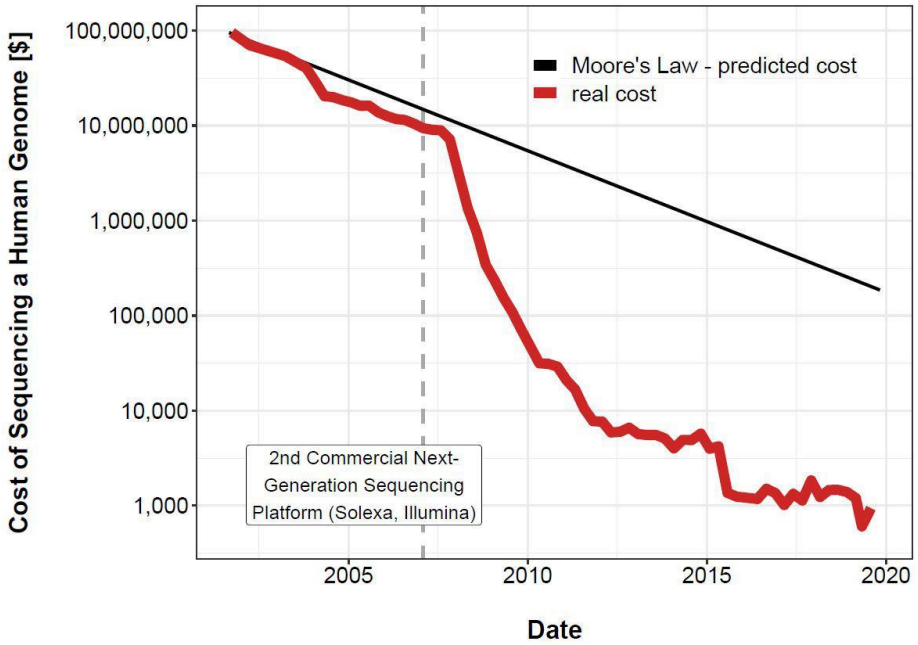


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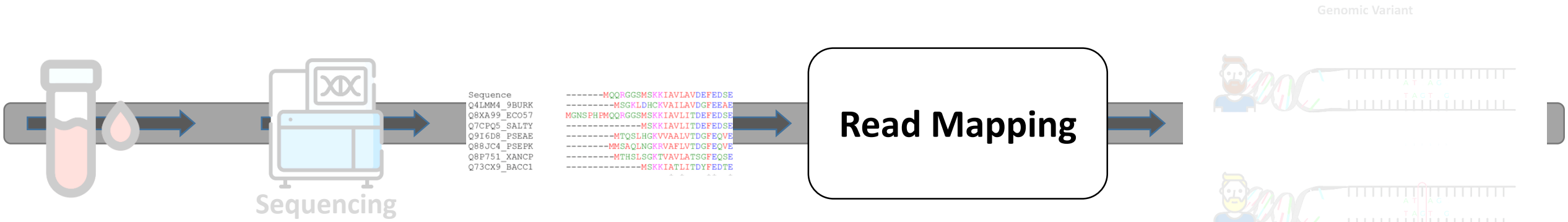





| | Reference-guided assembly | De-novo assembly |
|---|---|---|
| Short reads (~100bp) | ~200 CPU hours | ~2,000 CPU hours |
| Long reads (~10Kbp) | ~5,000 CPU hours | ~60,000 CPU hours |

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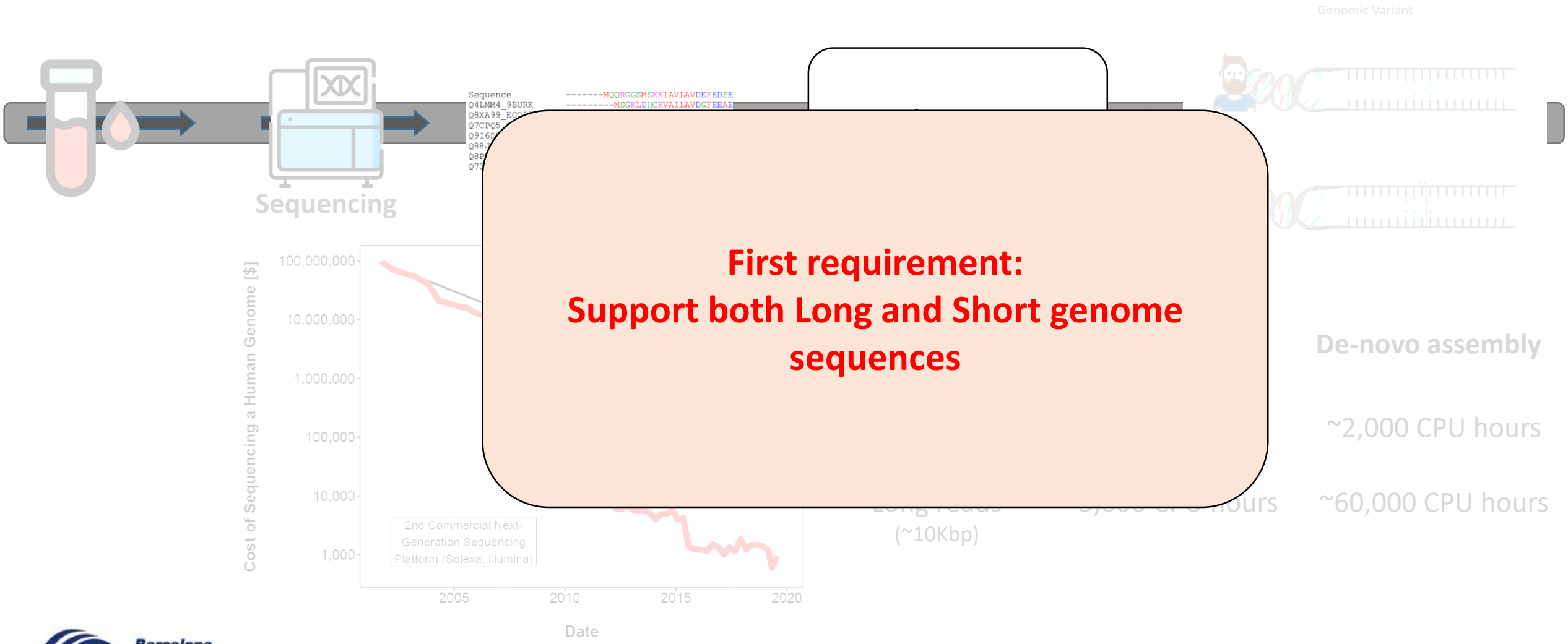


**First requirement:**
**Support both Long and Short genome sequences**

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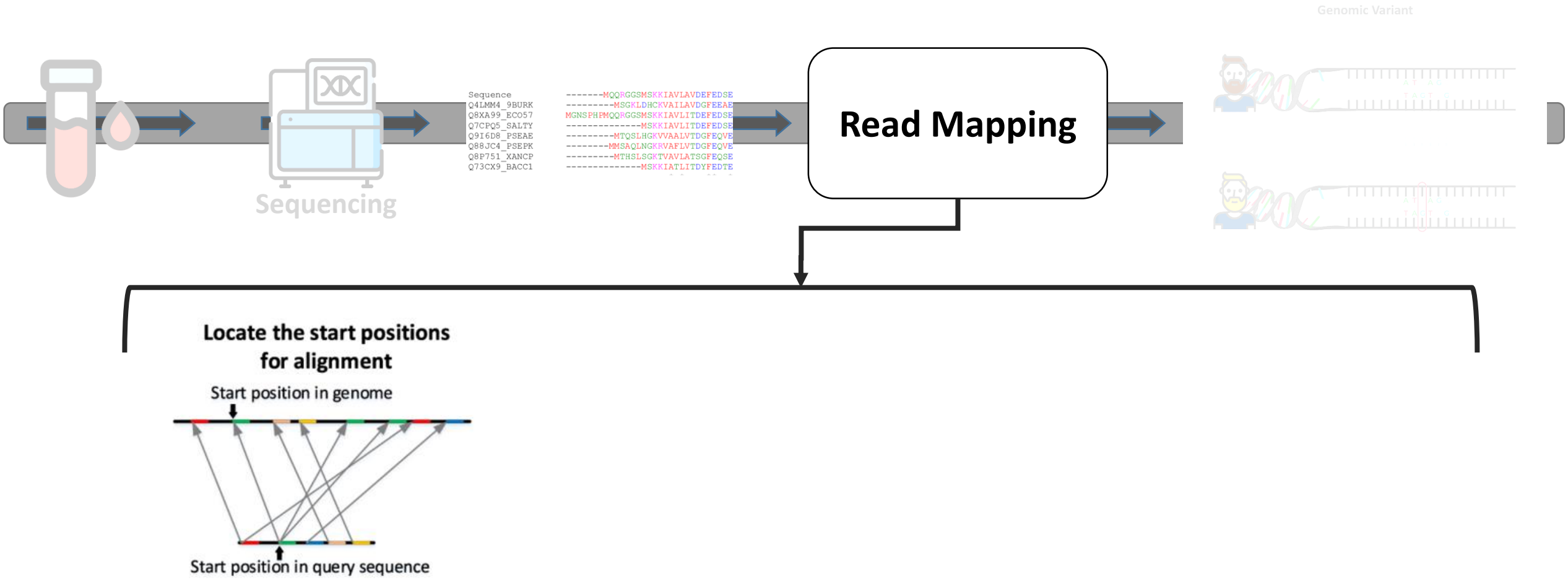
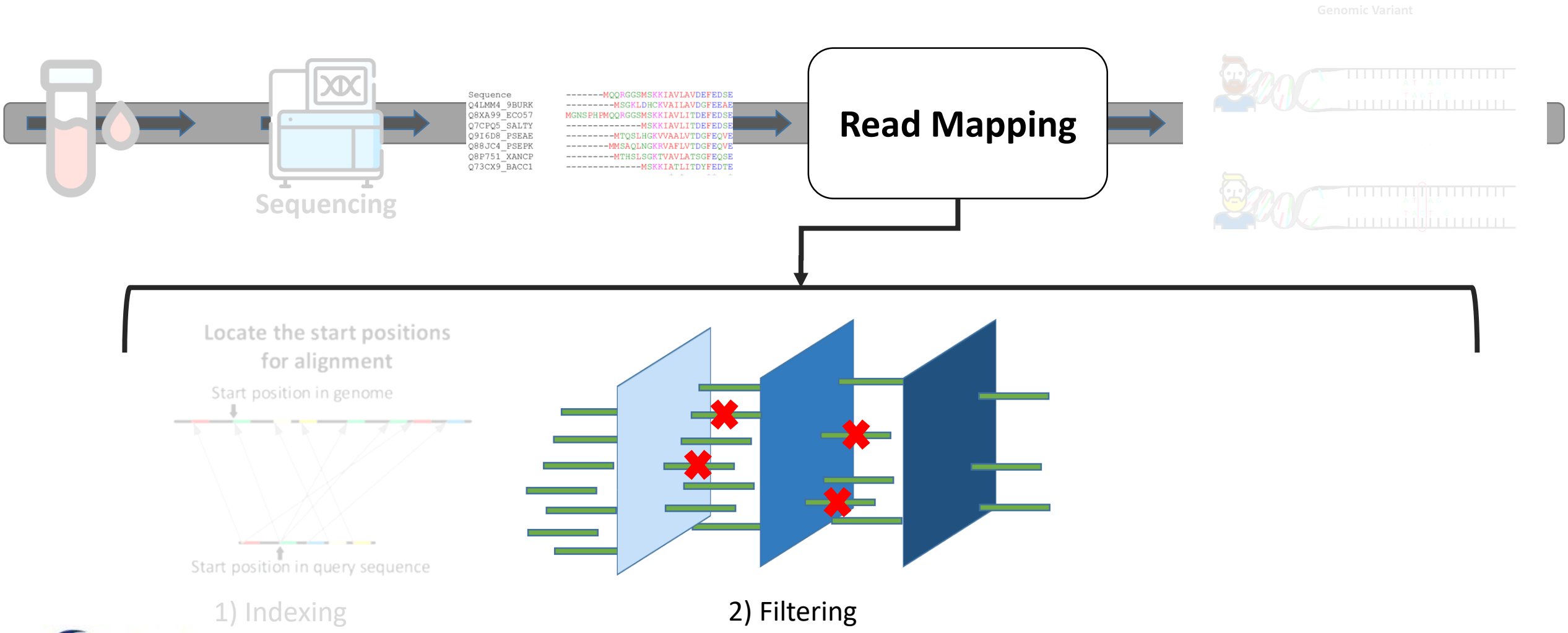
# Genome Analysis Pipeline




1) Indexing

# Genome Analysis Pipeline



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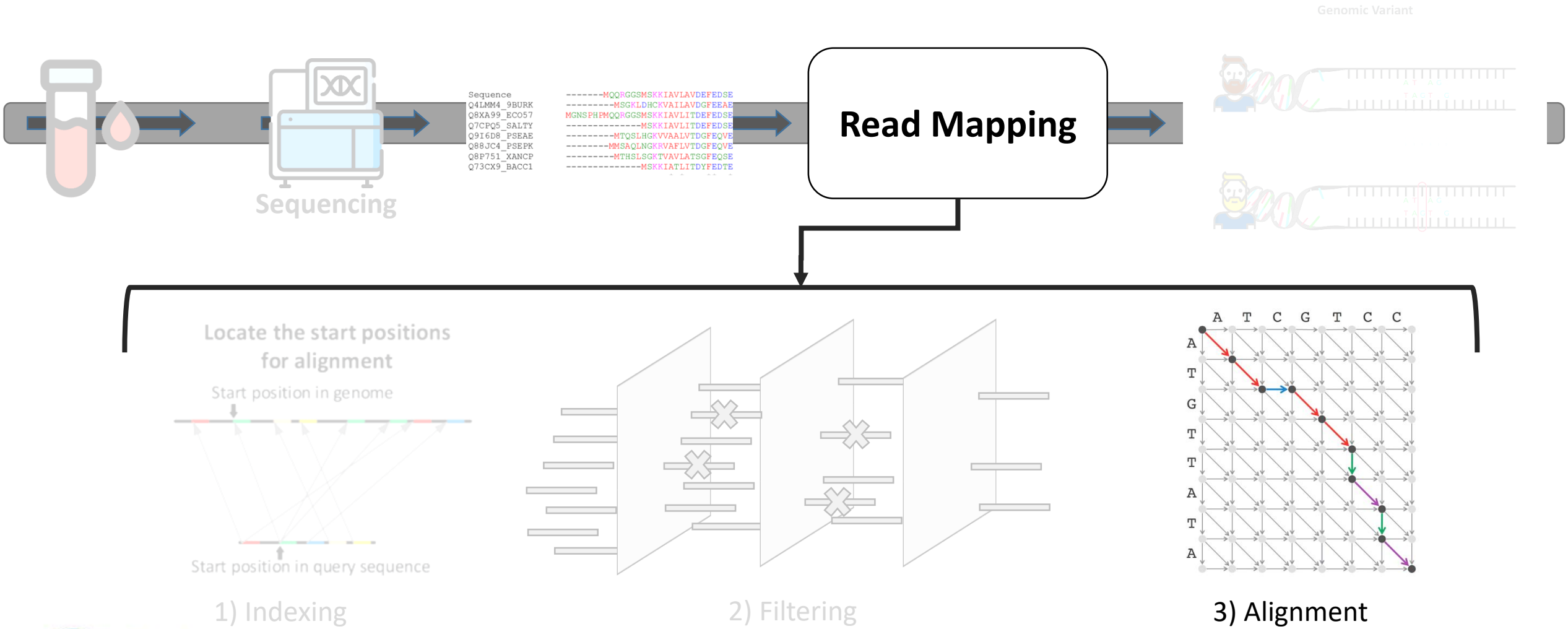


