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# **Symphony: Probabilistic Graphical Models for Scheduling Heterogeneous Processors**

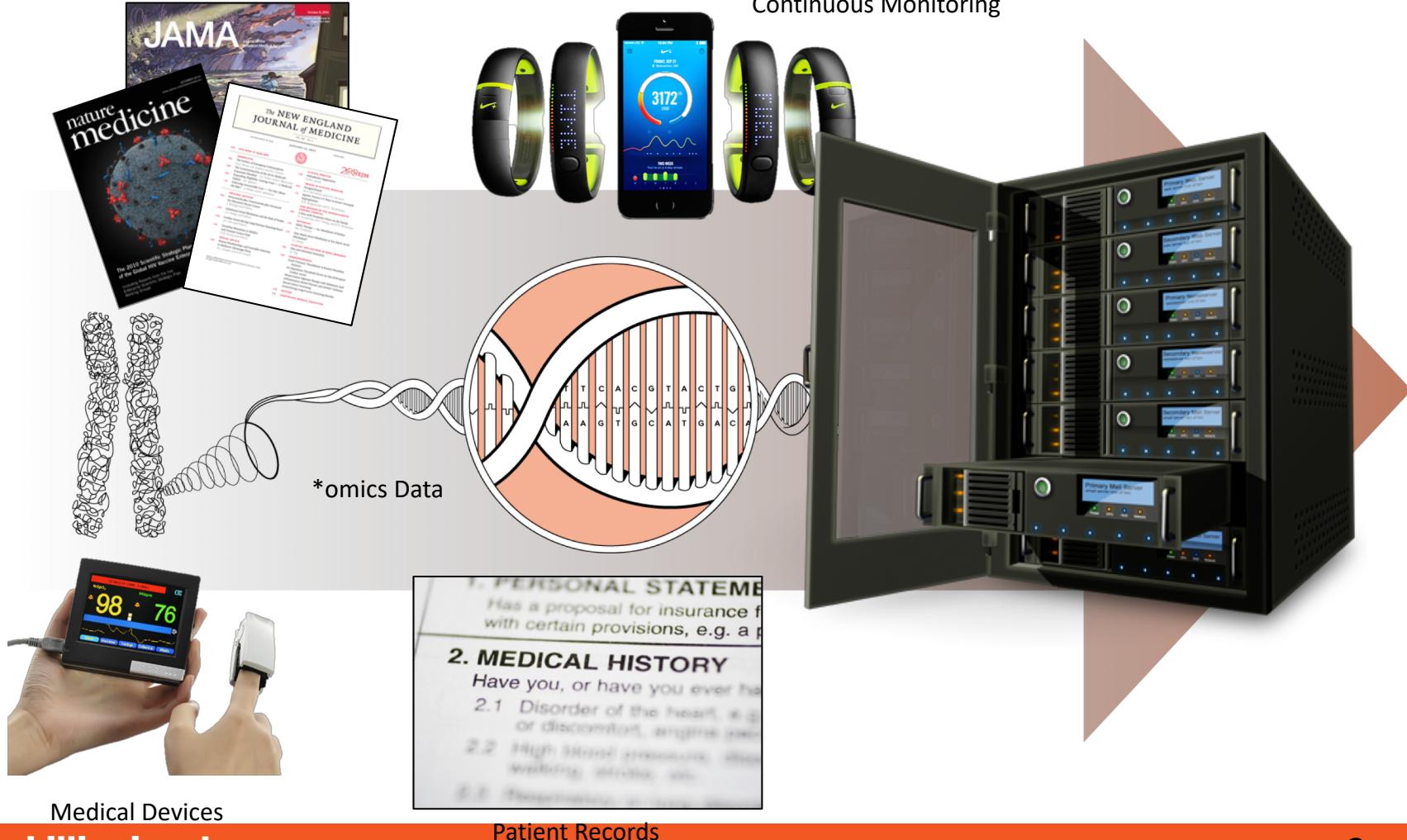




# Overview

Medical

Knowledge

**Timely Diagnosis****Personalized Drugs****Model Drug Response****New Biological Insight**

# Overview

Medical  
Knowledge

Continuous Monitoring

## Summary of Results

Top-down approach to building the CompGen machine  
Static analysis of genomic analyses algorithms  
Hardware Acceleration  
Scheduling strategies to deal with heterogeneous hardware

