Development of the SMART Coprocessor for Fuzzy Matching in Bioinformatics Applications

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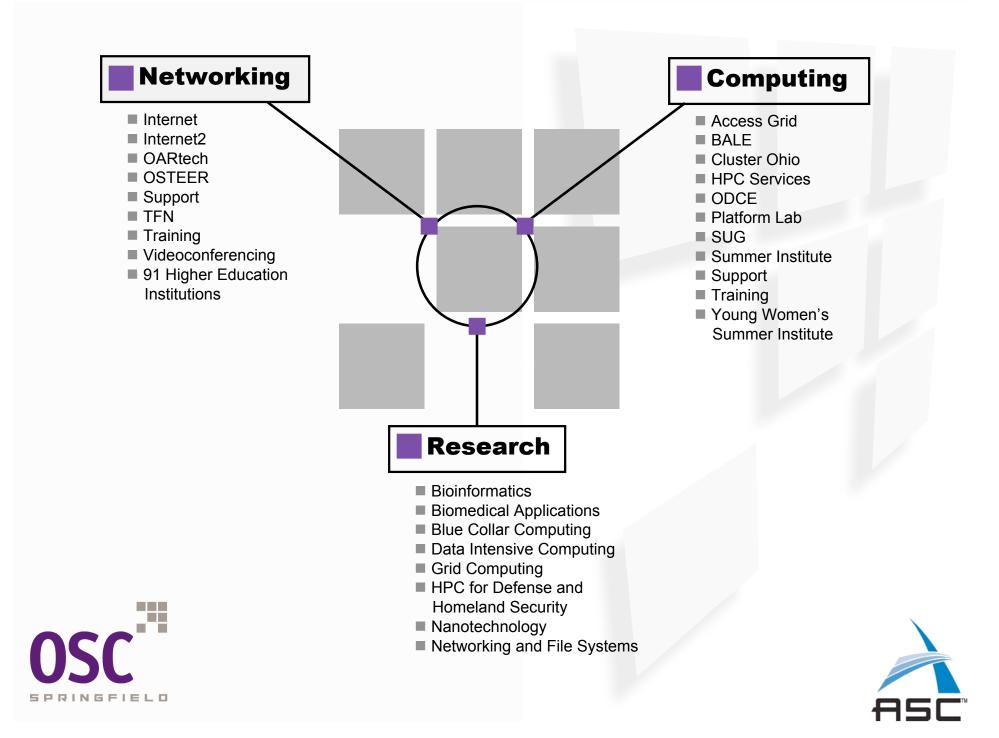


OSC Mission

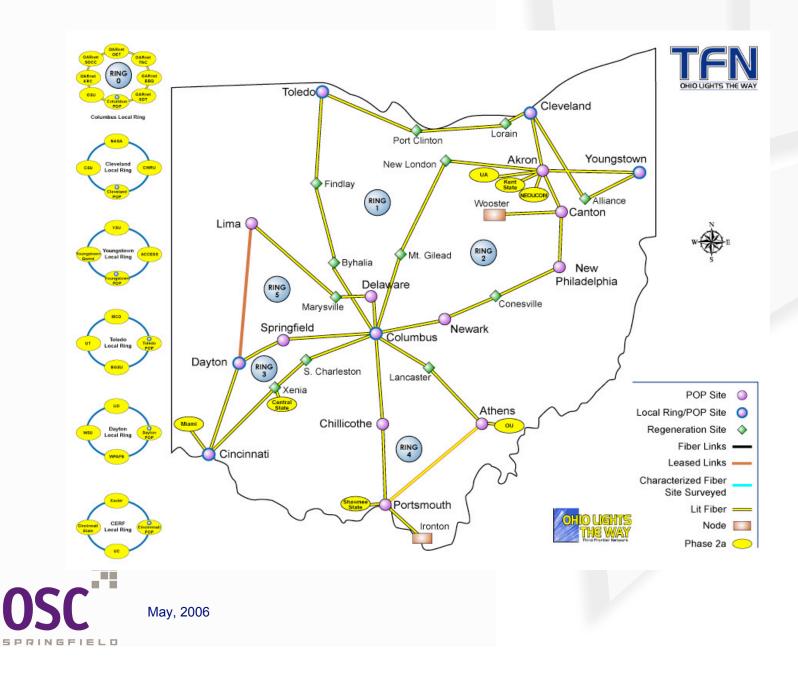
- OSC provides a reliable high-performance computing and high-performance communications infrastructure for a diverse, statewide/regional community including education, academic research, industry, and state government
- OSC promotes and stimulates computational research in order to act as a key enabler for the state's aspirations in advanced technology, information systems, and advanced industries, and,
- OSC acts as a catalytic partner of Ohio universities and industries to enable Ohio to compete for international, federal, and state funding, focusing on new research and business opportunities in:







OSC OARnet: TFN Overview





OSC HPC: Systems

- Columbus
 - 512p Intel Pentium 4 Xeon Cluster (2.5T)
 - 540p HP Intel Itanium2 Cluster (2.4T)
 - 32p SGI Altix (Itanium2) (.17T)
 - 3 16-way SGI Altix 350s (Itanium2 1.4GHz) (.27T)
 - 40p Sun SunFire 6800 (.07T)
 - 100p AMD Athlon Visualization Cluster (.3T)
 - IBM FastT900 and FastT600 (.5 PetaBytes of disk)
- Springfield
 - Cray X1 (.2T)
 - Cray XD1 (.32T+FPGA)
 - Apple Xserve G5 (.5T)











OSC and FPGAs

- Began using FPGAs in 2001
 - TimeLogic production system for bioinformatics
 - Users were pleased with performance
 - Wanted to program, but environment was closed
- Acquired XD1 in 2004
 - Beta site for XD1
 - Part of Data Intensive Computing Initiative
 - FPGAs became available to program for applications
 - Fortunate to have VHDL experience available
 - Tools were in infancy, but potential was getting sorted out
- Demonstrated potential
 - Papers at CUG 2005, FCCM 2006, etc.





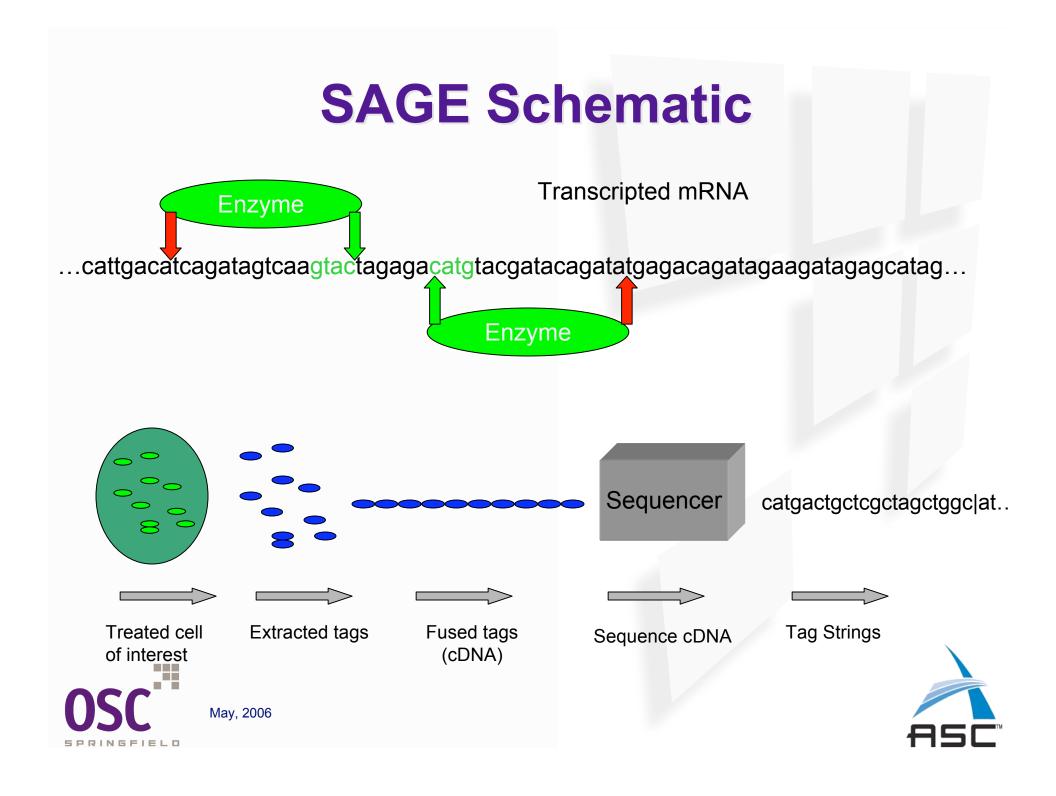


What is SAGE?