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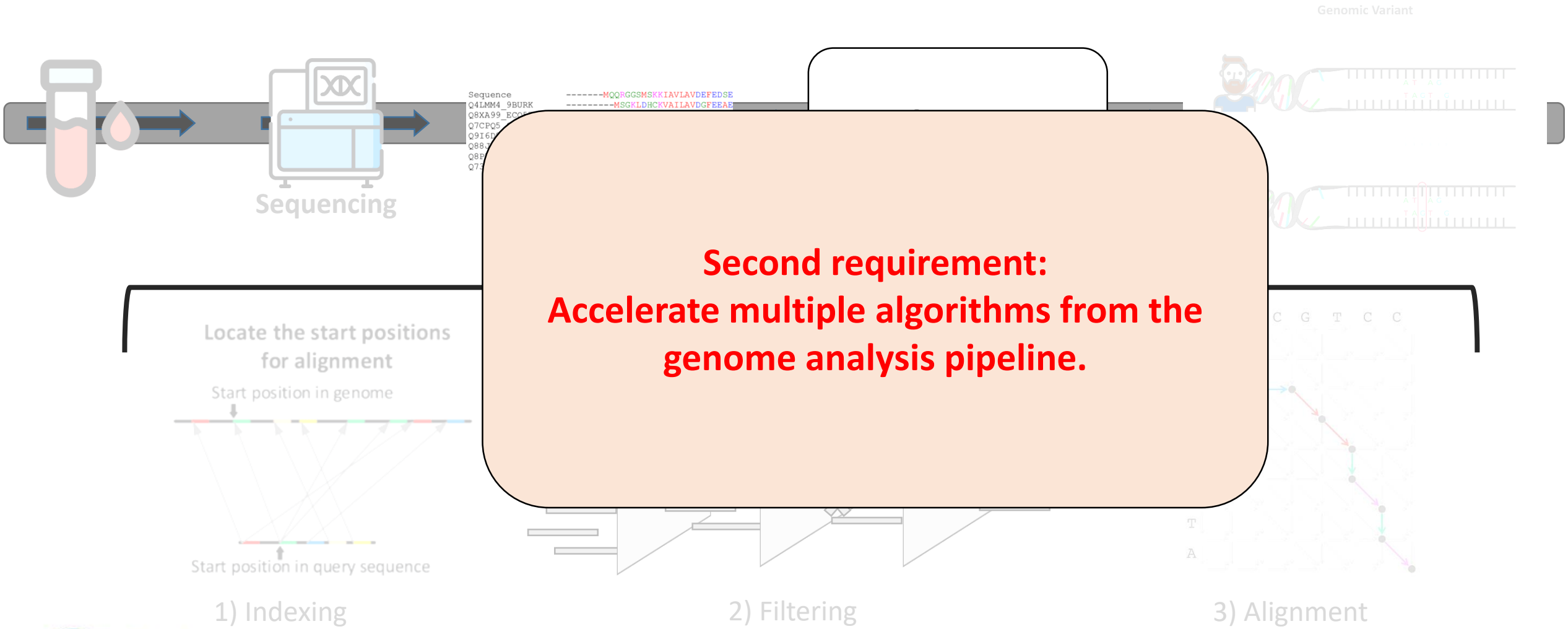
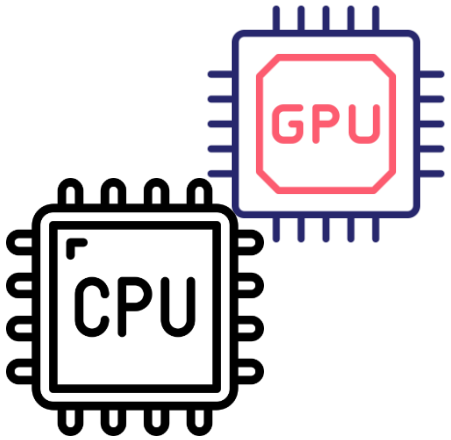
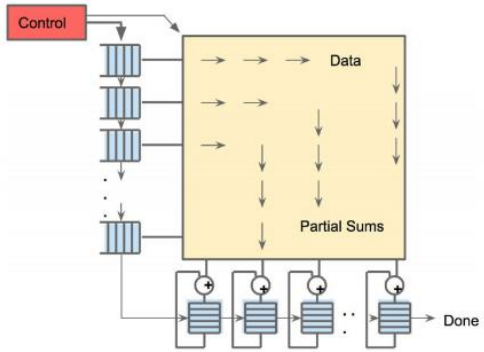



**Second requirement:**
**Accelerate multiple algorithms from the genome analysis pipeline.**

# Accelerating the Genome Analysis Pipeline

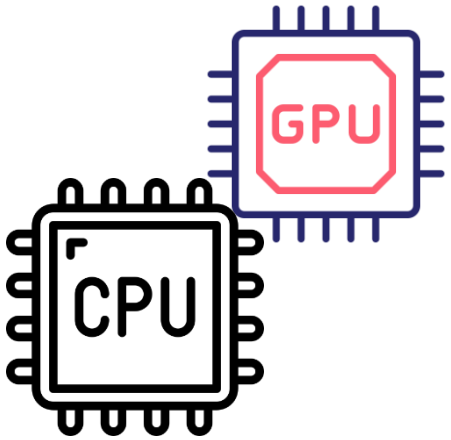



**CPU/GPU**



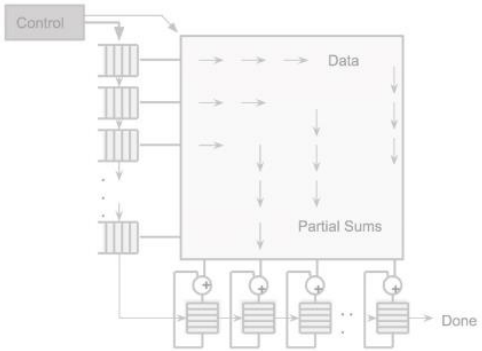

**Custom Accelerator**

# Accelerating the Genome Analysis Pipeline




**CPU/GPU**

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

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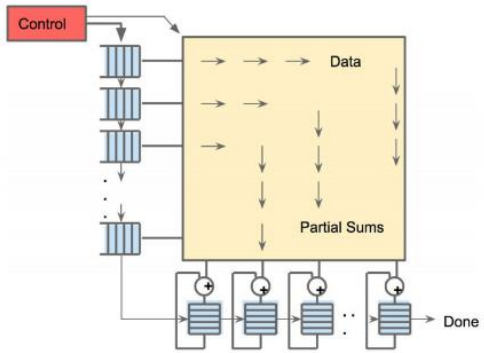


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- High performance and Energy efficiency.
- They are tight to a single algorithm or a single sequence length.
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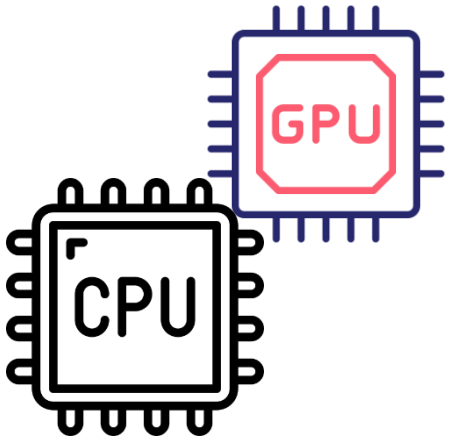


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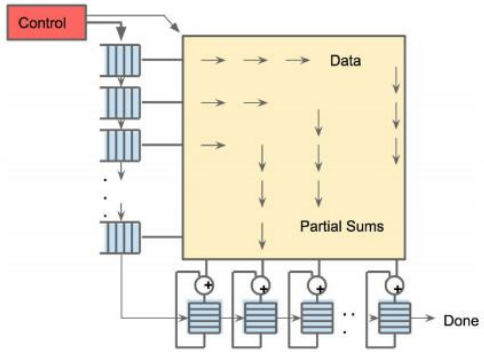


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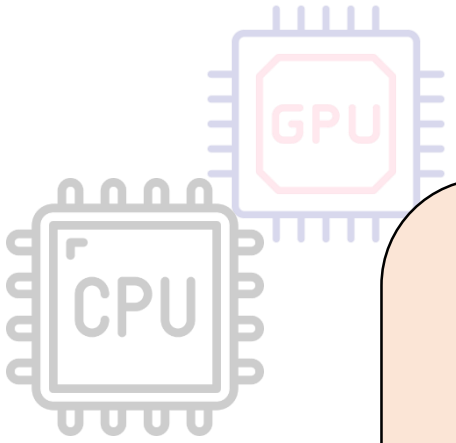


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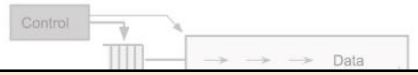


hm

¿?

**Answer:**
**We proposed QUETZAL, a hardware-software co-designed vector acceleration framework**

# Key Contributions

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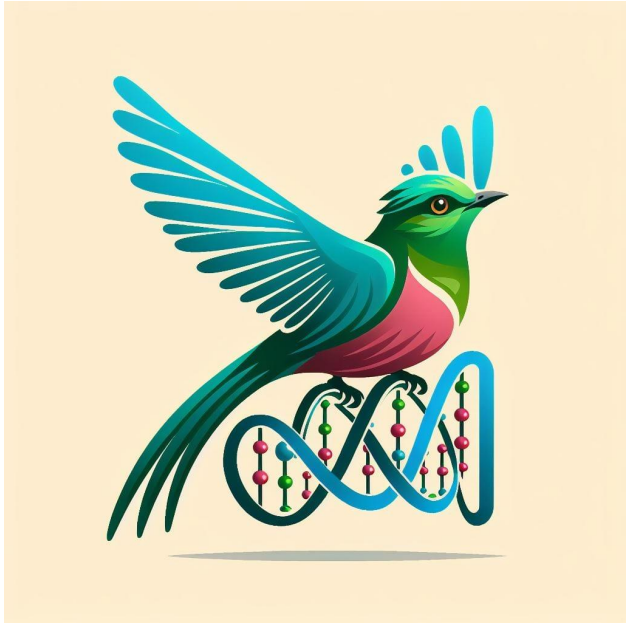
- QUETZAL addresses the bottlenecks from vector architectures when processing genome sequence analysis workloads.



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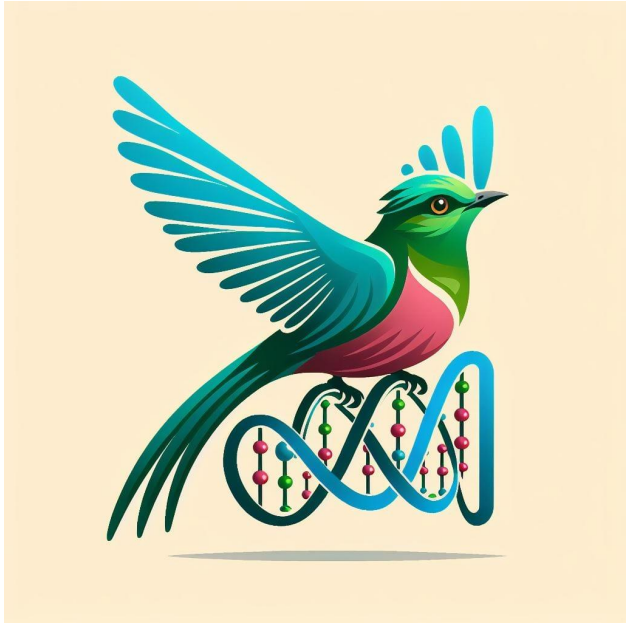
- QUETZAL addresses the bottlenecks from vector architectures when processing genome sequence analysis workloads.

- A CPU featuring QUETZAL, achieves 5.7x better performance compared to the baseline CPU architecture.



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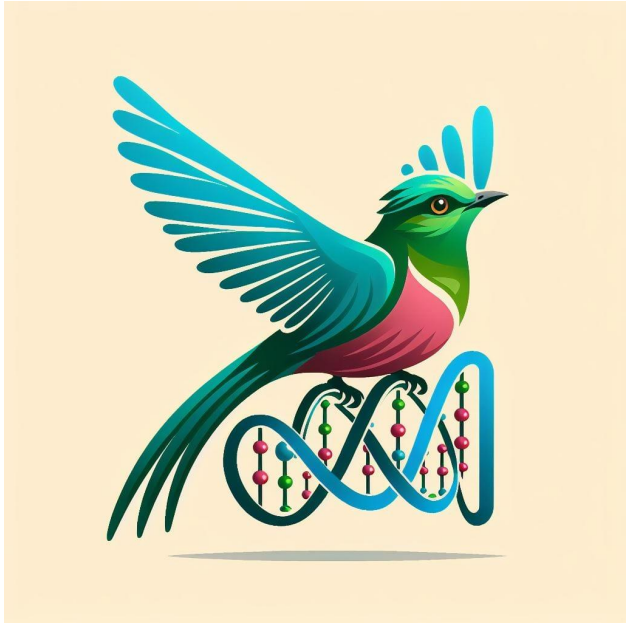
- QUETZAL addresses the bottlenecks from vector architectures when processing genome sequence analysis workloads.
- A CPU featuring QUETZAL, achieves 5.7x better performance compared to the baseline CPU architecture.
- QUETZAL outperforms GPUs when processing long genome sequences.



# Outline

1. Introduction and motivation
2. Background
   a) Modern Genome Analysis Algorithms
   b) Bottlenecks
3. QUETZAL
   a) Insights and Functionality
4. Evaluation
5. Conclusion

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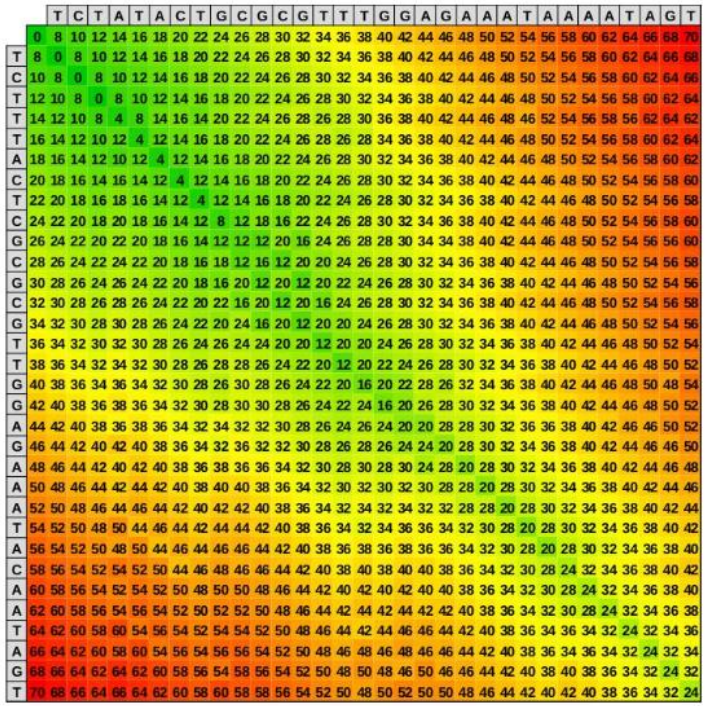
# Modern Genome Analysis Algorithms