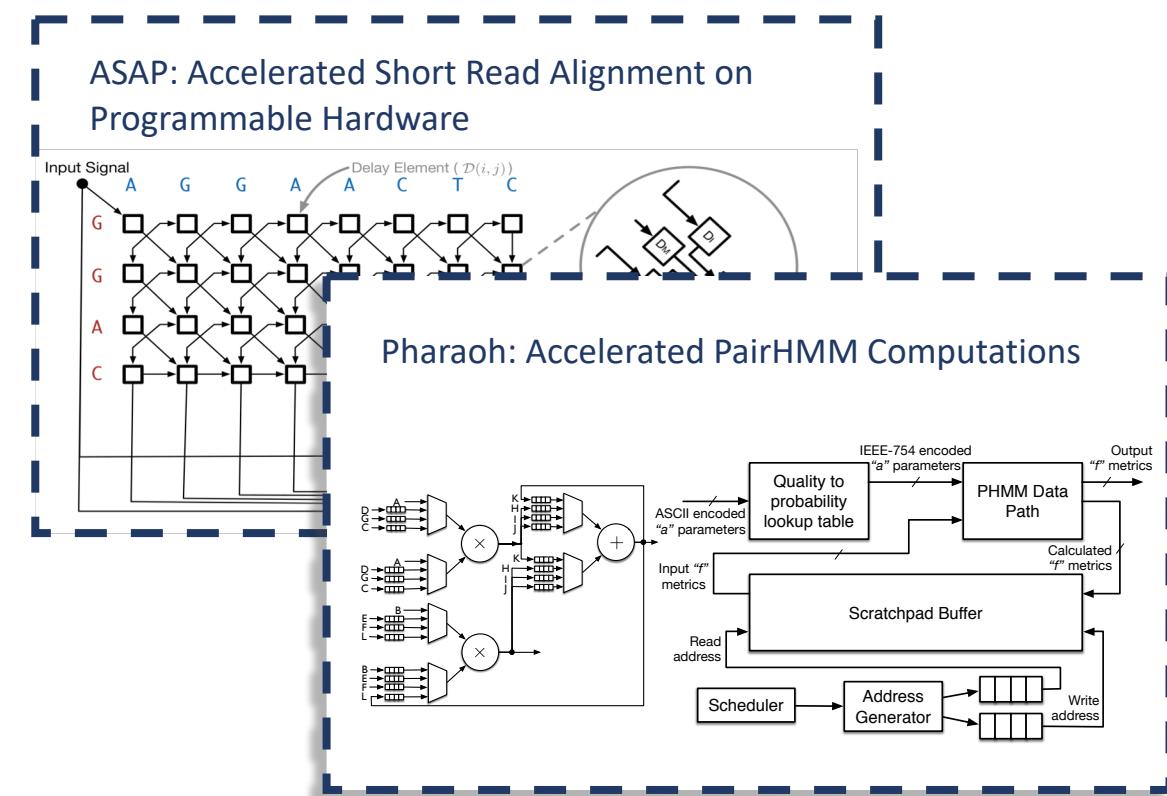
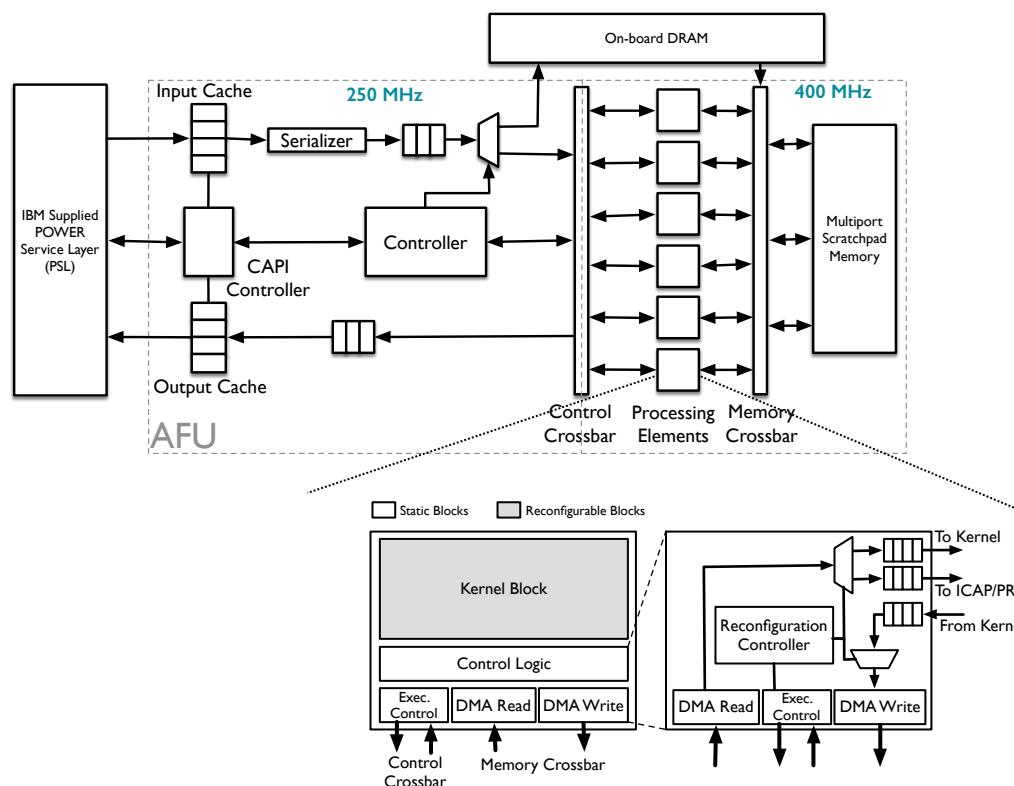
“Variant Calling and Genotyping” Workflow as the driver