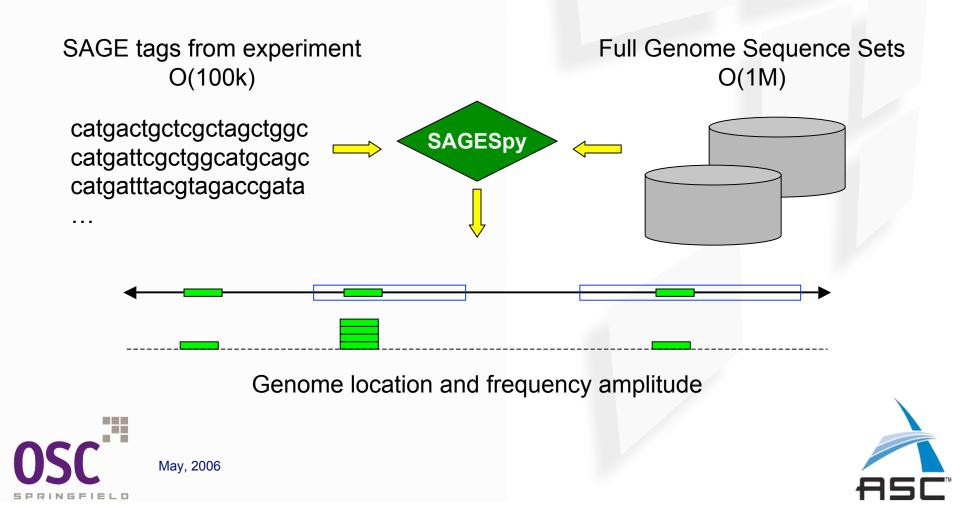
- SAGE = Serial Analysis of Gene Expression
- Originally developed in 1995 to study cancer
- Select for short unique segments that can be readily extracted, characterized and located
- Primary use
 - Transcriptome analysis creating a physical map of an organism's genome
 - Quantitative measurement of an organisms response to events
 - Alternative to gene expression micro-array analysis

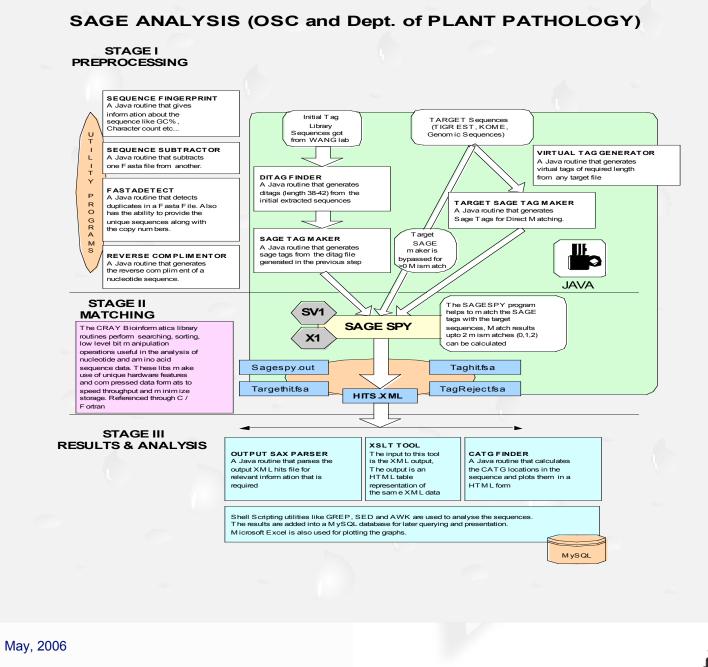






Map Back to Known Genome Regions





SPRINGFIELD



The Challenge

- To create a highly efficient means to compare very large quantities of short DNA sequences
 - All short tags (limited by chemistry of enzyme)
 - Theoretical limit for RL-SAGE: 4¹⁷ unique tags
 - Reality: millions matched against hundreds of thousands
- Scanning entire genomes for SAGE tag patterns
 - Identify matching single and double mismatches (compensate for experimental error)
 - Identify reverse complement matches



SAGE Background

- Originally designed for lengths of 9-10 nucleotides
- Various extensions to improve discriminating power when mapped back to original DNA locations
- Extended to 21 nucleotides in RL-SAGE
- Current capabilities demand
 - Files containing 3 million or more tags
 - Searching against entire genomes
 - Hit rates low in terms of absolutes





Motivations for Current Work

- Speed analysis of SAGE data
- Move analysis closer to experimental benchtop
- Lower costs to compare while maintaining turnaround time
- To determine if FPGA implementation can be faster than fastest other implementations