| | | T | C | T | A | T | A | C | T | G | C | G | C | G | T | T | T | G | G | A | G | A | A | A | T | A | A | A | A | T | A | G | T |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 0 | 8 | 10 | 12 | 14 | 16 | 18 | 20 | 22 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 | 58 | 60 | 62 | 64 | 66 | 68 | 70 |
| T | 8 | 0 | 8 | 10 | 12 | 14 | 16 | 18 | 20 | 22 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 | 58 | 60 | 62 | 64 | 66 | 68 |
| C | 10 | 8 | 0 | 8 | 10 | 12 | 14 | 16 | 18 | 20 | 22 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 | 58 | 60 | 62 | 64 | 66 |
| T | 12 | 10 | 8 | 0 | 8 | 10 | 12 | 14 | 16 | 18 | 20 | 22 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 | 58 | 60 | 62 | 64 |
| T | 14 | 12 | 10 | 8 | 4 | 8 | 14 | 16 | 14 | 20 | 22 | 24 | 26 | 28 | 26 | 28 | 30 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 46 | 52 | 54 | 56 | 58 | 56 | 62 | 64 | 62 |
| T | 16 | 14 | 12 | 10 | 12 | 4 | 12 | 14 | 16 | 18 | 20 | 22 | 24 | 26 | 28 | 26 | 28 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 | 58 | 60 | 62 | 64 |
| A | 18 | 16 | 14 | 12 | 10 | 12 | 4 | 12 | 14 | 16 | 18 | 20 | 22 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 | 58 | 60 | 62 |
| C | 20 | 18 | 16 | 14 | 16 | 14 | 12 | 4 | 12 | 14 | 16 | 18 | 20 | 22 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 | 58 | 60 |
| T | 22 | 20 | 18 | 16 | 18 | 16 | 14 | 12 | 4 | 12 | 14 | 16 | 18 | 20 | 22 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 | 58 |
| C | 24 | 22 | 20 | 18 | 20 | 18 | 16 | 14 | 12 | 8 | 12 | 18 | 16 | 22 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 | 58 | 60 |
| G | 26 | 24 | 22 | 20 | 22 | 20 | 18 | 16 | 14 | 12 | 12 | 12 | 20 | 16 | 24 | 26 | 28 | 28 | 30 | 34 | 34 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 | 56 | 60 |
| C | 28 | 26 | 24 | 22 | 24 | 22 | 20 | 18 | 16 | 18 | 12 | 16 | 12 | 20 | 20 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 | 58 |
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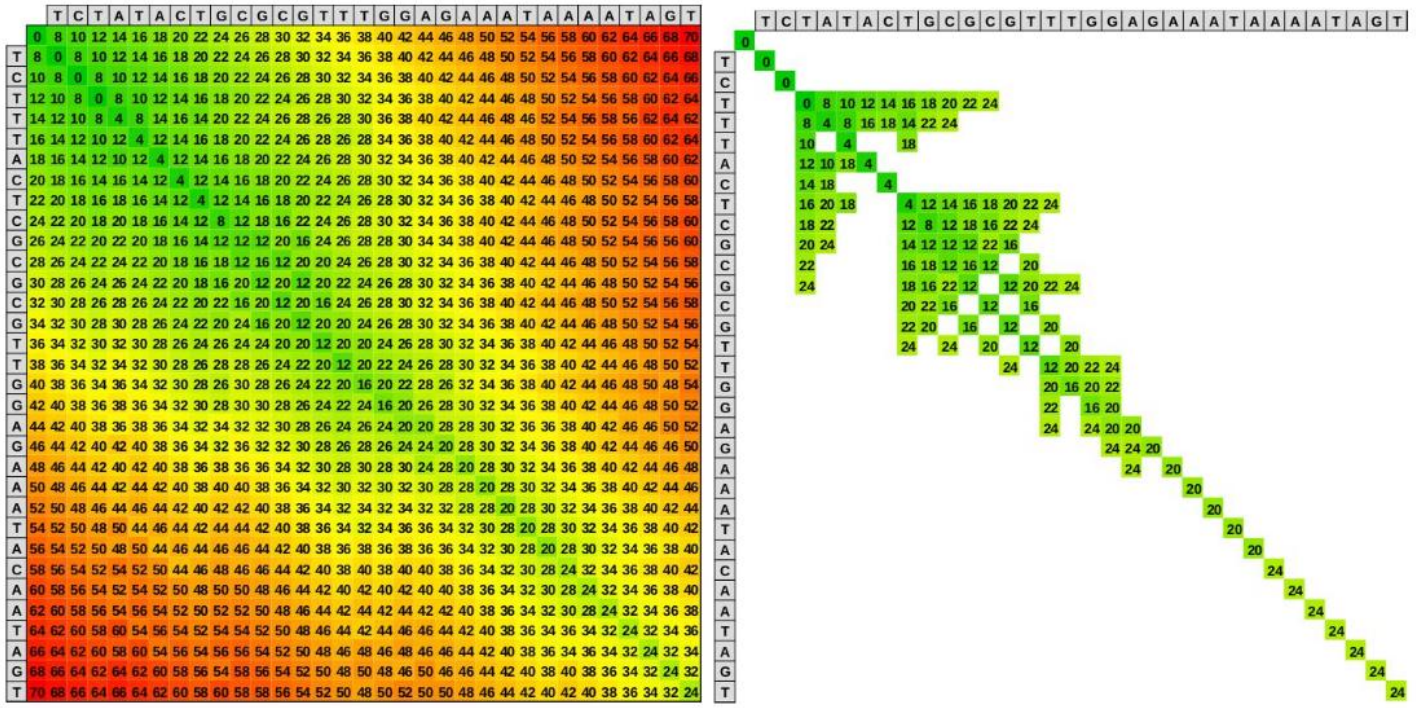
| C | 32 | 30 | 28 | 26 | 28 | 26 | 24 | 22 | 20 | 22 | 16 | 20 | 12 | 20 | 16 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 | 58 |
| G | 34 | 32 | 30 | 28 | 30 | 28 | 26 | 24 | 22 | 20 | 24 | 16 | 20 | 12 | 20 | 20 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 | 56 |
| T | 36 | 34 | 32 | 30 | 32 | 30 | 28 | 26 | 24 | 26 | 24 | 24 | 20 | 20 | 12 | 20 | 20 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 | 54 |
| T | 38 | 36 | 34 | 32 | 34 | 32 | 30 | 28 | 26 | 28 | 28 | 26 | 24 | 22 | 20 | 12 | 20 | 22 | 24 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 |
| G | 40 | 38 | 36 | 34 | 36 | 34 | 32 | 30 | 28 | 26 | 30 | 28 | 26 | 24 | 22 | 20 | 16 | 20 | 22 | 28 | 26 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 48 | 54 |
| G | 42 | 40 | 38 | 36 | 38 | 36 | 34 | 32 | 30 | 28 | 30 | 30 | 28 | 26 | 24 | 22 | 24 | 16 | 20 | 26 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 | 50 | 52 |
| A | 44 | 42 | 40 | 38 | 36 | 38 | 36 | 34 | 32 | 34 | 32 | 32 | 30 | 28 | 26 | 24 | 26 | 24 | 20 | 20 | 28 | 28 | 30 | 32 | 36 | 36 | 38 | 40 | 42 | 46 | 46 | 50 | 52 |
| G | 46 | 44 | 42 | 40 | 42 | 40 | 38 | 36 | 34 | 32 | 36 | 32 | 32 | 30 | 28 | 26 | 28 | 26 | 24 | 24 | 20 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 46 | 50 |
| A | 48 | 46 | 44 | 42 | 40 | 42 | 40 | 38 | 36 | 38 | 36 | 36 | 34 | 32 | 30 | 28 | 30 | 28 | 30 | 24 | 28 | 20 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 | 48 |
| A | 50 | 48 | 46 | 44 | 42 | 44 | 42 | 40 | 38 | 40 | 40 | 38 | 36 | 34 | 32 | 30 | 32 | 30 | 32 | 30 | 28 | 28 | 20 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | 46 |
| A | 52 | 50 | 48 | 46 | 44 | 46 | 44 | 42 | 40 | 42 | 42 | 40 | 38 | 36 | 34 | 32 | 34 | 32 | 32 | 32 | 28 | 28 | 20 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 | 44 | |
| T | 54 | 52 | 50 | 48 | 50 | 44 | 46 | 44 | 42 | 44 | 44 | 42 | 40 | 38 | 36 | 34 | 32 | 34 | 36 | 36 | 34 | 32 | 30 | 28 | 20 | 28 | 30 | 32 | 34 | 36 | 38 | 40 | 42 |
| A | 56 | 54 | 52 | 50 | 48 | 50 | 44 | 46 | 44 | 46 | 46 | 44 | 42 | 40 | 38 | 36 | 38 | 36 | 38 | 36 | 36 | 34 | 32 | 30 | 28 | 20 | 28 | 30 | 32 | 34 | 36 | 38 | 40 |
| C | 58 | 56 | 54 | 52 | 54 | 52 | 50 | 44 | 46 | 48 | 46 | 46 | 44 | 42 | 40 | 38 | 40 | 38 | 40 | 40 | 38 | 36 | 34 | 32 | 30 | 28 | 24 | 32 | 34 | 36 | 38 | 40 | 42 |
| A | 60 | 58 | 56 | 54 | 52 | 54 | 52 | 50 | 48 | 50 | 50 | 48 | 46 | 44 | 42 | 40 | 42 | 40 | 42 | 40 | 40 | 38 | 36 | 34 | 32 | 30 | 28 | 24 | 32 | 34 | 36 | 38 | 40 |
| A | 62 | 60 | 58 | 56 | 54 | 56 | 54 | 52 | 50 | 52 | 52 | 50 | 48 | 46 | 44 | 42 | 44 | 42 | 44 | 42 | 42 | 40 | 38 | 36 | 34 | 32 | 30 | 28 | 24 | 32 | 34 | 36 | 38 |
| T | 64 | 62 | 60 | 58 | 60 | 54 | 56 | 54 | 52 | 54 | 54 | 52 | 50 | 48 | 46 | 44 | 42 | 44 | 46 | 46 | 44 | 42 | 40 | 38 | 36 | 34 | 36 | 34 | 32 | 24 | 32 | 34 | 36 |
| A | 66 | 64 | 62 | 60 | 58 | 60 | 54 | 56 | 54 | 56 | 56 | 54 | 52 | 50 | 48 | 46 | 48 | 46 | 48 | 46 | 46 | 44 | 42 | 40 | 38 | 36 | 34 | 36 | 34 | 32 | 24 | 32 | 34 |
| G | 68 | 66 | 64 | 62 | 64 | 62 | 60 | 58 | 56 | 54 | 58 | 56 | 54 | 52 | 50 | 48 | 50 | 48 | 46 | 50 | 46 | 46 | 44 | 42 | 40 | 38 | 40 | 38 | 36 | 34 | 32 | 24 | 32 |
| T | 70 | 68 | 66 | 64 | 66 | 64 | 62 | 60 | 58 | 60 | 58 | 58 | 56 | 54 | 52 | 50 | 48 | 50 | 52 | 50 | 50 | 48 | 46 | 44 | 42 | 40 | 42 | 40 | 38 | 36 | 34 | 32 | 24 |

**Classical approach**

# Modern Genome Analysis Algorithms



**Classical approach** **Modern approach (WFA[1])**

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[1] Marco-sola et al., Fast gap-affine pairwise alignment using the wavefront algorithm, Bioinformatics, 2020.

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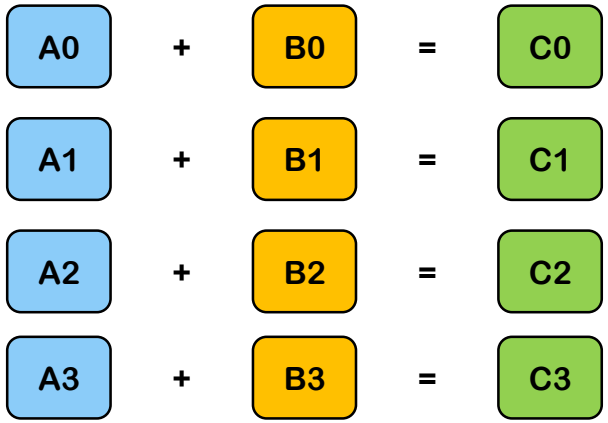


**Scalar Operation**

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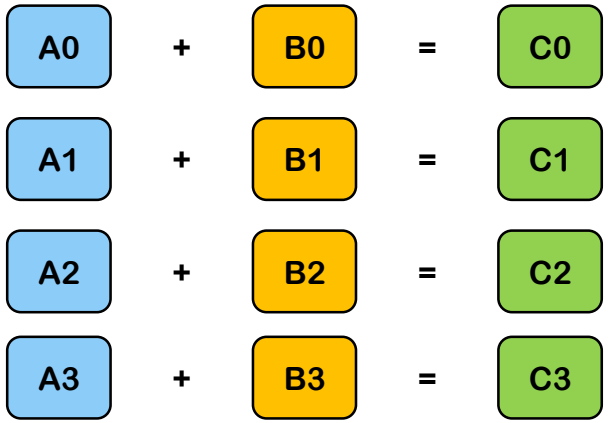
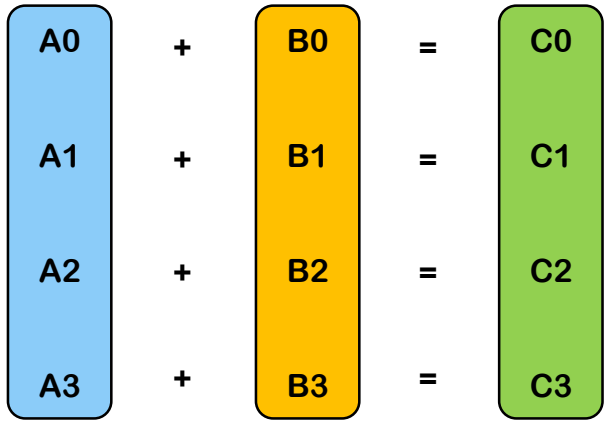
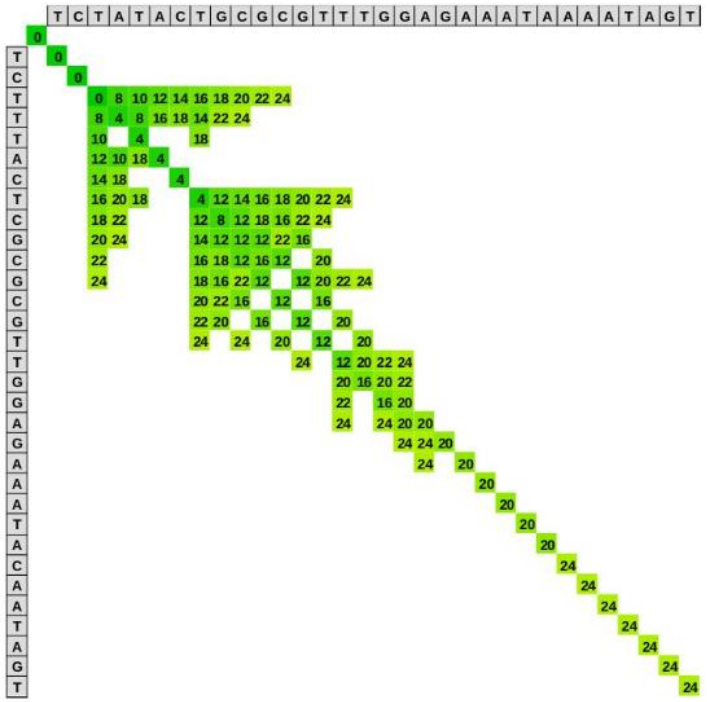



**Scalar Operation**




**Vector Operation**

# Bottlenecks for Vector Architectures

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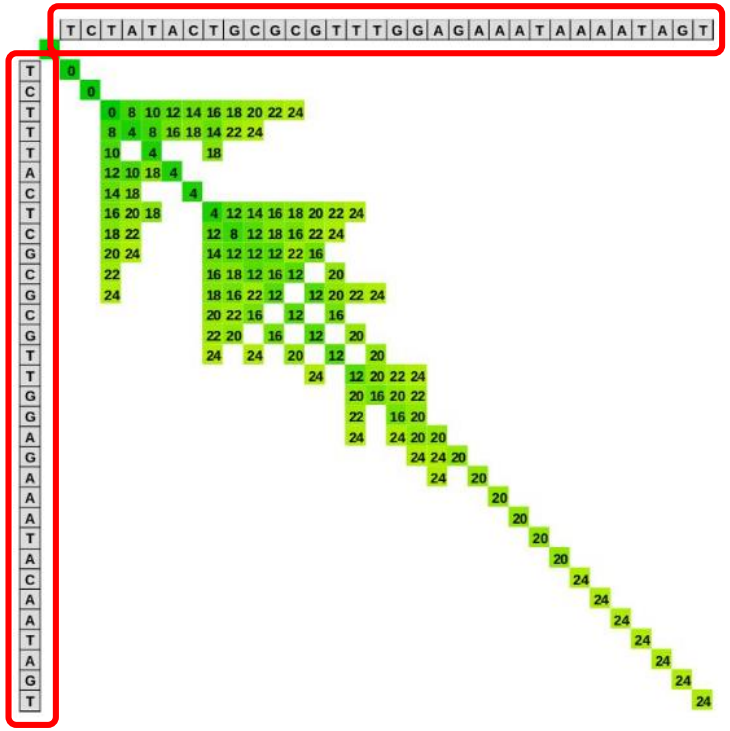


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# Bottlenecks for Vector Architectures

Memory

Pattern

| T | C | T | A | T | A | C | T | G | C | G | C | G | T | T | T |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|

Text

| T | C | T | T | T | A | C | T | C | G | C | G | C | G | T | T |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|

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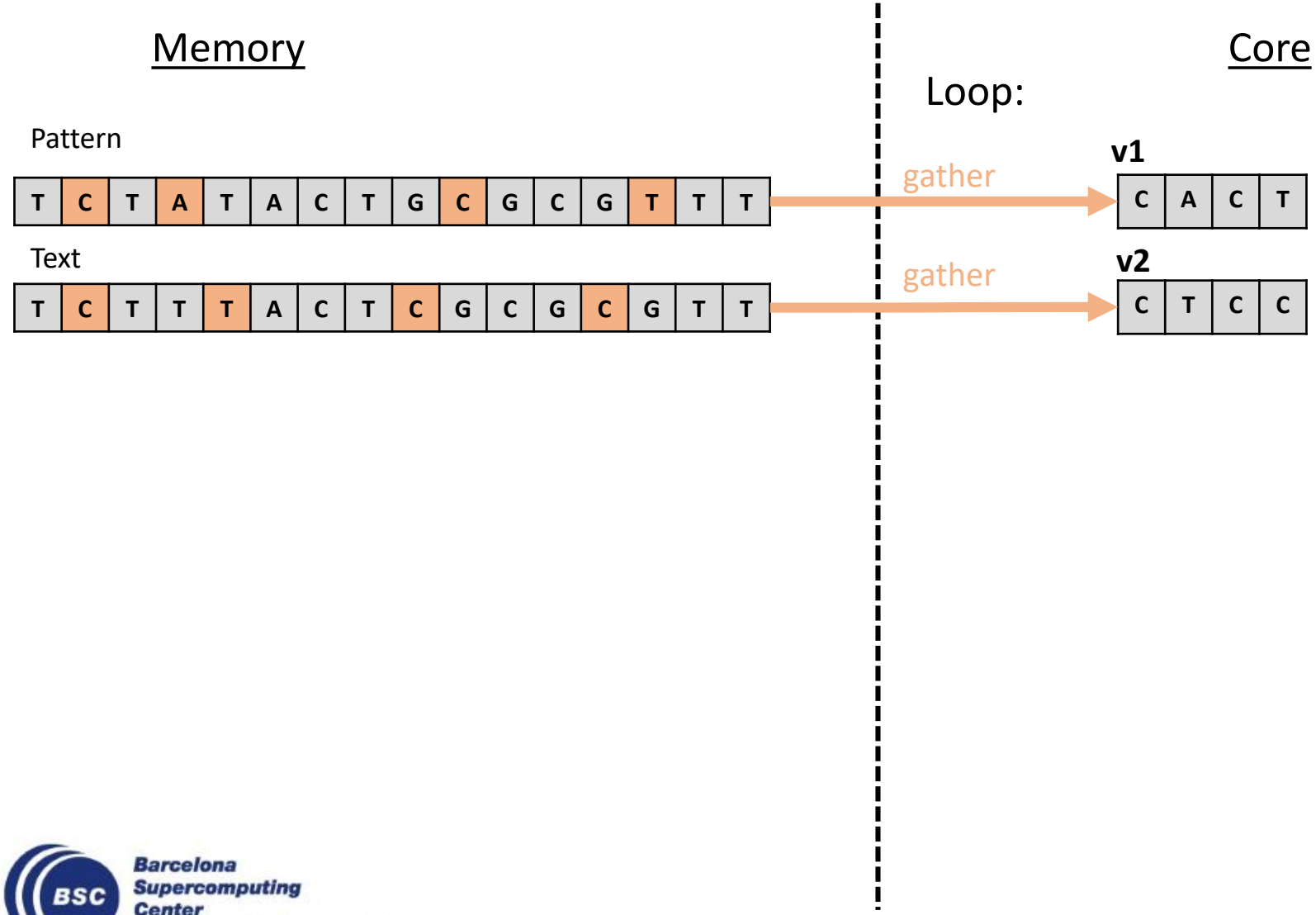