	Baseline Runtime	CompGen Accelerated Runtime **	Speedup
Blue Waters – Single Node (CPU)	59 hr	28 hr	2.1x
IBM Power 8 – Single Node (CPU + GPU + FPGA)	36 hr	42 min	84x, 51x
Blue Waters – 10 Nodes (CPU)	-	2 hr	29.5x

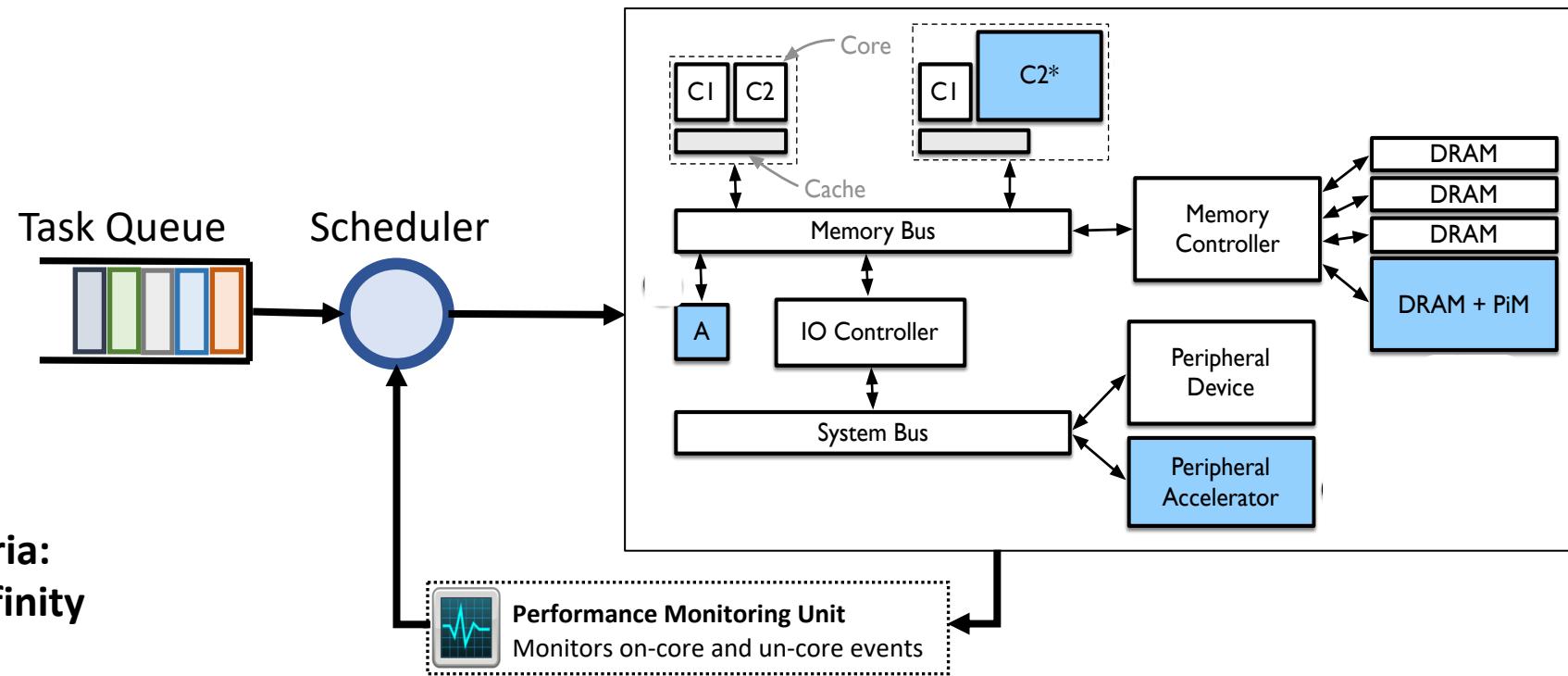
# TCGA: The Computational Genomics Accelerator