SMART Solution

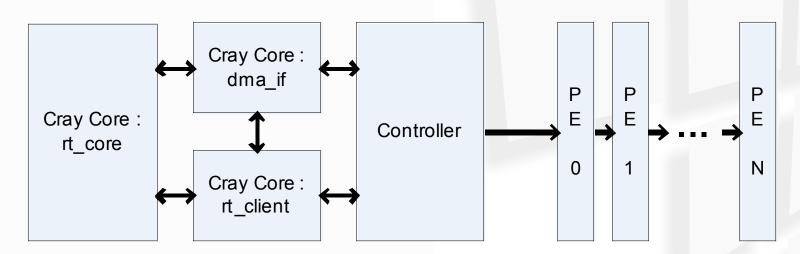
- SMART
 - Sage Method Analysis with Reconfigurable Technology
- Guiding philosophy for the solution
 - Fuzzy matching likely to be more efficient on FPGA
 - Keep it simple (maximize parallel operations)
 - Data flow choice
 - Flow target more rapidly than query (each PE has a unique pattern to capture)
 - Rather than flowing query more rapidly than target
 - Design for portability







SMART Solution



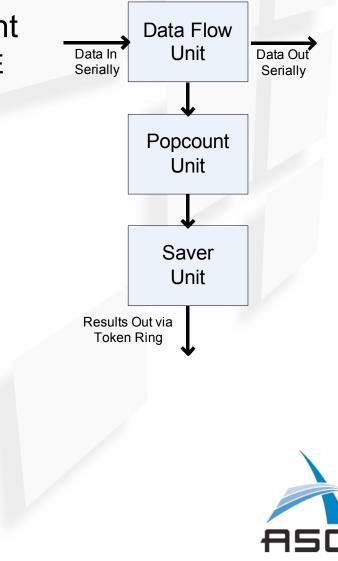
- Major architectural features
 - Processing Element (PE) easily replicated to achieve parallelism on larger FPGAs
 - Controller to isolate machine dependence and manage data flow





SMART Processing Element

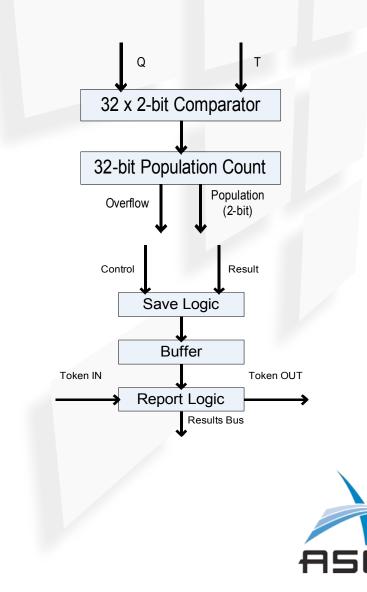
- Overall Design Linear Array Element
 - All data/control signals passed to next PE
 - Allows for design expandability
 - Three main subcomponents
- Component 1 Dataflow Unit
 - Handles the passing and buffering of all data needed by the processor
 - Simple but large unit to achieve high buffering efficiency





SMART Processing Element

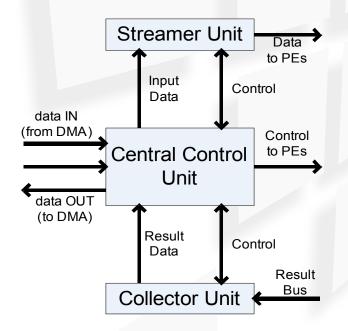
- Component 2 Pop Count Unit
 - Six level pipelined unit
 - Actual "comparisons" done here
 - Optimization possible by collapsing pipeline stages
- Component 3 Saver Unit
 - Analyzes popcount output and buffers hits
 - Handles reporting results via token ring bus





SMART Controller

- Single Controller Terminates
 Chain of Processors
 - Handles all communication minimizing impact of changes required for new environments
 - Contains all state associated with the system (control FSM)
 - Whenever possible, functionality moved from PEs to Controller
 - Also three major subcomponents

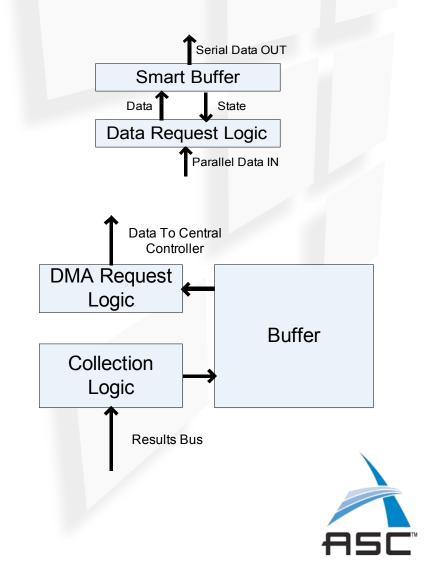






SMART Controller

- The Data Streamer
 - Requests DMA reads from the Central Control Unit
 - Passes characters to the PE chain serially
- The Data Collector
 - Monitors the reporting token ring for results
 - Requests DMA writes from the Central Control Unit