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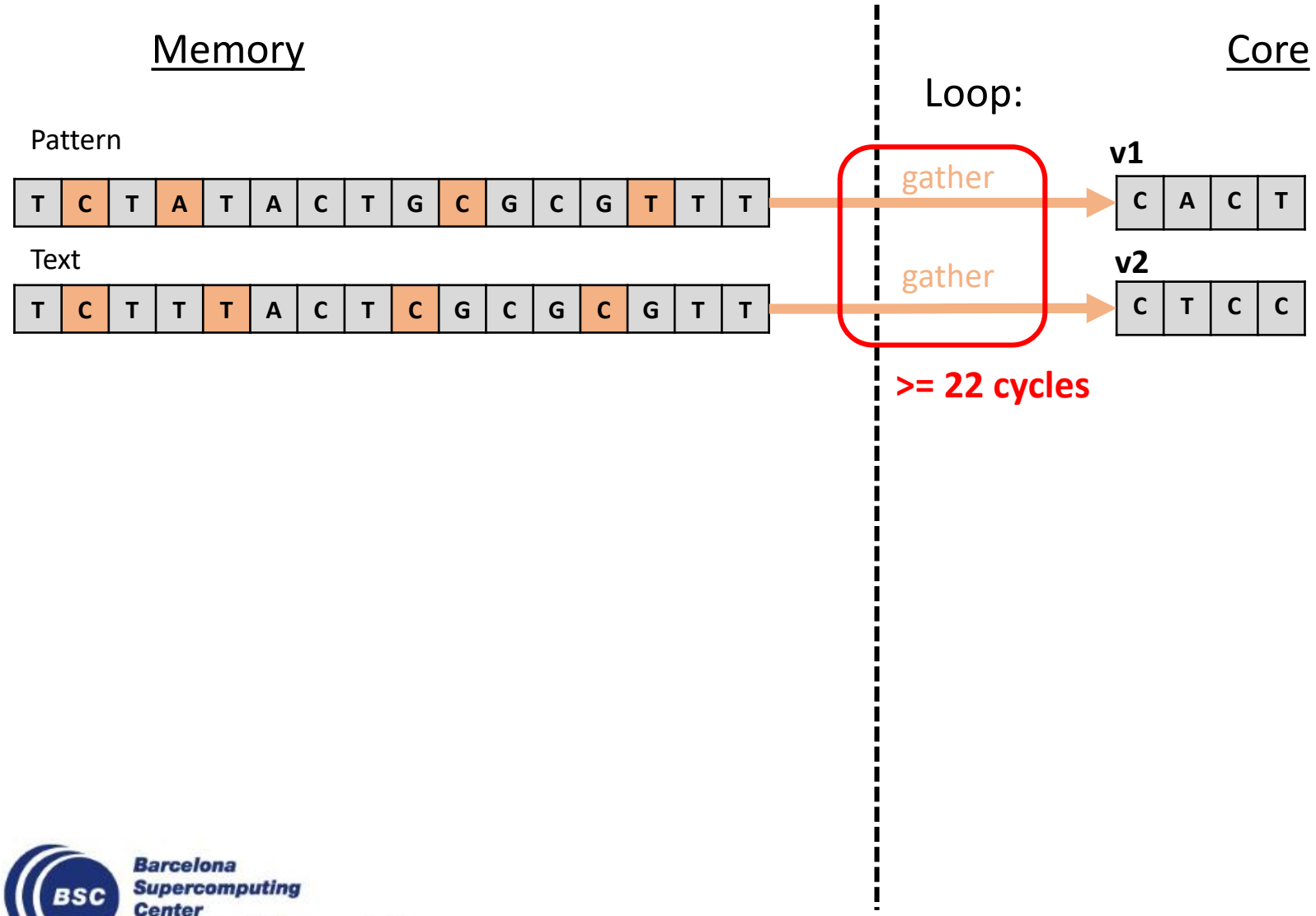


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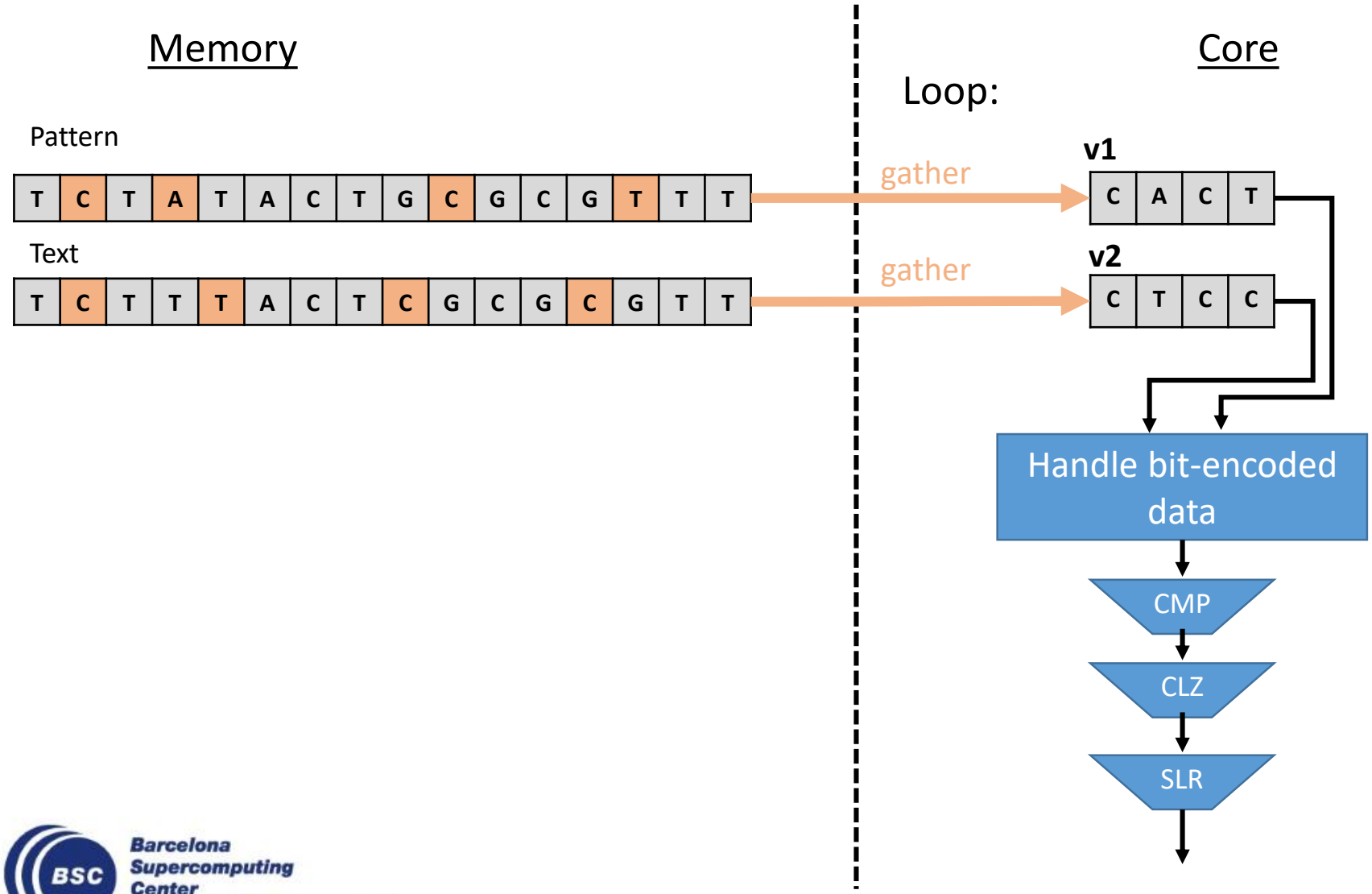
# Bottlenecks for Vector Architectures

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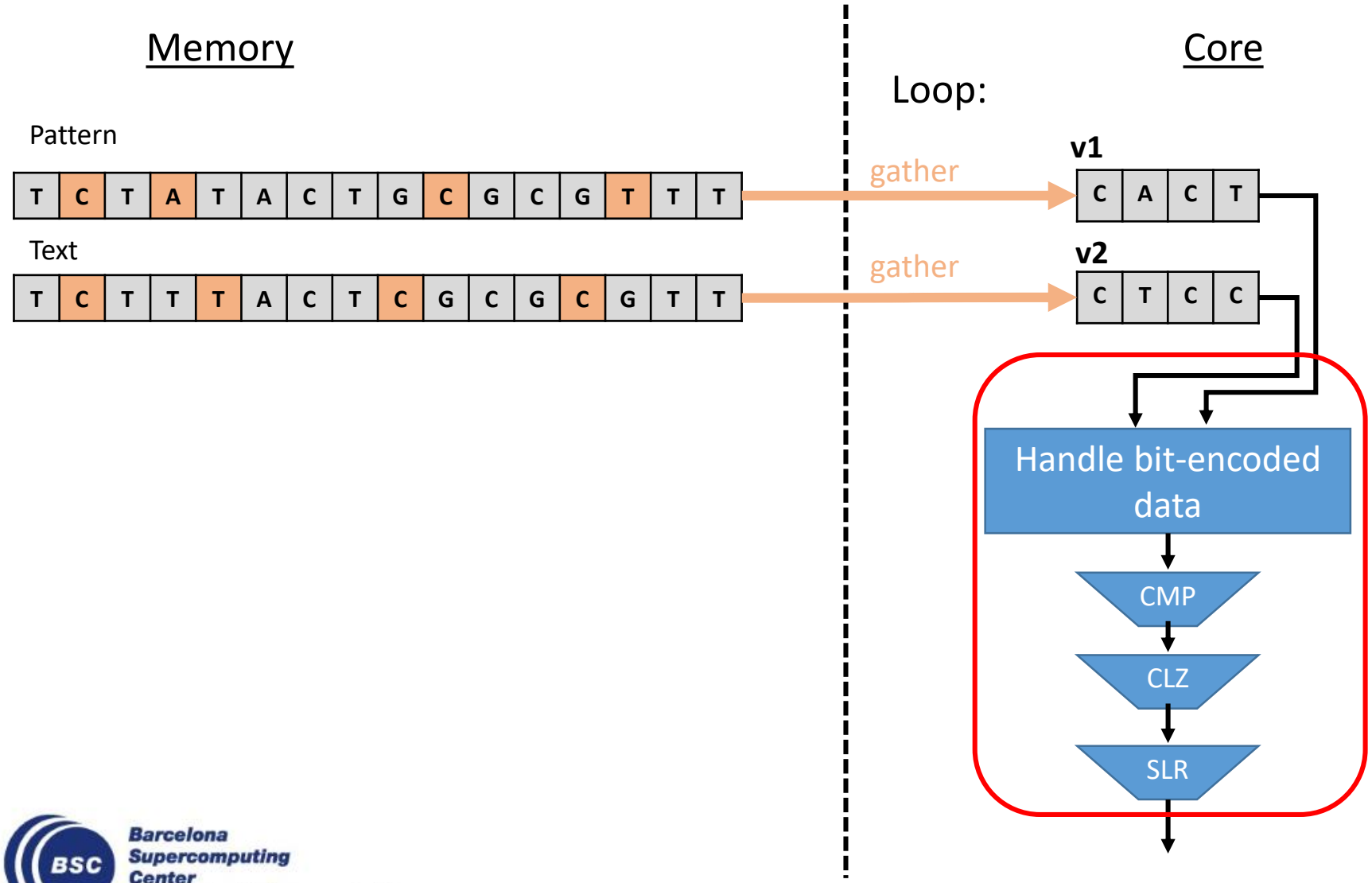
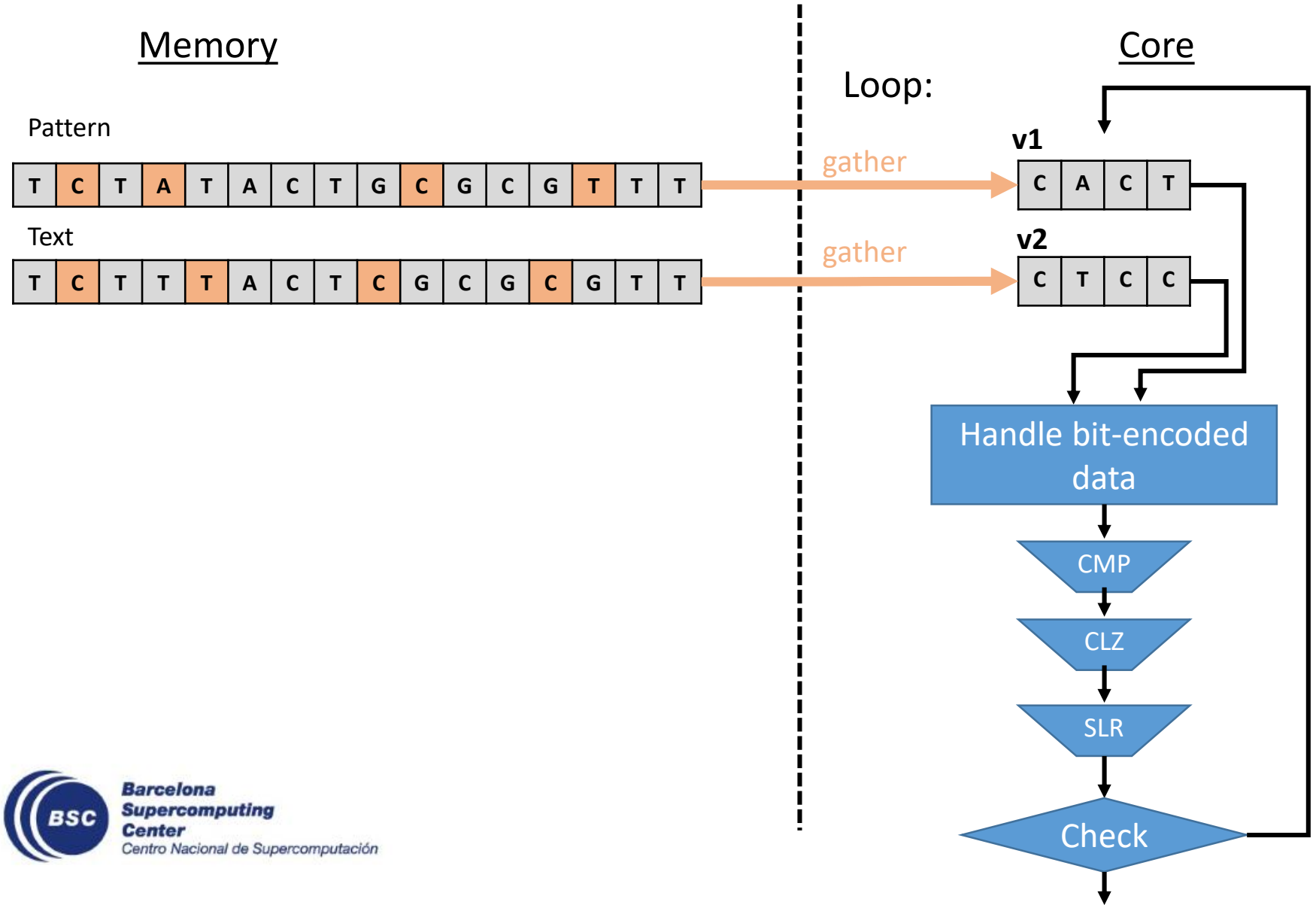
# Bottlenecks for Vector Architectures




