ENGINEERING AT ILLINOIS

CSL: COORDINATED SCIENCE LAB

IGen: The Illinois Genomics Execution Environment

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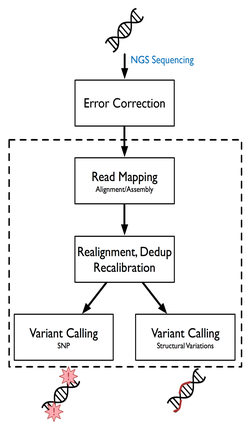
Goals

- Identify system performance bottlenecks in variant calling workflows running on extreme scale systems
- Identify algorithmic patterns in the variant calling workflow to exploit available parallelism
- Inform the design of future genomics algorithms and their implementations on large computing systems

Application: Variant Calling Workflow

- Identifies and characterizes mutations in NGS data
  - Map NGS data to reference genome
  - Correct for noisy data
  - Differentiate strings in the presence of noise and ploidy
- First phase of the personalized medicine flow
  - Recurrently used
  - Data intensive part of NGS analytics



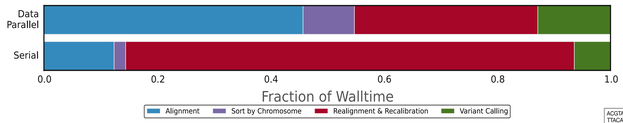
Variant Calling and Genotyping Workflow

- Data filtering process
  - In: 100GB
  - Out: 50 MB
- Best Practices Workflow:
  - BWA for alignment
  - GATK for BQSR and realignment
  - GATK for SNP calling
- Data-parallel distributed computation

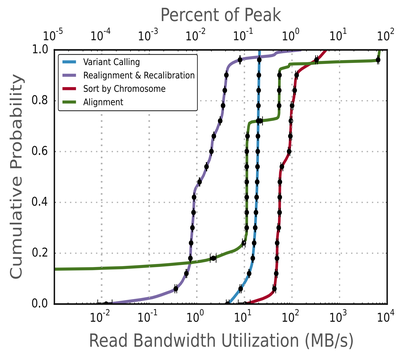
Performance Bottlenecks

Walltime for human genome @ 50x coverage

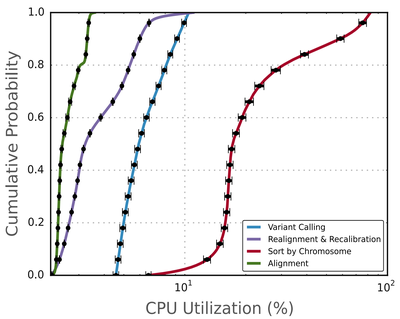
- 43.7 ± 0.01 h on a single node
- 28.3 ± 0.2 h on 22 Blue-Waters nodes



- Very poor resource utilization
- IO dependent performance limitations:
  - File system as distributed memory
  - Htslib: Inefficient for distributed file systems
  - Sorting large alignments on-disk



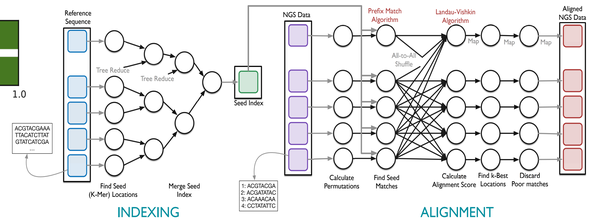
- Compute dependent performance limitations:
  - Serialization across threads in GATK
  - Poor cache locality in Java



Efficient NGS Analytics

Genome Analytics as Data-Flow Graphs

- "Kernels" (Vertices): Data transformations
- "Patterns" (Edges): Data dependencies



Single Ended NGS Read Alignment as a DFG

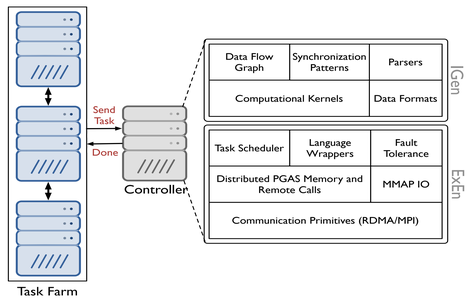
- Implicitly data parallel
- Composable and pluggable model
- Reuse of computational kernels
  - Potential for system level optimizations
  - Potential for accelerators

Workflow stage	Kernels
Error Correction	K-mer computation
Alignment	K-mer computation, prefix tree, Edit-distance computation
Indel Re-Alignment	Edit-distance computation, Table lookup
Re-Calibration	Yates correction, Table lookup
Variant Calling	Entropy, Convolution, Assembly, Edit-distance, Bayesian inference

Common kernels in the Variant Calling Workflow

Distributed DFG executions over heterogeneous clusters

- **Ex**ecution **En**gine: Runtime framework for distributed data-parallel executions of data flow graphs on heterogeneous clusters
- **I**llinois **G**enomics Execution **En**vironment: Accelerated genomic analyses tools for ExEn

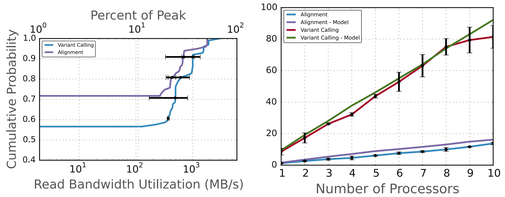


High level view of the ExEn-IGen framework

Performance Enhancements:

- Distributed execution of kernel functions
- RDMA to cut down data-serialization costs
  - RPC: Control Transfer
  - PGAS Memory: Data Transfer
- Efficient data formats
  - Columnar store
  - Use in-memory representation
  - Memory Mapped IO
- High performance kernel functions

Preliminary Results



- Synthetic human chromosome 1 @ 50x
- IGen Aligner (vs. SNAP)
  - Single Node: **1.2x** (35 min to 30 min)
  - Multiple Node (10): **14x**
- IGen Variant Caller (vs. GATK HaplotypeCaller)
  - Single Node: **9x** (36 min to 4.1 min)
  - Multiple Node (10): **81x**

Conclusions

- Measurement driven study of performance bottlenecks in existing NGS analytics tools
- Similar performance pathologies across multiple tools. Scope for system level optimization
- Present a data-flow based abstraction for NGS analytics
- Demonstrate preliminary results of significant performance acceleration
- Simpler to build high performance parts

Ongoing Work

Improved Kernel Scheduling

- Optimal task assignment under constraints of:
  - Affinity
  - Shared resource contention
  - Data Locality

Accelerators

- Explore the use of GPUs for computationally heavy kernels
- Custom hardware accelerators

Deployment Mechanisms

- Containerized deployments using Docker
- Integration with HDFS and Tachyon

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