



When Apache Spark Meets FPGAs: A Case Study for Next-Generation DNA Sequencing Acceleration

Yu-Ting Chen, Jason Cong, Zhenman Fang, Jie Lei and Peng Wei

University of California, Los Angeles





We are forced to explore heterogeneity

- When Dennard scaling comes to the end and Moore's law slows down as components reach atomic scale
 - Shift from single-core to multi-core
 - Take the pain to learn parallel programming
 - Memory ordering, locking, load balancing, ...
 - Even homogeneous multi-core architectures are not able to drive continued perf. and energy improvement that we have come to expect in the past



Heterogeneous Architecture

- Why heterogeneity?
 - Customized accelerators promise orders-ofmagnitude perf./watt gains
- > Accelerator-centric architectures
 - Application-specific functional units
 - Domain-specific building blocks
 - Reconfigurable/reprogrammable logic
 - GPUs, CGRAs, FPGAs, ...



Source: Bob Broderson, Berkeley Wireless group



What is an FPGA?

- > Field Programmable Gate Array (FPGA)
 - Reconfigurable hardware
 - Can be used to solve any problem which is computable
 - Not always fast, though
 - Is well-known to be used for ASIC prototyping and hardware emulation
 - Prototype accelerators
 - Can also be directly used as a compute accelerator





Altera Stratix-10 FPGA Source: Altera



http://www.slideshare.net/omutukuda/presentation-1993175

Why FPGAs in datacenter?

- FPGAs are reconfigurable
 - You do not want to be as extravagant as Google to tape-out an ASIC chip only for one app
 - Not many applications are so important as to be equipped with a customized chip
- FPGAs are energy-efficient
 - A high-end FPGA board typically consumes ~20 watt
- > Concrete examples have demonstrated harnessing FPGAs in datacenter
 - Microsoft Catapult for the Bing search engine: 2x speedup with 10% more power consumption
- > An FPGA fabric is (probably) going to be a "free lunch" in the near future
 - Altera, now part of Intel => An FPGA fabric will probably be a default component in a server
- > CPU-FPGA systems are not fully elucidated
 - So many research opportunities, so much potential

The Objectives of This Case Study

- > Accelerating an application that is a matter of life or death
 - DNA sequencing is expected to be widely used in precision medicine, like cancer treatment
 - A cancer cell's genome mutates probably in a few days
 - The state-of-the-art sequencing pipeline typically takes a week or so to sequence a patient's genome, which, for clinic use, is too long
- > Proposing an approach to efficient integration of FPGAs into Apache Spark
- > Presenting what issues need to be addressed to operate FPGAs at scale
- Attracting more attention from system architects to make better CPU-FPGA systems

Next-Generation DNA Sequencing

An individual's genome samples •••••



The Solution: Heterogeneous Cluster Computing

- Processing billions of reads (strings) independently
 - Fit the MapReduce programming model perfectly
 - As for the long reference genome? Spark's broadcast variables
- Inside each read's alignment process
 - Step #1: Seeding
 - Exact string matching
 - Linear time complexity
 - Step #2: Extending
 - Approximate string matching
 - The Smith-Waterman dynamic programming algorithm (Quadratic time complexity)
 - Accelerated by FPGAs

Straightforward Integration: 1+1 < 0.001

The Spark Program

- CS-BWAMEM [HitSeq `15]
- Aligning billions of short reads onto the reference human genome in parallel
- The Accelerator [FCCM`15]
 - A throughput-oriented FPGA accelerator for the Smith-Waterman DP kernel

The Straightforward JNI Integration

- CPU: 2.1 x 10³ reads per second
- FPGA: 1.6 reads per second



While <u>JNI</u> serves as a standard approach to connect JVMs with FPGAs, a straightforward integration through JNI degrades the performance by <u>1000x</u>.

What happened in a CPU-FPGA communication instance?



Why communication matters?

- Each map function is likely to process only a small volume of data with a small amount of execution time
 - One read is only 101 ASCII characters
 - One line of a text file

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- One record of a NoSQL table
- Communication overhead can be amortized by batch processing

def map func(input:U):V = { // U => P => O => V t1:P = cnv1(input)t2:Q = cnv2(t1)t3:V = cnv3(t2)t 3 rdd out = rdd in.map(ele=>map func(ele)) def map func(input:Array[U]):Array[V] = { // Array[U] => ... => Array[V] t1:Array[P] = cnv1 batch(input) t2:Array[Q] = cnv2 batch(t1)t3:Array[V] = cnv3 batch(t2)t 3 rdd out = rdd in.map(ele=>map func(ele))

Let's first do batch processing manually



Dependency/Irregularity-Aware Batch Processing

Accelerator-as-a-Service



Source: https://spark-summit.org/2016/events/deploying-accelerators-at-datacenter-scale-using-spark/

Lessons Learned and Open Discussion

- From homogeneous to heterogeneous => requirement of corresponding systems
 - lightweight, unified and efficient processor-accelerator communication
- While various FPGA-based accelerators have been proposed, CPU-FPGA systems are being built on top of "naive" communication stack
 - Pageable memory => pinned memory => device memory
- MapReduce does not take accelerators into consideration, and does not seem to be accelerator-friendly
 - A map function often has little execution time, but considerable aggregate time
 - It must be greatly helpful if automatic code transformation for batch processing works
- A generic accelerator-aware big-data framework is needed, even if not now

Acknowledgement



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