

### HPC-BLAST Scalable Sequence Analysis for the Intel® Many Integrated Core Future

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### **HPC-BLAST Development**

- HPC-BLAST is a high-throughput, highly parallel version of the NCBI Basic Local Alignment Search Tool.
  - > Designed for use with the Intel® Many Integrated Core architecture
- The **NCBI BLAST** algorithm is used extensively in bioinformatics for comparative sequence analysis.
- **HPC-BLAST** is scalable, employing **MPI** and **OpenMP**.
  - > Executes **natively** on Xeon processors or Xeon Phi coprocessors
  - Executes symmetrically across Xeon processors and Xeon Phi coprocessors
- The development of HPC-BLAST extensively used tools.
  - > Rogue Wave TotalView
  - > Allinea DDT
  - > Intel VTune and Inspector
  - > 2013 and 2015 Intel C++ compilers

# Look Inside

# The NCBI-BLASTp algorithm: Overview

[1] Concatenate queries. Query **Concatenated Query** Query [5] Perform gapped Query alignment allowing for blanks to be inserted. Offset Word Seeds YVF 13 Word Offset YVF 13 VED 14 VED 14 **EDI** 15 DIY 15 16 EDI IYR 17 DIY 16 Gaps IYR 17 [3] Mark matches **Query: YVEDIYRDHGALPPMS** (seeds) in the VED+ R+HG ++ +[2] Build a lookup lookup table. Subject: RVEDDCRCHGVTMMRR table. [6] Report high-scoring matches.

[4] Perform ungapped alignment.

## **HPC-BLAST Approach – MPI Level**



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within a replication group allow for distribution of the **search database**.

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# **HPC-BLAST Approach – Thread Level**



- A thread group consists of one or more leader threads that collectively contain a complete copy of the subject database.
- Multiple thread groups allow for distribution of the query database.
- Multiple leader threads within a thread group allow for distribution of the search database.
- Multiple search threads provide threads to the core BLAST search algorithm.



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# **Performance: Strong Scaling**

### Relative Performance: Comparison of BLAST implementations

Xeon Phi 5110p v.s. Xeon E5-2670 pair



- Single Xeon Phi performance compared to pair of Xeon E5-2670
- Speedup relative to single NCBI thread on Phi
- 4 HPC-BLASTp ranks on Phi
- 1 HPC-BLASTp rank on Xeons

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Subject database: nr.01 partition; Query database: 1065 random sequences from nr.01

• BLAST+ 2.2.28; mpiBLAST 1.6.0

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### **Performance: Weak Scaling**



- 32 nodes
- 4 coprocessors per node
- 1 MPI rank per coprocessor
- 4 threads per coprocessor core
- Identical workload on each rank

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Subject database: nr.01 partition; Query database: 500 sequences of length 350 amino acids

• BLAST+ 2.2.28

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### **Performance: Throughput**

The HPC-BLAST approach enables **scientific impact** with impressive throughput.



• Xeon + Xeon Phi provides improved performance per dollar for sufficiently large searches of the entire nr database from NCBI

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• Subject database: nr (entire database)

• Query database sampled from subjects: 444 (red) and 1065 (blue)

• BLAST+ 2.2.28; mpiBLAST 1.6.0

### **Observations, Insights, & Future Work**

- Different sequence analysis problems exhibit different performance characteristics.
- Problem decomposition impacts performance pattern.
- Standard BLAST algorithm does not vectorize well.
- Flexibility in expressing parallelism at all levels is crucial for tuning performance.
- VTune is very helpful for performance analysis; Inspector is useful in finding race conditions.

### • Future work:

- > Implement scalable, parallel I/O
- Improve load balancing currently 30% 40% imbalanced
- Refactor to utilize SIMD operations while matching canonical output challenging to maintain compatibility with heuristics

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