**Processing bit-encoded data requires multiple chained instructions.**

# Bottlenecks for Vector Architectures

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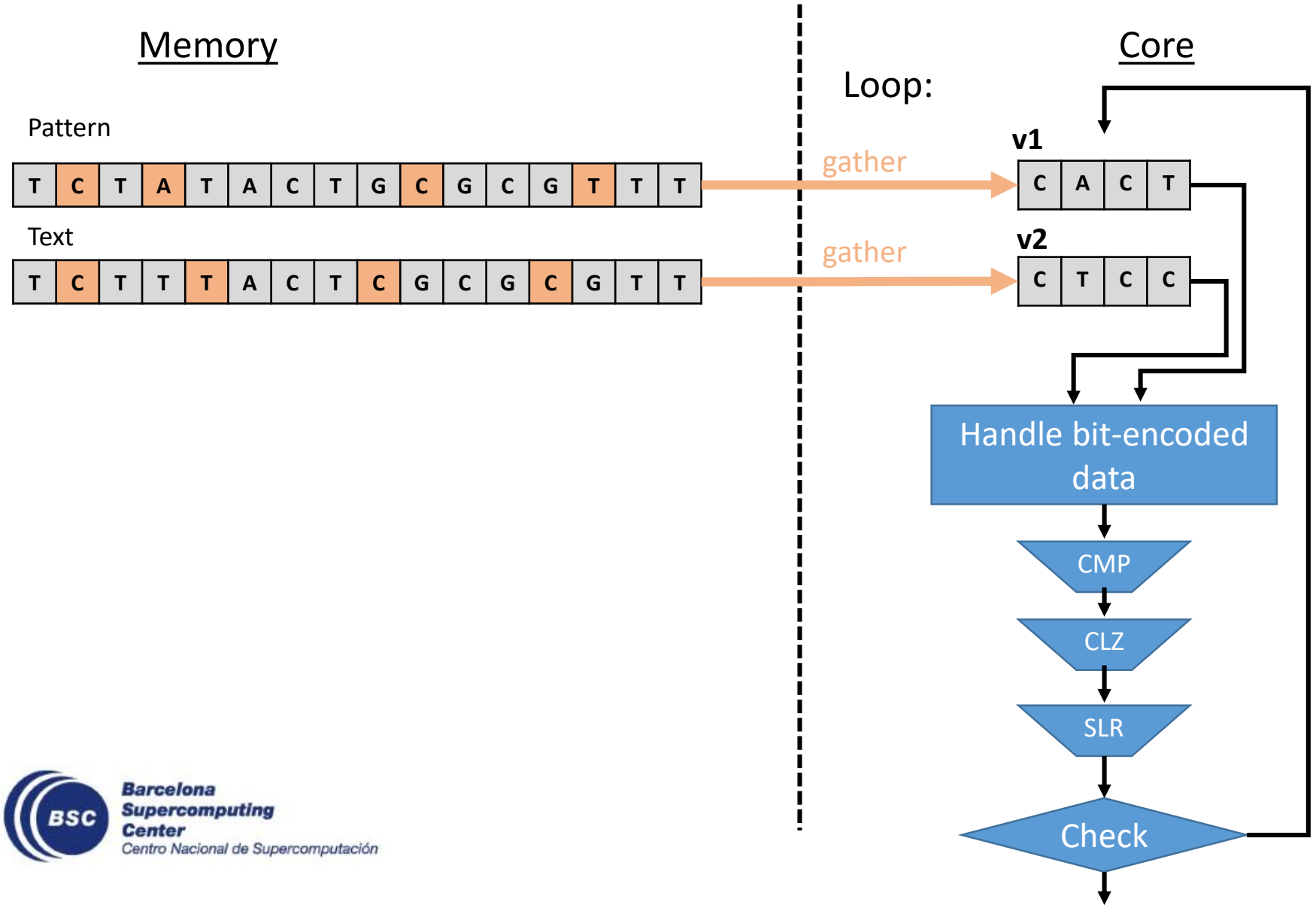
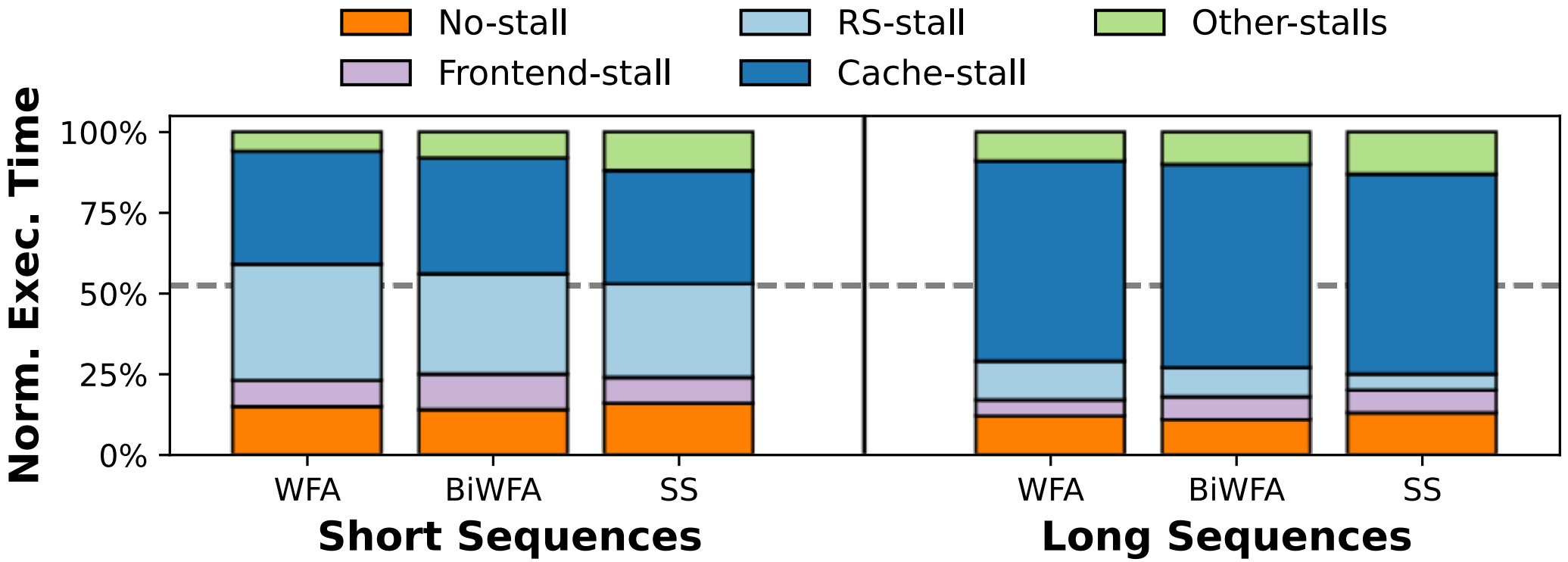
# Bottlenecks for Vector Architectures




**Two major bottlenecks:**
**1) Scatter/gather instructions**
**2) The large number of instructions to handle bit-encoded data.**

# Bottlenecks for Vector Architectures

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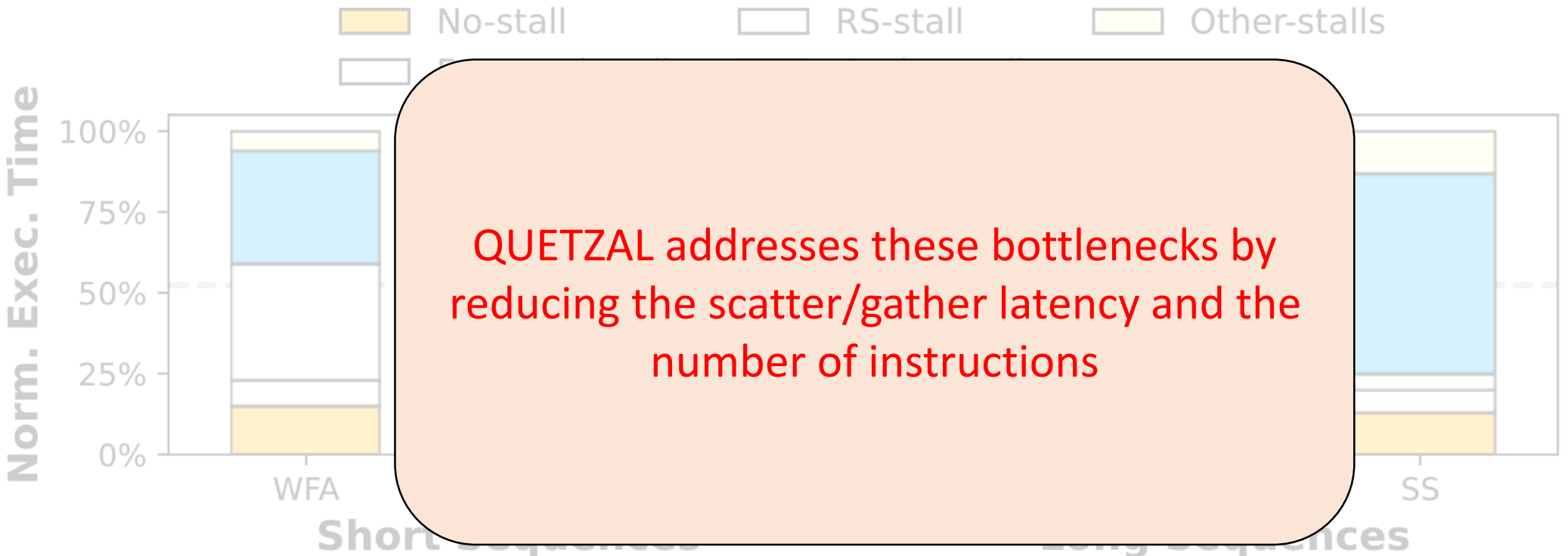
# Bottlenecks for Vector Architectures

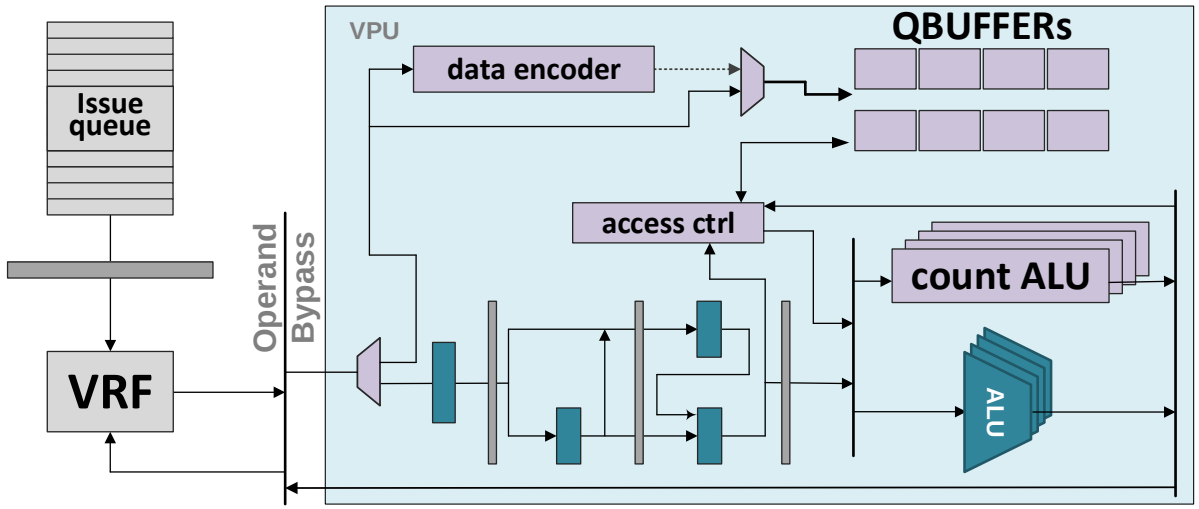



QUETZAL addresses these bottlenecks by reducing the scatter/gather latency and the number of instructions

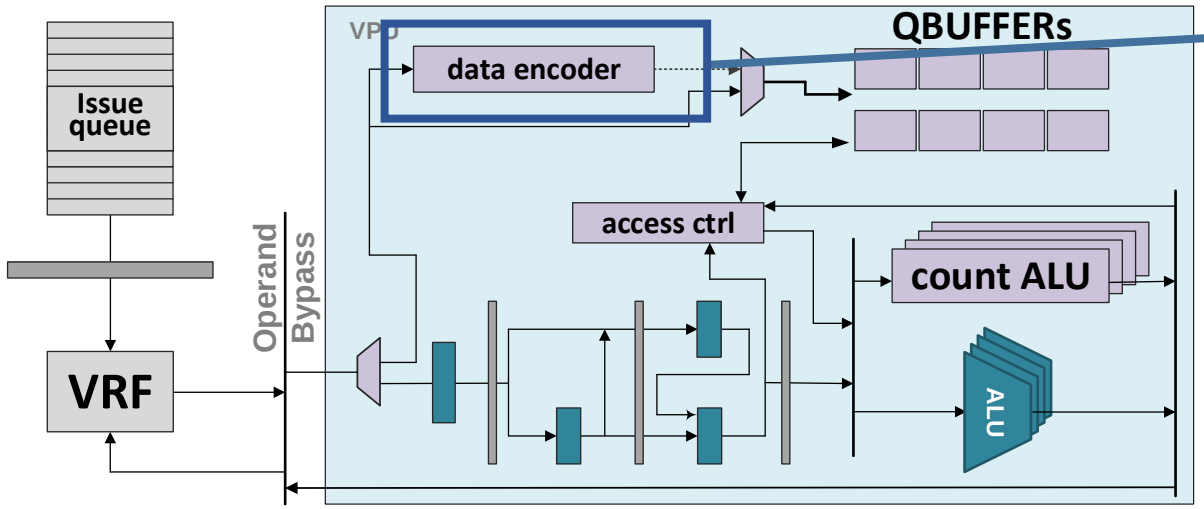
# Outline

1. Introduction and motivation
2. Background
   a) Modern Genome Analysis Algorithms
   b) Bottlenecks
3. QUETZAL
   a) Insights and Functionality
4. Evaluation
5. Summary

# QUETZAL

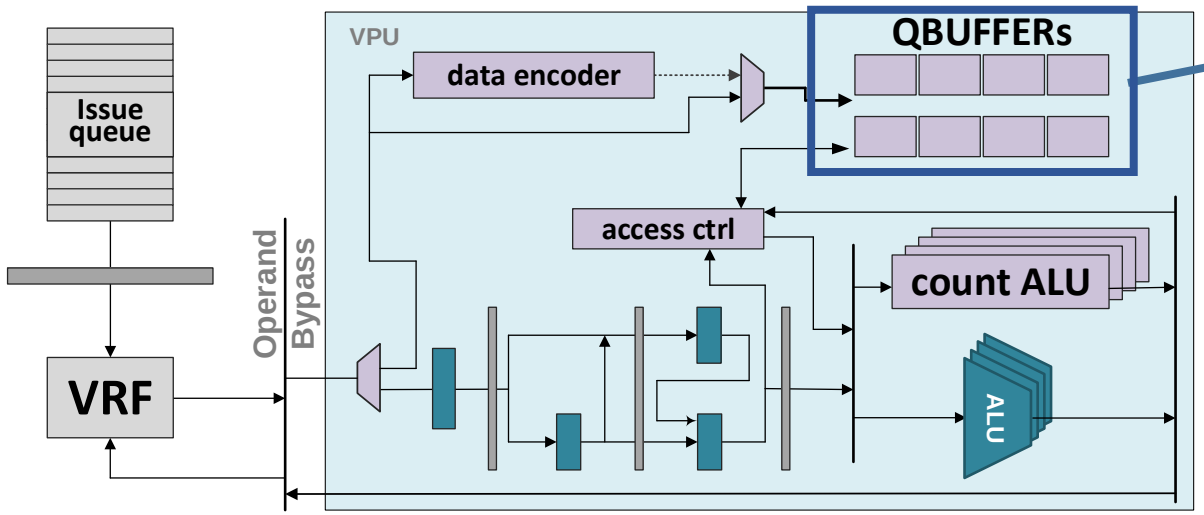

Issue queue
VRF
Operand Bypass
VPU
data encoder
QBUFFERs
access ctrl
count ALU
ALU

# QUETZAL



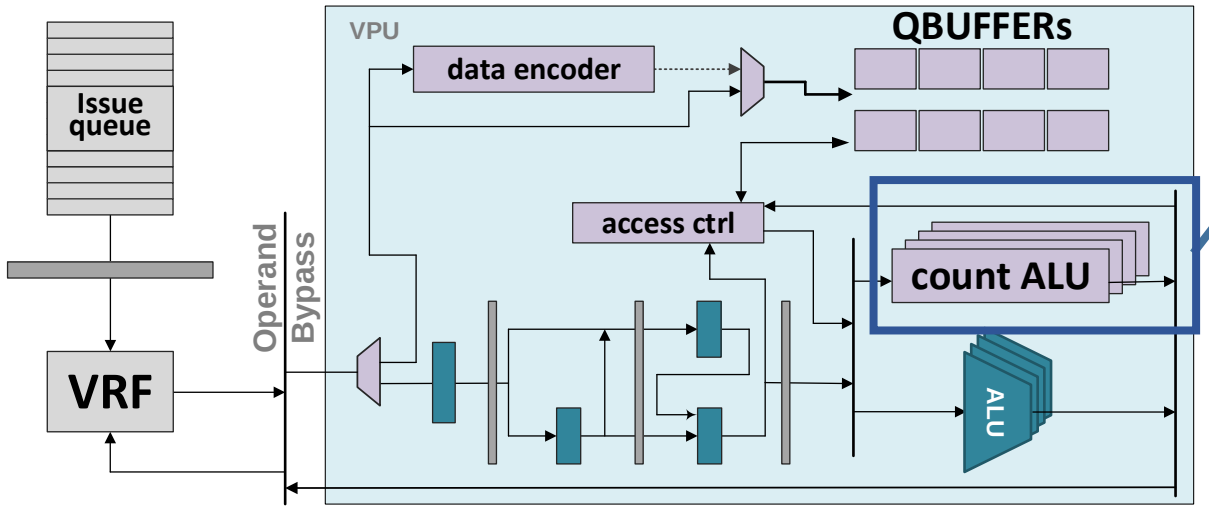

- QUETZAL supports bit-encoded operations without extra instructions.

# QUETZAL



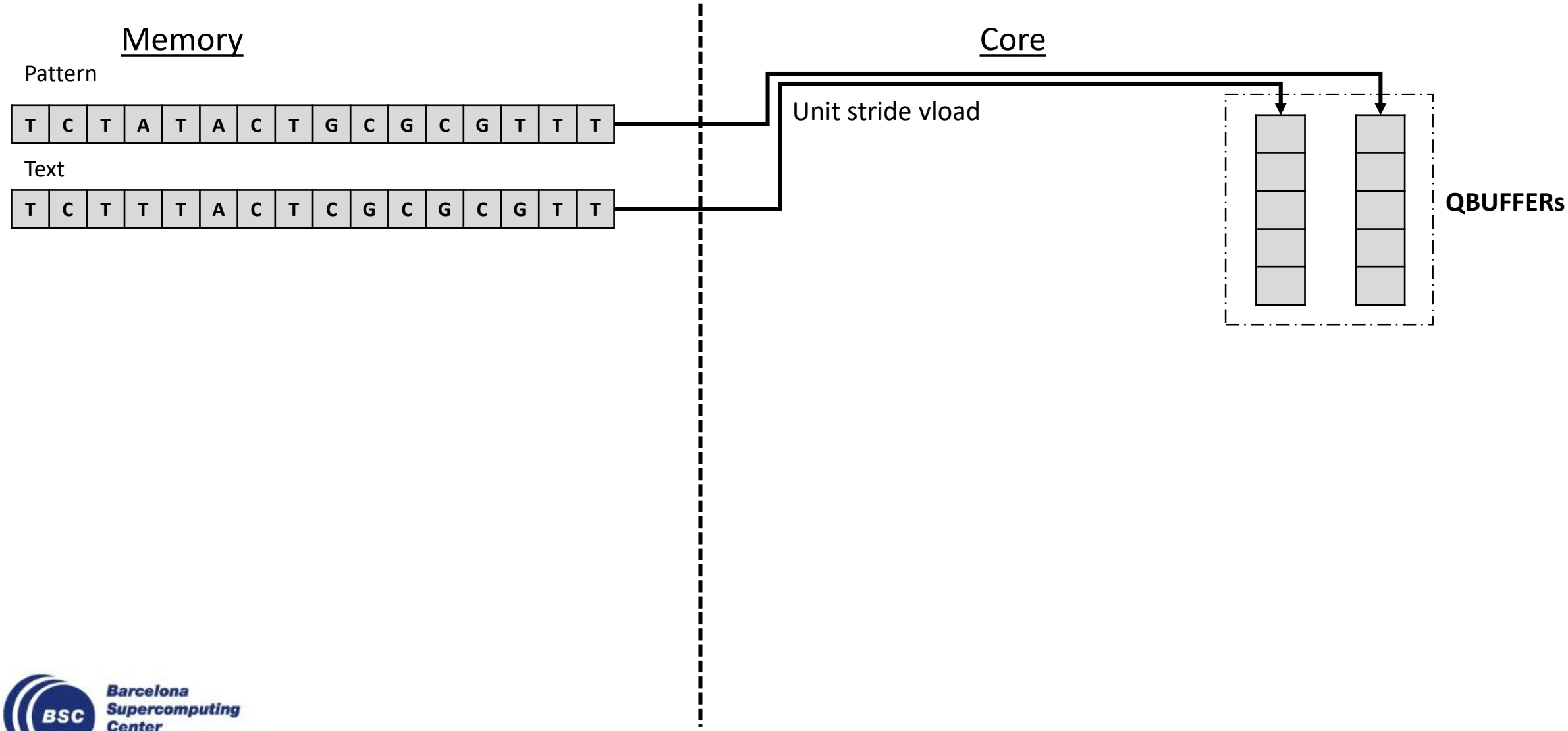

- QUETZAL supports bit-encoded operations without extra instructions.
- QBUFFERS reduce the access latency from 22 cycles to only 2 cycles.