SMART Controller

- Central Control Unit
 - Contains FSM that runs the whole show
 - Provides monitored access to the Cray provided DMA read/write core
 - Passes state information to the PEs via control lines
 - Contains all configuration information





SMART Solution Design Elements

- Design uses preexisting Cray provided IP cores for data transfer
- DMA used for bulk of sequential data transfer
- Solution utilizes duplex nature of interconnect
- Configuration and input data contained in same memory space







Design Elements Continued

- Token ring / results bus combination provides efficient data reporting
- Linear array allows for scaling, efficient usage of resources
- PEs can be expanded to accommodate additional functionality easily



ASC

Development Overview

Development Stages

- 1. System Design
- 2. System Implementation
- 3. System Simulation
- 4. System Synthesis
- Software Interface
 - Lightweight reads file, compresses data, sets up DMA regions
 - In development







SMART Design and Implementation

- Initial Design Strategy
 - Space scalability was important
 - Influenced by other OSC/XD1 work
 - Objective: exceed performance of Opteron and X1 version of SAGESpy
- The Implementation/Redesign Cycle
 - Standard practice





SMART Solution Status

- Unit Testing [done]
 - Testing functionality of individual components
- Data Path Testing [done]
 - Testing functionality of strings of components
- Full Controller/Full PE Testing [done]
 - Testing of our complete unit
- Full Unit Testing [simulation in process]
 - Testing of the full hardware





SMART Synthesis

Synthesis results

- Single Virtex2Pro FPGA will hold up to 60 PEs running at 180MHz at least
- Virtex4 could possibly hold 300
 PEs running at an estimated 350MHz

Unit	Slices	MHz	
Controller – Full Unit	299	240	
dma_if (Cray) – Full Unit	727	190	
rt_client (Cray) – Data Collector	468	270	
Processing Element - Dataflow	119	344	
Processing Element - Popcount	65	307	
Processing Element - Saver Unit	102	280	



SMART Software

- Software development and specification
 - All efforts were made to keep software simple
 - Target use within SAGESpy application and OBL
 - Cray BioLib used in FASTA file read and compression
 - Program arranges data in DMA memory space, then signals FPGA and waits
 - Program outputs results in simple ASCII.
 - XML, other formats planned





SMART Results

- SMART Raw number projections:
 - Will be able to perform 10.8B comparisons per second (Virtex2Pro)
 - 60 processors
 - 180 MHz clock rate
 - One compare per clock
 - Not as compelling as hoped for





Performance Comparison

		Computation time in seconds				
	Number of target bps	SV1	X1	XD1 w V2P (estimated)	XD1 w V4 (theoretical)	Number of Hits
Chrom1	13333992	1.35	0.36	0.066	0.0165	29
Chrom4	9923256	1.00	0.27	0.049	0.0124	34
Chrom10	5964420	0.61	0.16	0.030	0.0074	8
TIGR(EST)	9889404	1.00	0.26	0.049	0.0124	333

Table 1. Performance of SAGESpy XOR comparison approach relative to estimates for SMART co-processor. Speed was measured for one hundred query tags with a two mismatch threshold.

- Assumptions:
 - 200 MHz speed of FPGA (Virtex2Pro)
 - 100 processing elements per FPGA (Virtex2Pro)
 - 20 billion comparisons/second/FPGA





SMART Future

- SMART not yet finished expecting to:
 - Enhance functionality
 - Simultaneous reverse string comparison
 - Variable sizes for queries/tags
 - Decode output into standard C types
 - Improve performance
 - Use increasing memory on FPGA more effectively
 - Internal buffer overflow protection
 - Consolidate compression with reading of original data
 - Multiple FPGA implementation





What We Learned Along the Way

- Writing hardware is a more dynamic experience than writing software
- Don't grow attached to your initial ideas. If something isn't working, find another way!
- Reduce communication protocols between functional units as much as possible
- Naming conventions are very, very important
- Keep detailed development logs
- Unit testing will save you time and frustration







Conclusion

- Reconfigurable computing application development still hard with VHDL
- Virtex2Pro is good, but isn't quite compelling
- Virtex4 becomes compelling
- I/O is still a major factor
- Anxious to compare with C-based solutions to FPGA algorithm specification





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Thank you.

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