A reconfigurable *many-kernel* coprocessor for computational genomics applications

- Common computational kernels across applications
- Memory centric computation: IBM CAPI, Hazard free scheduling, runtime reconfiguration
- Specialized Compute: Algorithmic Approximations, Delay based computation



# Symphony: Scheduling across heterogeneous systems and clusters



## Scheduling Criteria:

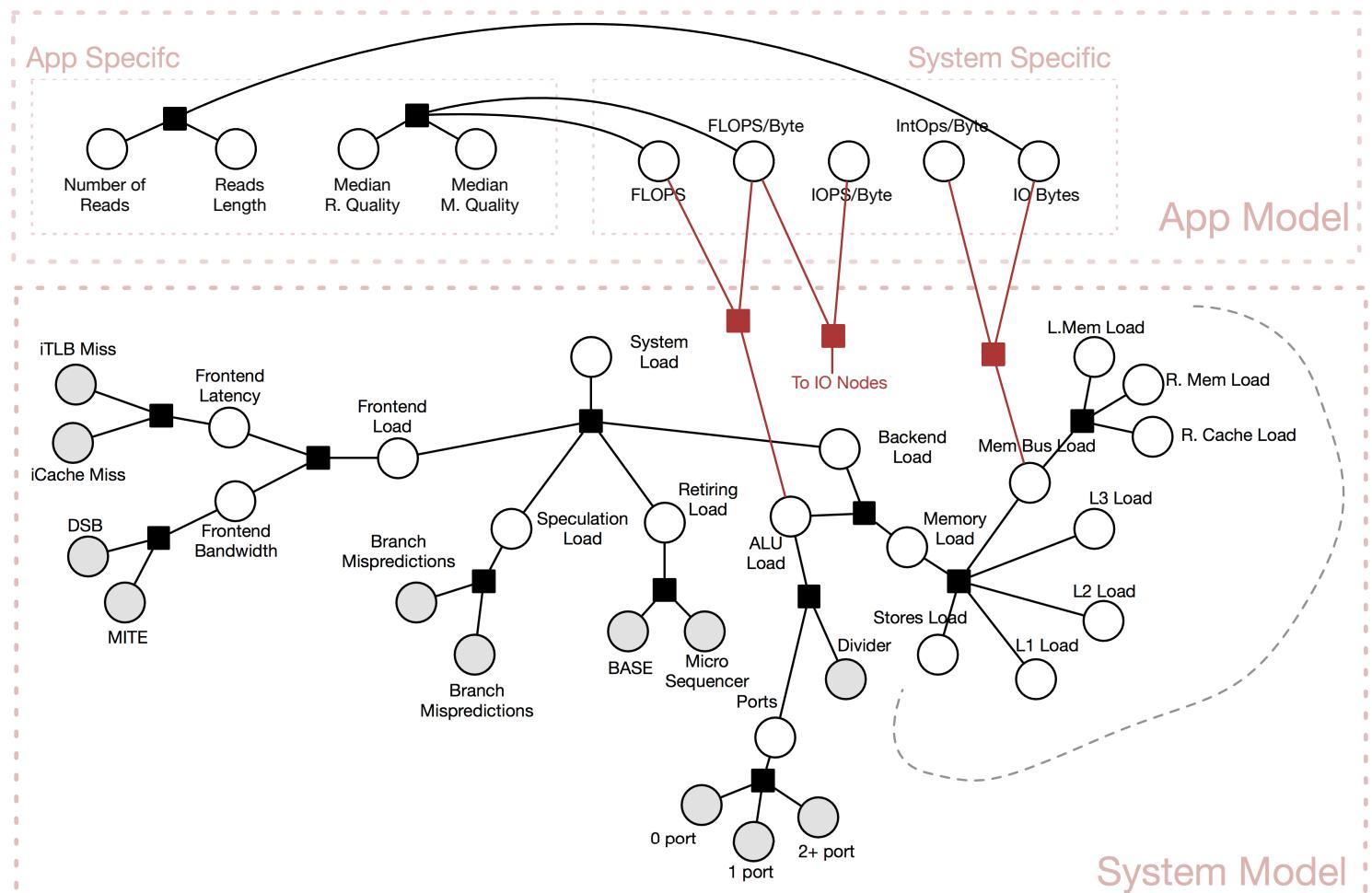
- Processor Affinity
- Data Locality
- Shared Resource Contention

# Sympho systems

## Scheduling Criteria:

- Processor Affinity
- Data Locality
- Shared Resource

- Using probabilistic inference and reasoning to
  - Inexact measurements
  - Time synchronization issues
  - Model processor architectures (Black box)





# Questions?

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