# QUETZAL

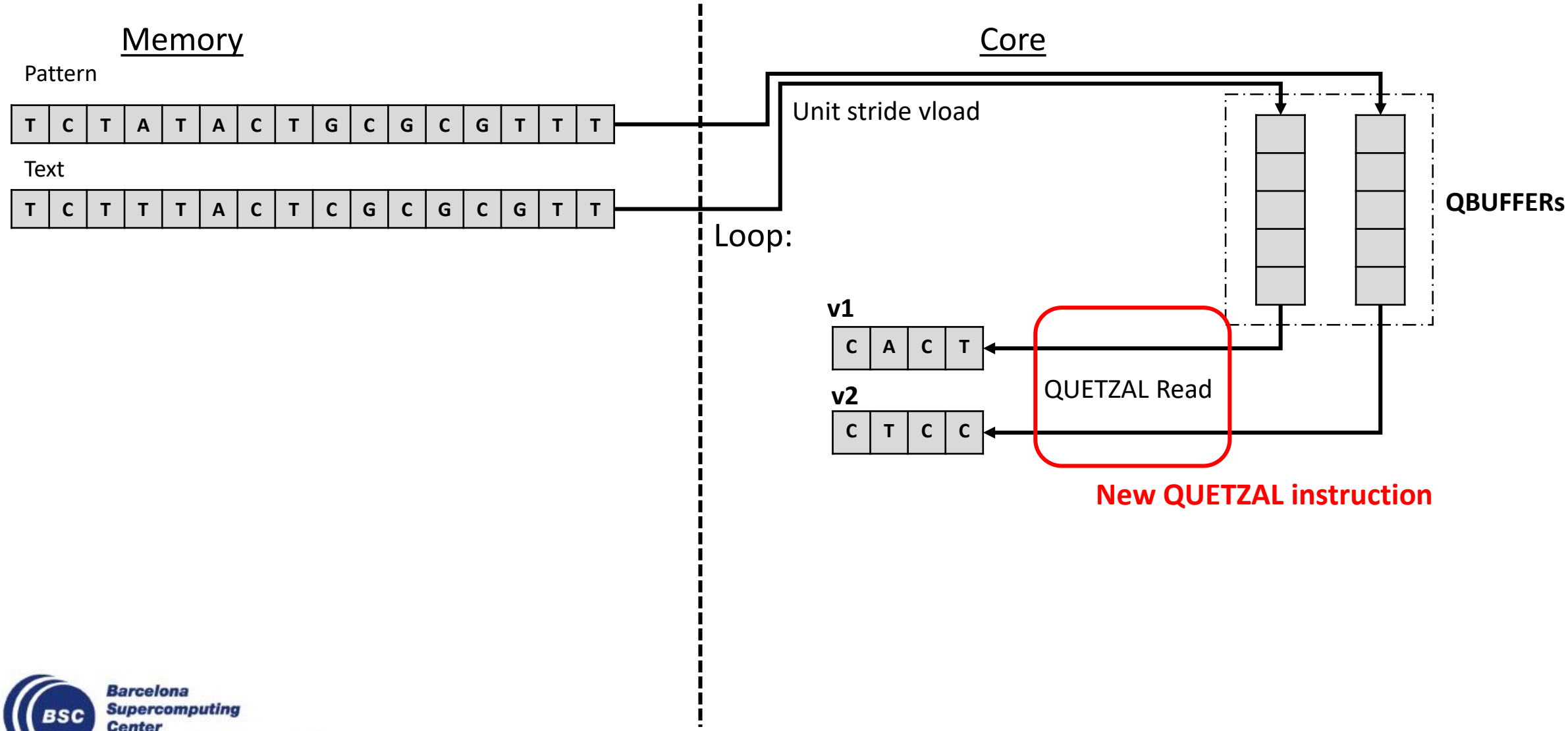



- QUETZAL supports bit-encoded operations without extra instructions.
- QBUFFERS reduce the access latency from 22 cycles to only 2 cycles.
- QUETZAL features custom hardware to calculate the maximum number of exact matches.

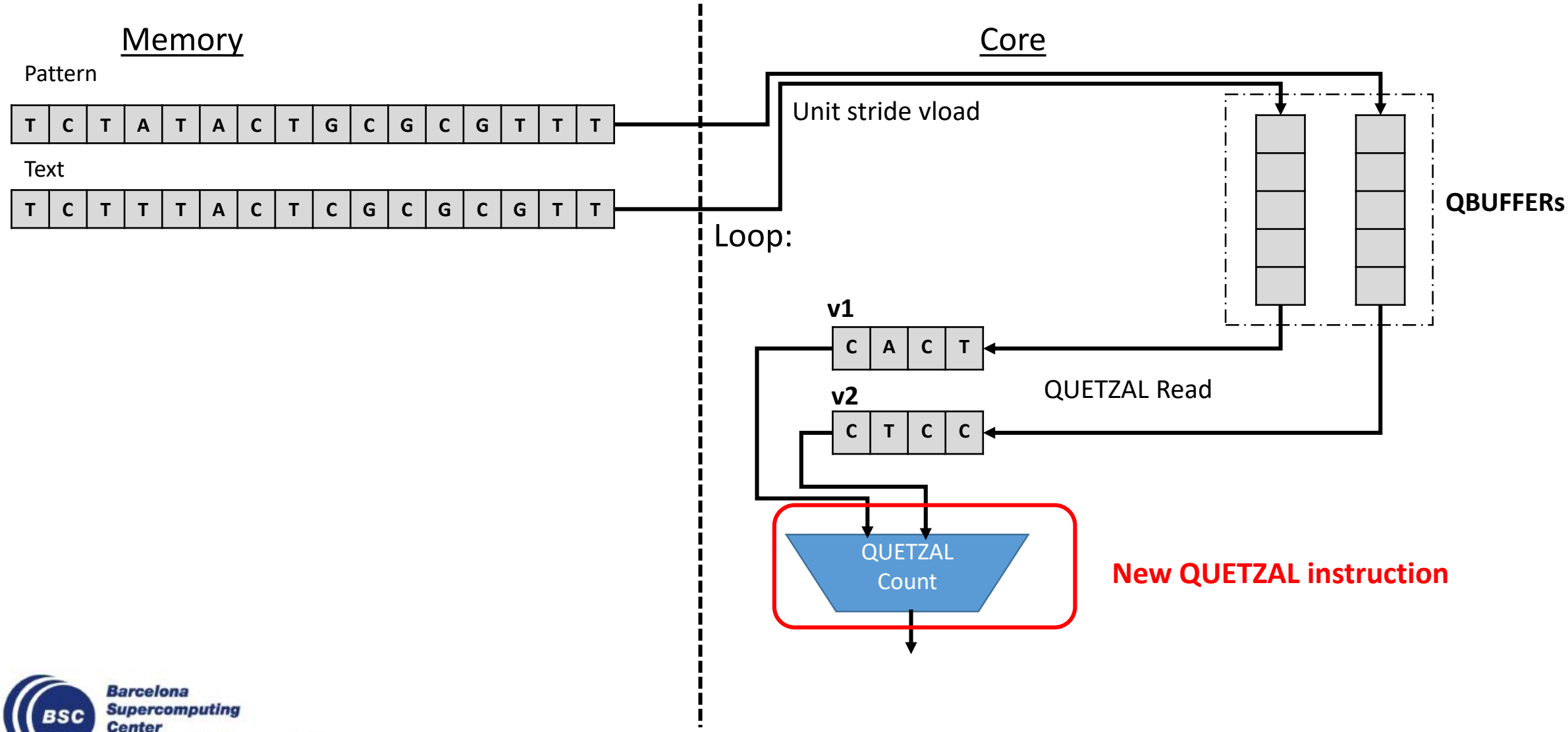
# Bottlenecks for Vector architectures



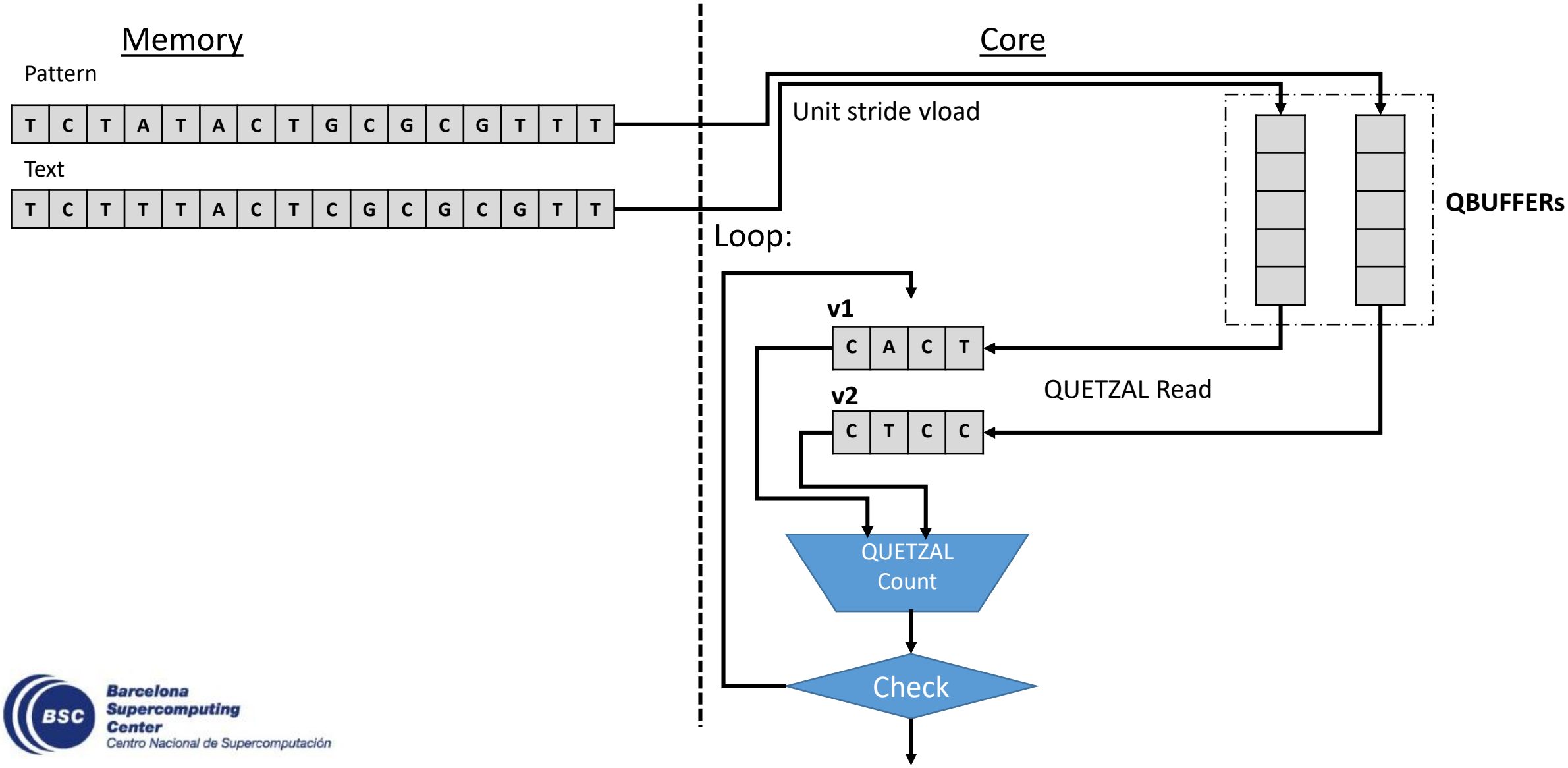
# Bottlenecks for Vector architectures



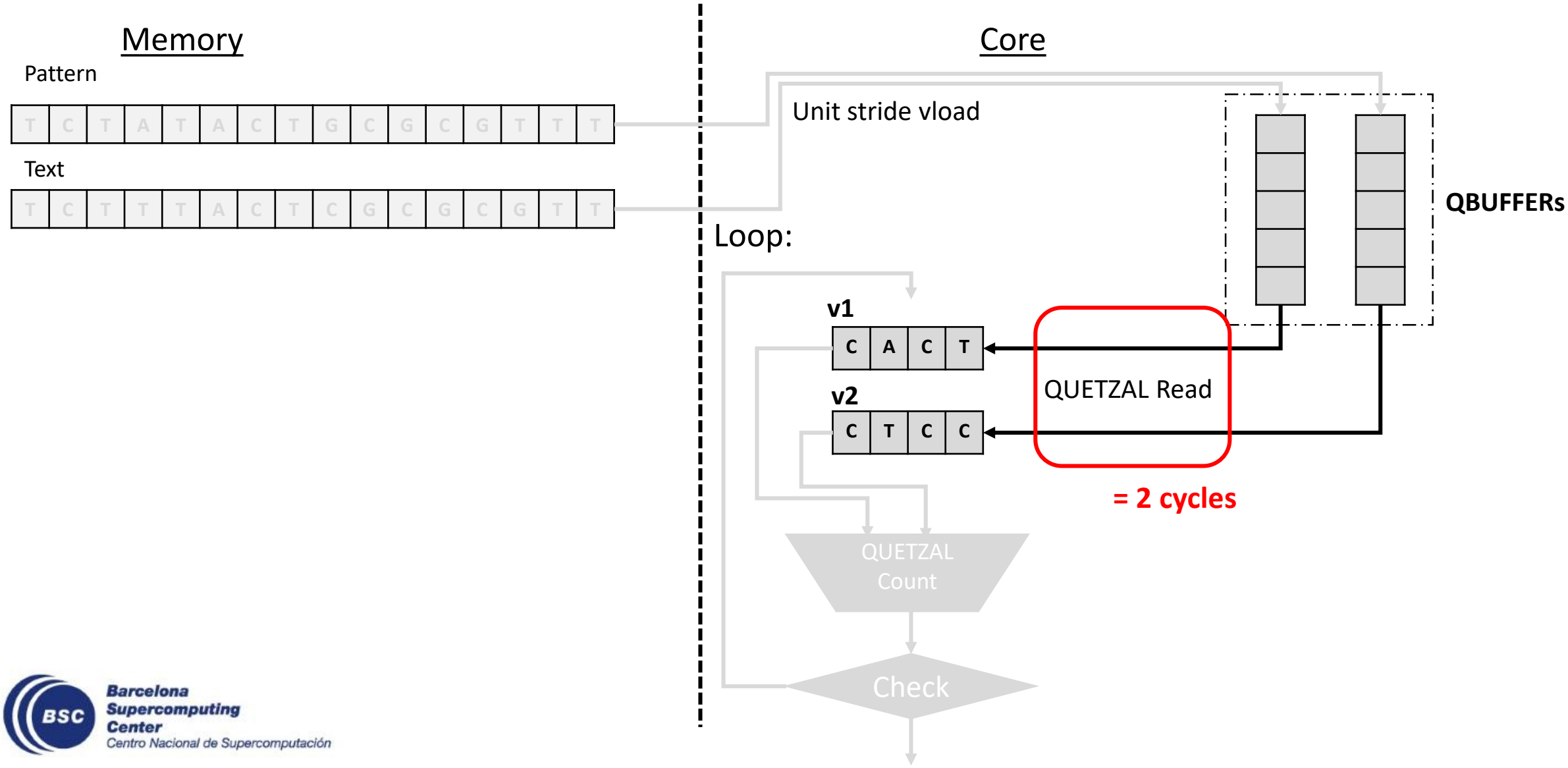
# Bottlenecks for Vector architectures



# Bottlenecks for Vector architectures



# Bottlenecks for Vector architectures



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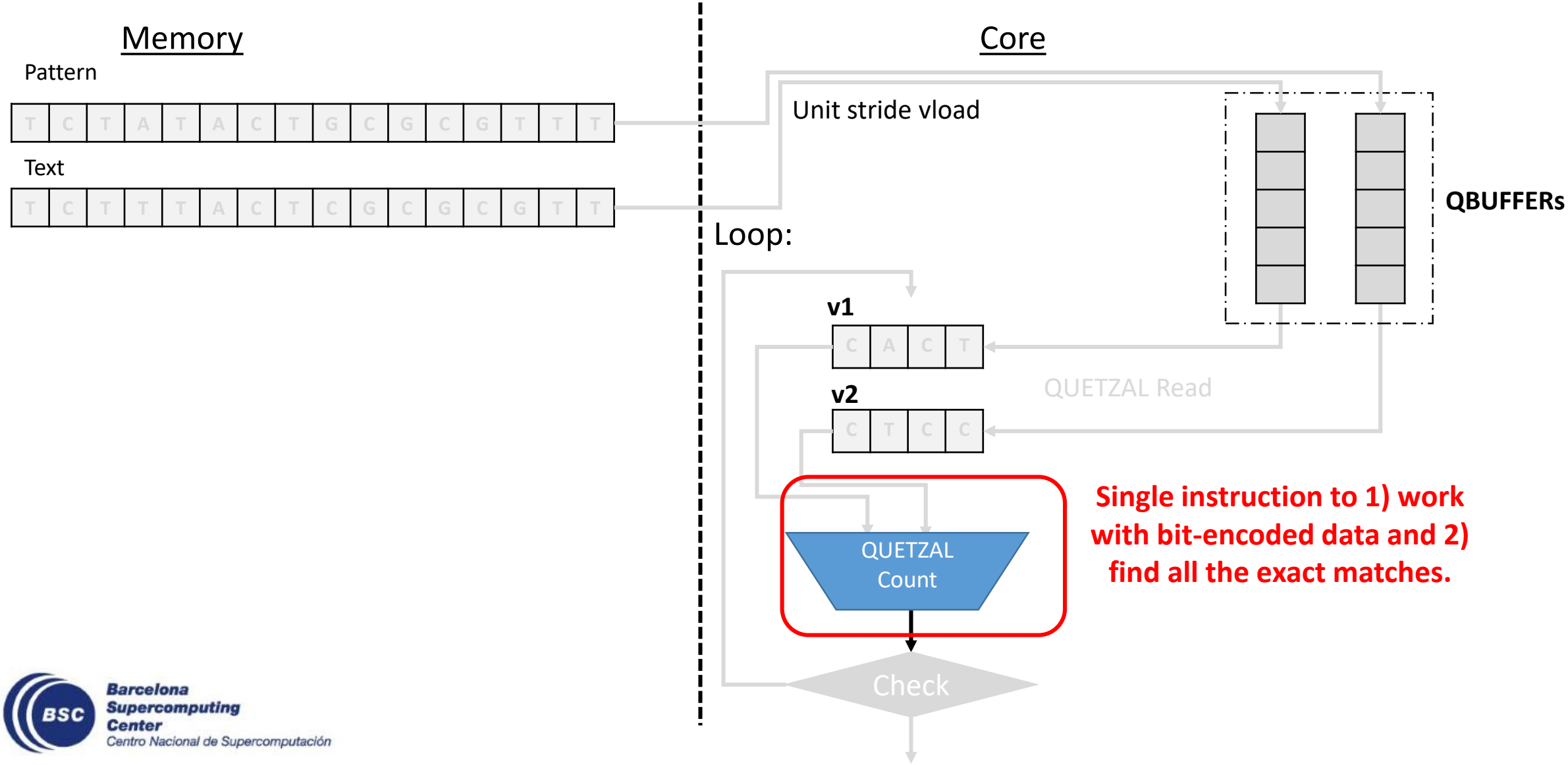

# Outline

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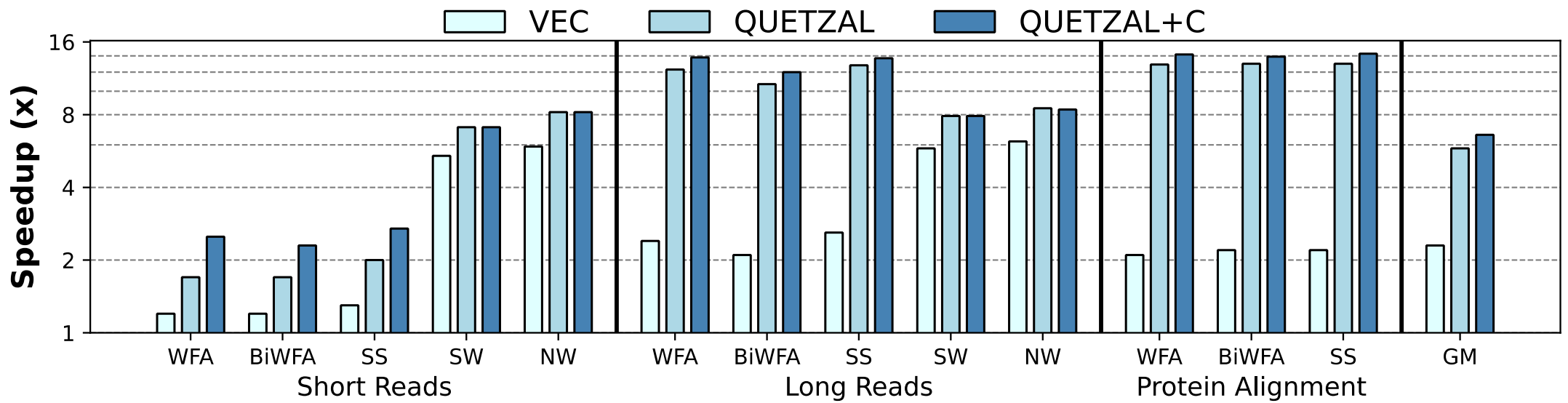
3. QUETZAL
   a) Insights and Functionality
4. Evaluation
5. Conclusion

# Evaluation

- We use the **gem5 simulator** to model a **16-core ARM 64-bit full-system** running an **Ubuntu 20.04** with a 4.18.0+ Linux Kernel.
- All results are normalized to a CPU baseline.

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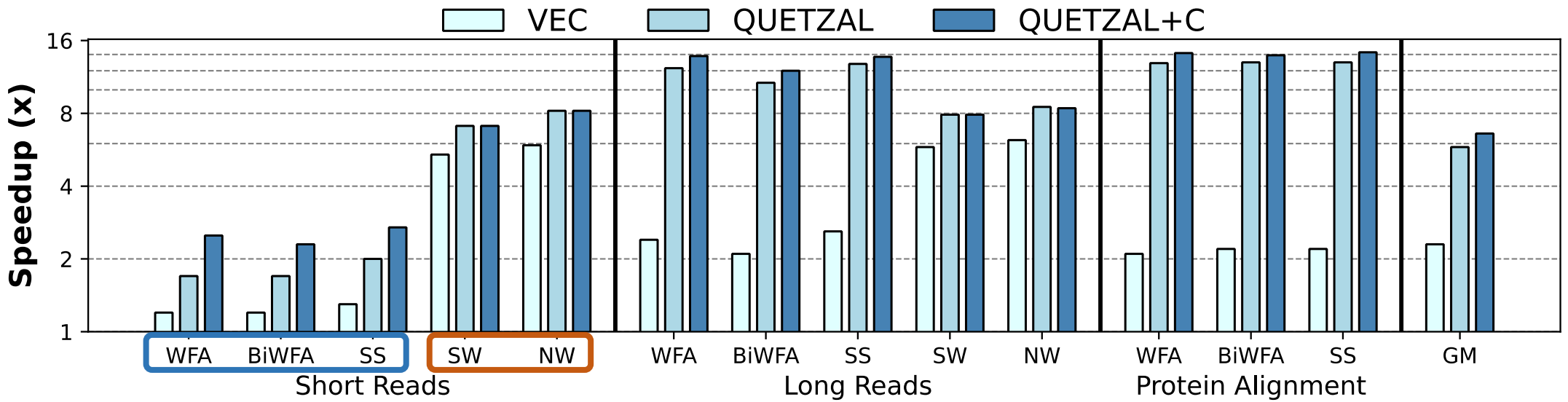
# Evaluation

- Five algorithms: **three modern** and **two classical** algorithms.

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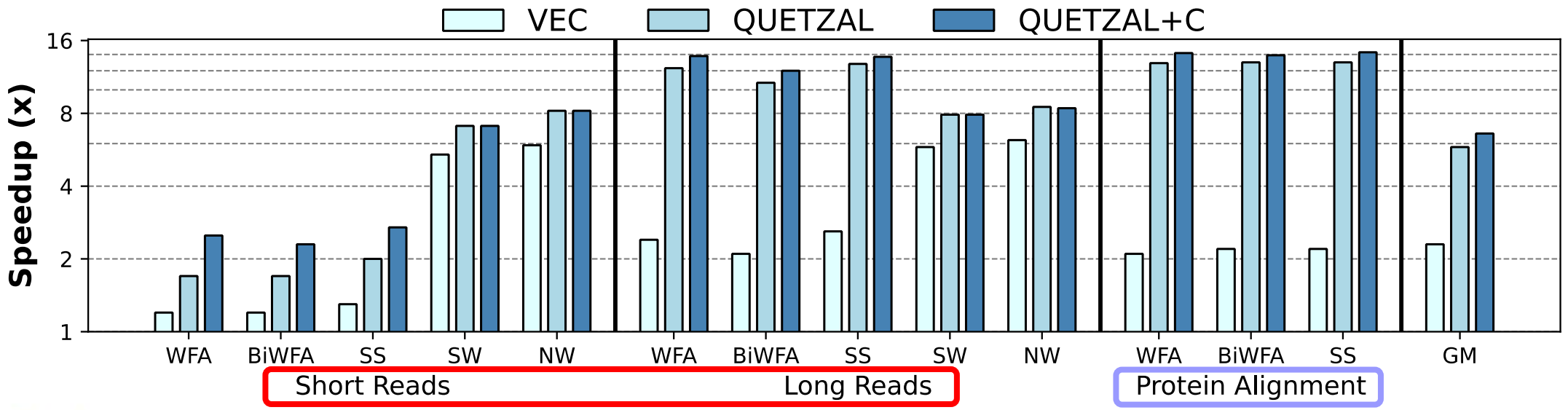
# Evaluation

- Five algorithms: **three modern** and **two classical** algorithms.
- Two alphabets: DNA/RNA and Proteins.

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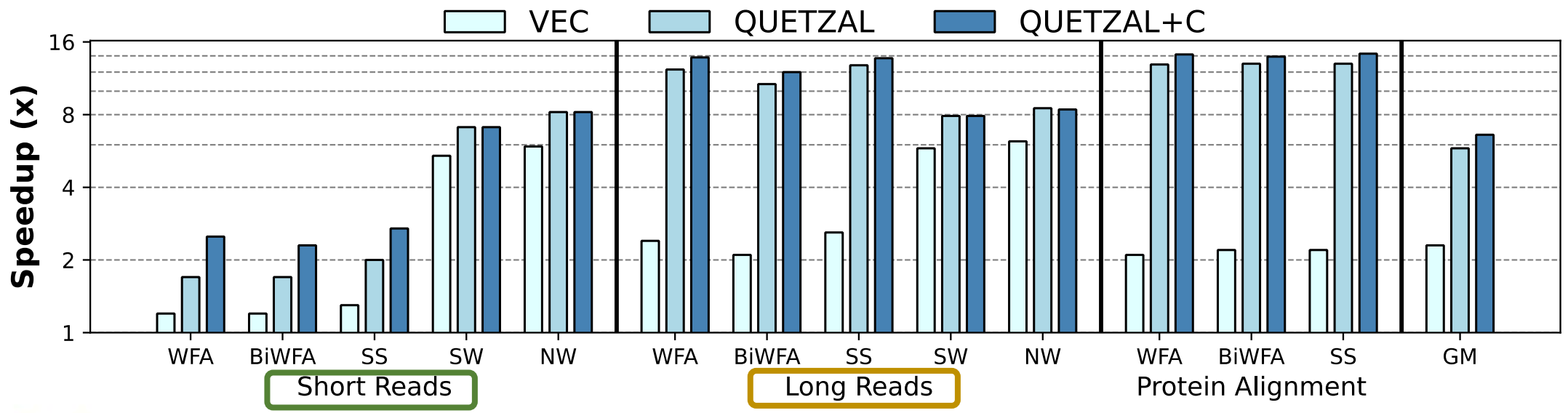
- Five algorithms: **three modern** and **two classical** algorithms.
- Two alphabets: DNA/RNA and Proteins.
- Both short and long DNA/RNA sequences.

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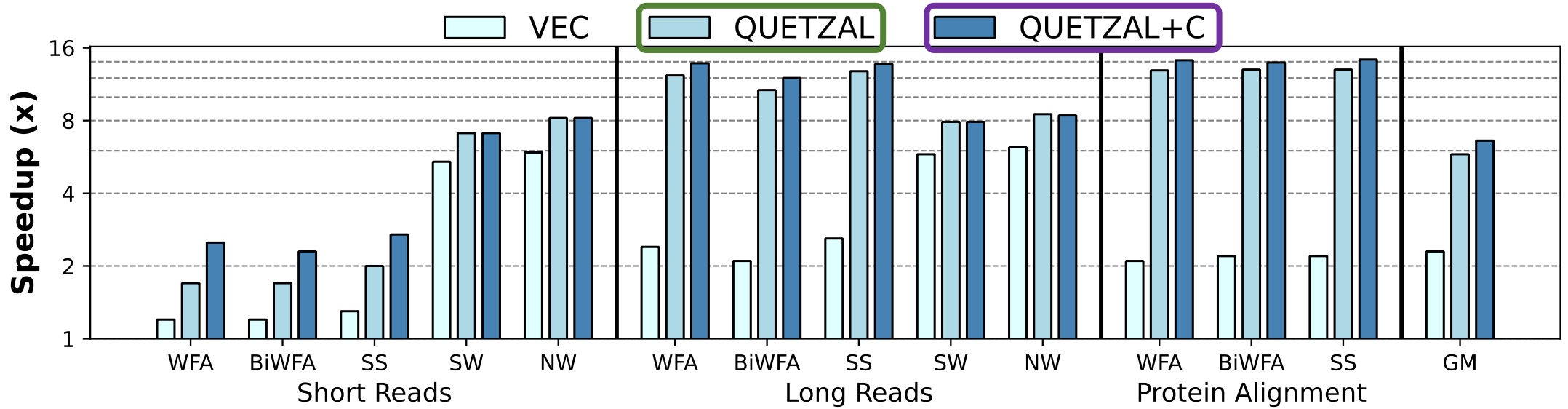
# Evaluation

- Five algorithms: **three modern** and **two classical** algorithms.
- Two alphabets: DNA/RNA and Proteins.
- Both short and long DNA/RNA sequences.
- Two QUETZAL implementations

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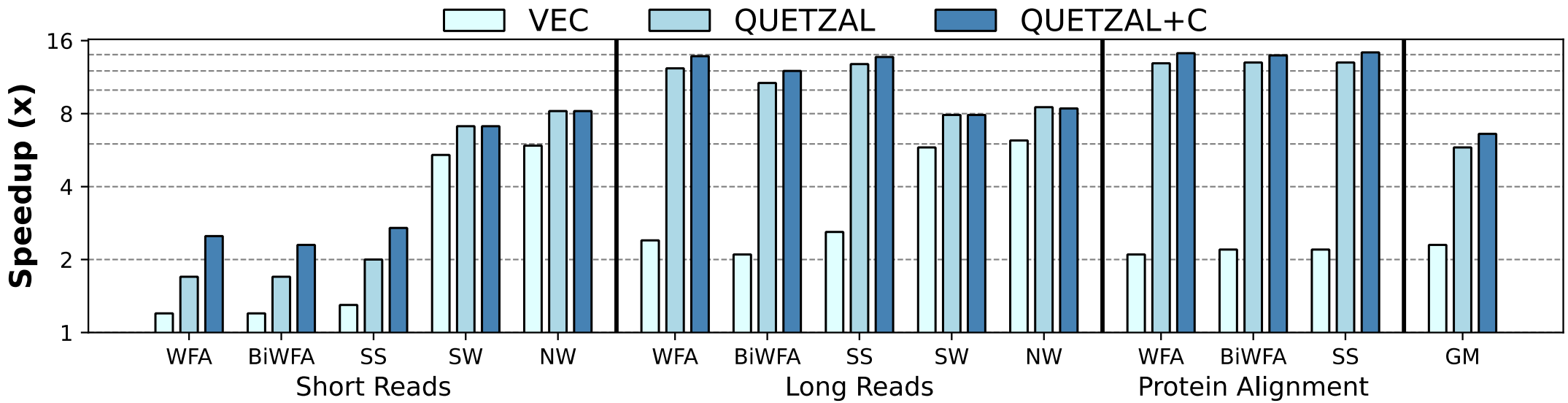
# Evaluation

- QUETZAL significantly outperforms all the evaluated algorithms.

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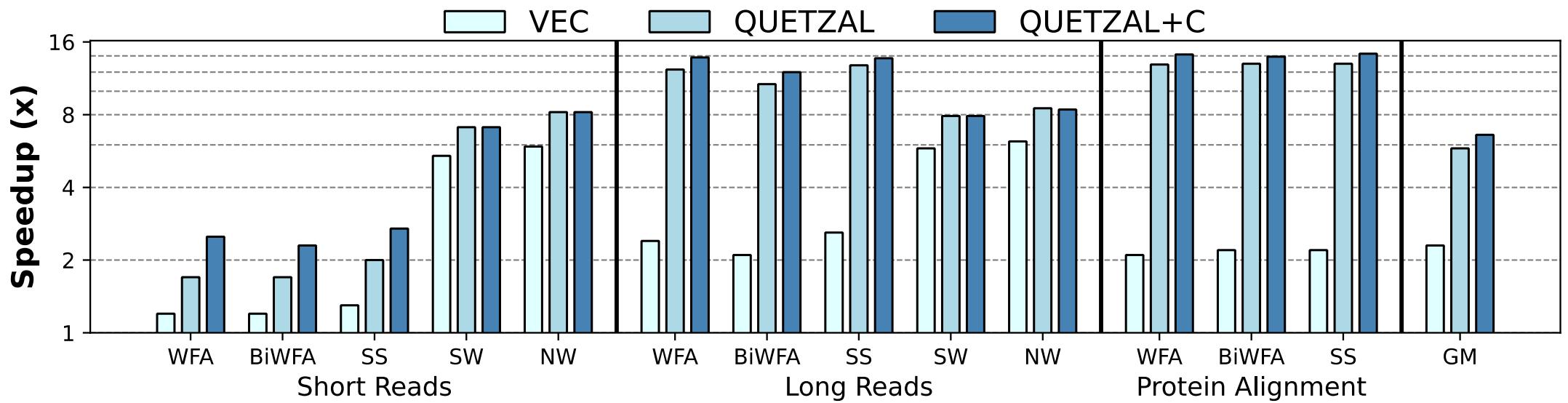
# Evaluation

- QUETZAL significantly outperforms all the evaluated algorithms.
- **Speedup:** 5.7x better performance compared to other vectorized algorithms.

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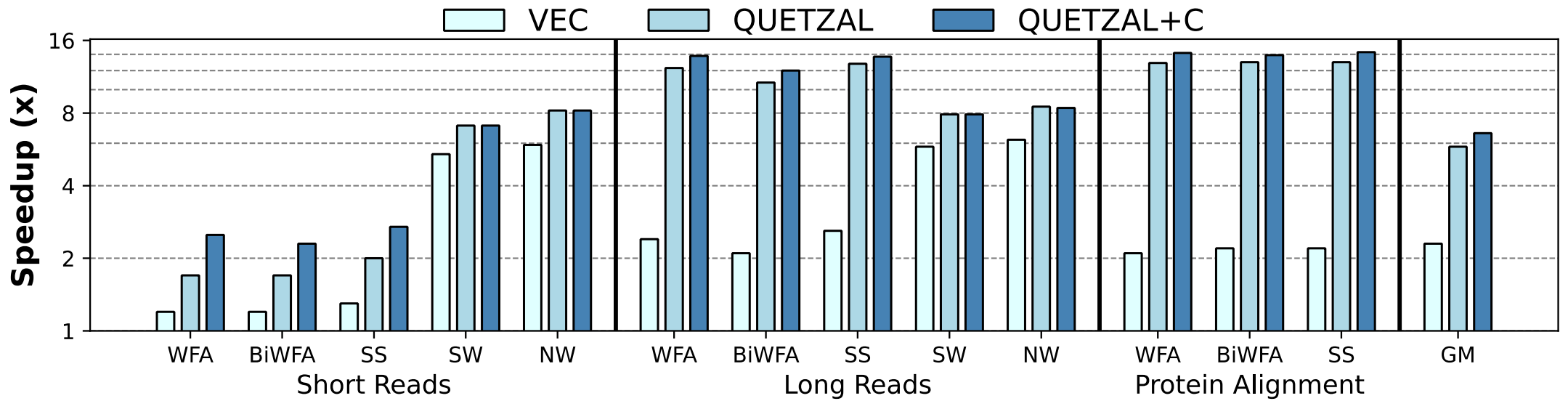
# Evaluation

- 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.

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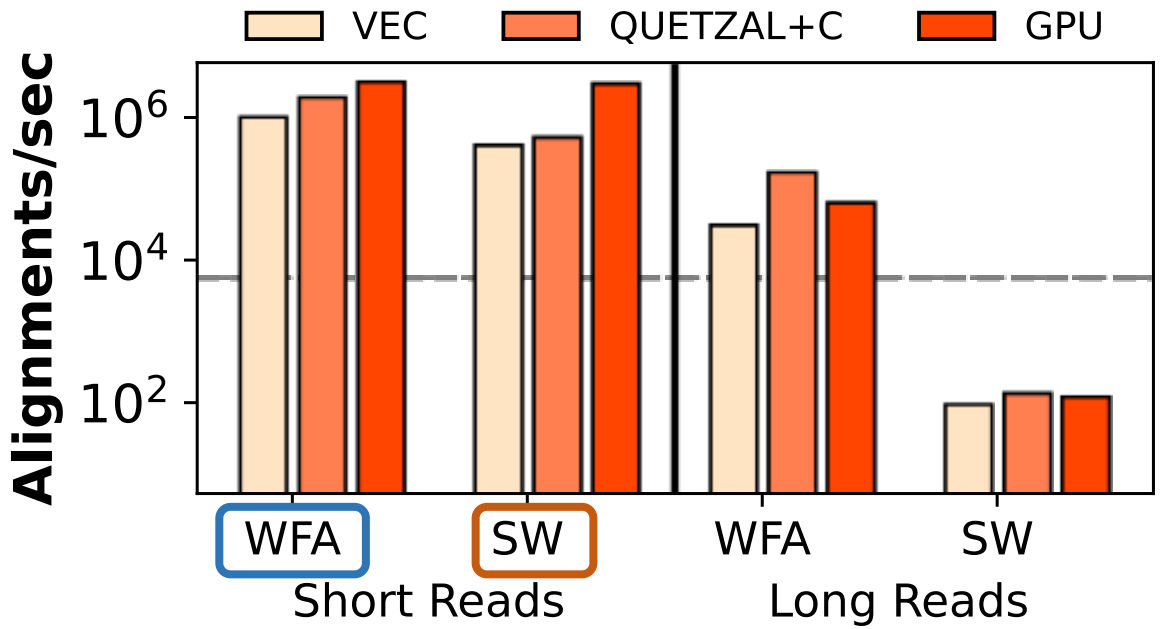
# Evaluation

- Two algorithms: **one modern** and **one classical** algorithms.

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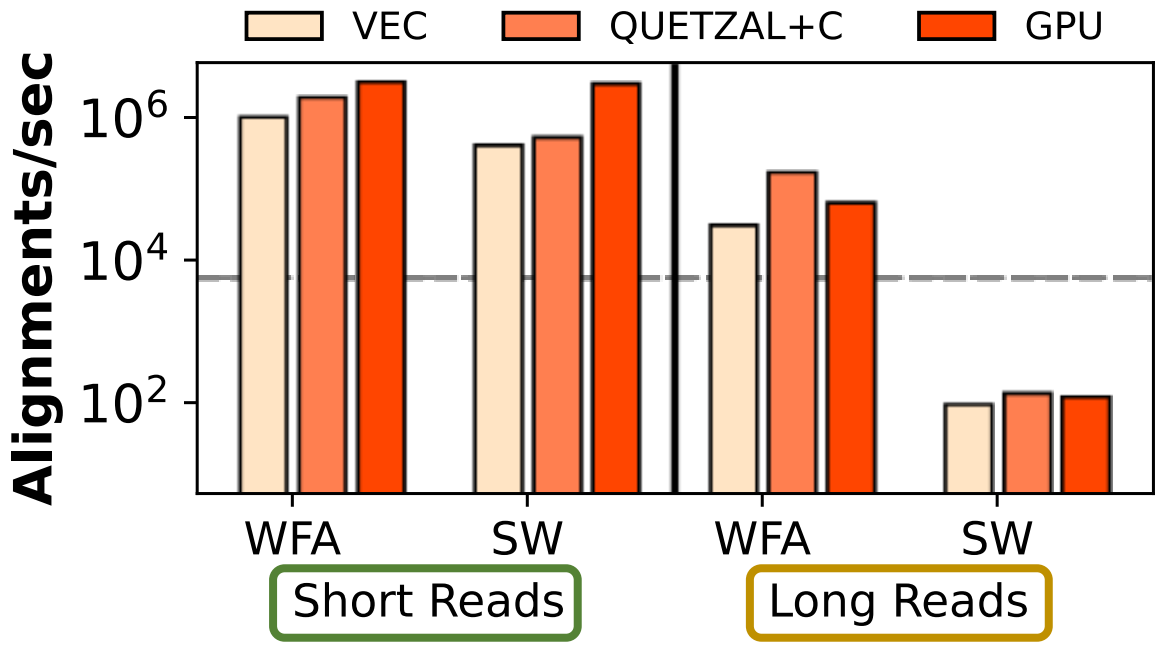
# Evaluation

- Two algorithms: **one modern** and **one classical** algorithms.
- Both short and long DNA/RNA sequences.

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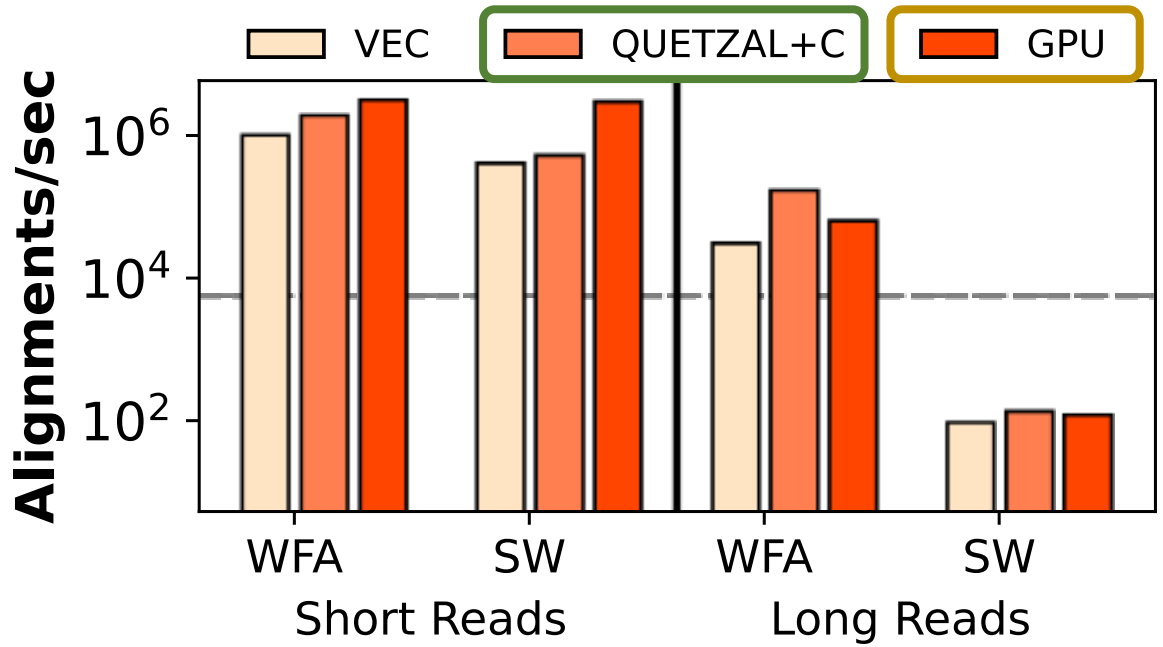
# Evaluation

- Two algorithms: **one modern** and **one classical** algorithms.
- Both short and long DNA/RNA sequences.
- we compared a **16-core** CPU featuring **QUETZAL** and an **NVIDIA A40 GPU**.

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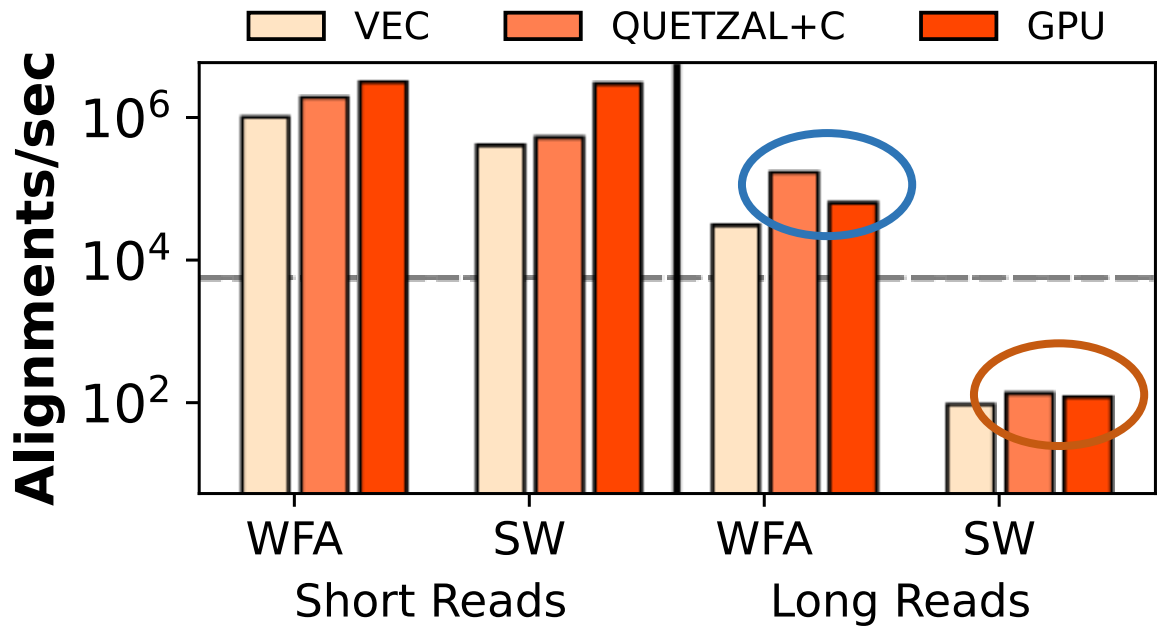
# Evaluation

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



# Area overhead results

We evaluated the area overhead of QUETZAL by going all the way **from RTL to Place&Route** our design using **SystemVerilog** and the **Synopsys' ICC2 Place and Route tool** targeting **7nm** node technology and **2GHz** frequency.

Our evaluation shows a small area overhead of

1.4%

compared to a Fujitsu A64FX SoC.

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# Other content of the paper

1. Detailed explanation of all the hardware components in QUETZAL.
2. Examples to integrate QUETZAL in a C++ code.
3. Single- and multi-core scalability.
4. Design Space Exploration to right-size the QBUFFERS.
5. QUETZAL performance for non-genomic applications.
6. Comparison to ASIC accelerators.

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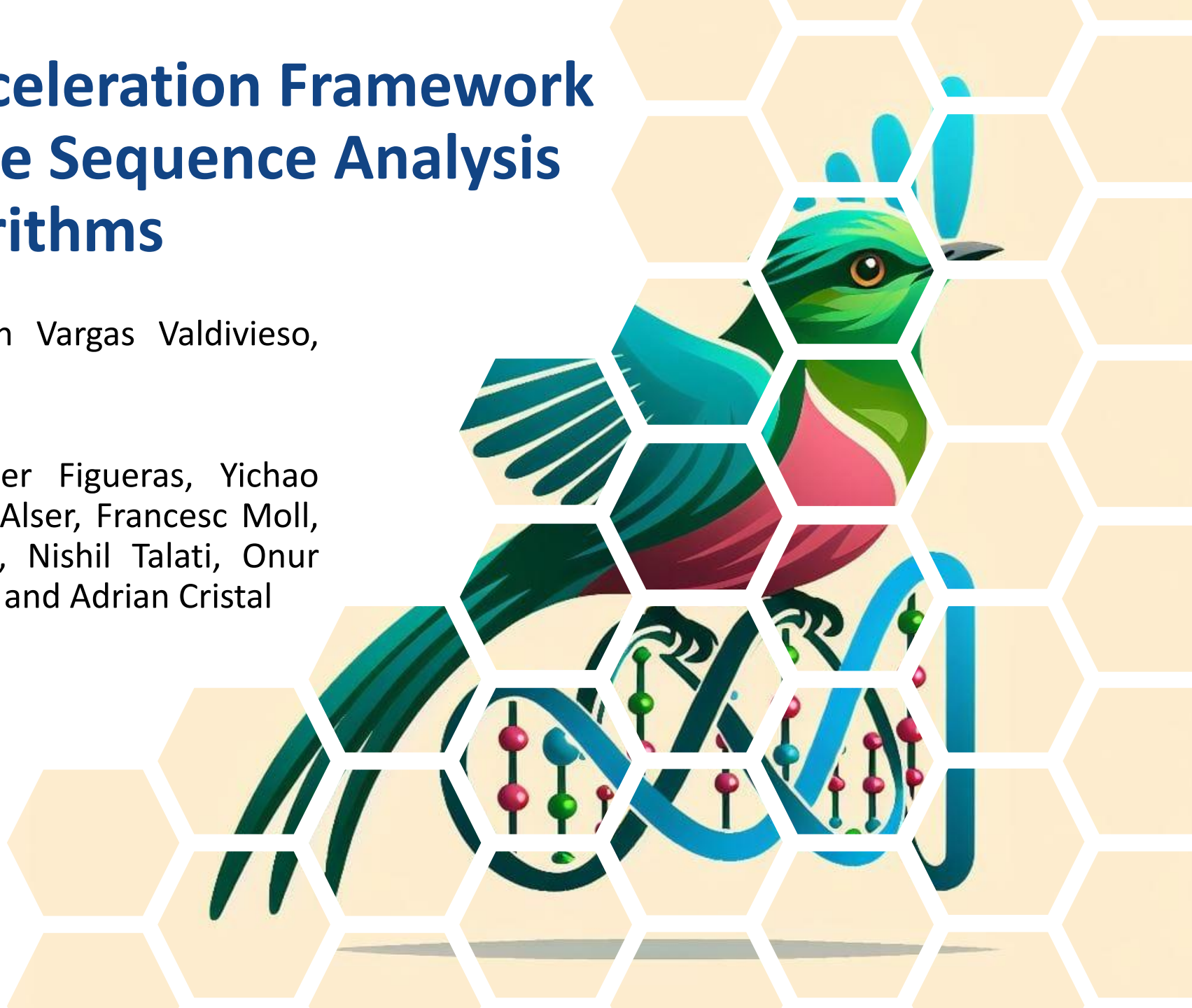
# Conclusion

- Striking a balance between high performance and generality is critical
- CPU's vector data path offers an attractive design choice for data parallel applications
- QUETZAL – hardware-software co-design for genome sequencing with 5.7x compared to baseline CPU

# QUETZAL: Vector Acceleration Framework for Modern Genome Sequence Analysis Algorithms

**Lead authors: Julian Pavon**, Ivan Vargas Valdivieso, Carlos Rojas, Cesar Hernandez

**Co-authors:** Mehmet Aslan, Roger Figueras, Yichao Yuan, Joel Lindegger, Mohammed Alser, Francesc Moll, Santiago Marco Sola, Oguz Ergin, Nishil Talati, Onur Mutlu, Osman Unsal, Mateo Valero and Adrian Cristal



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