Many-core Acceleration for Biomedical Applications

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  - Dana Schaa
- Undergrads
  - Chanelle Green, Chawandia Mack – Spelman
  - Justin White - Northeastern

GPUs are Everywhere!

- Every desktop and laptop has a GPU on board
- Graphics Processing Units – NVIDIA, AMD Firestream/Fusion, IBM Cell, Intel Larrabee
  - Cost-effective desktop supercomputing!!
- User-friend programming interfaces and tools
  - CUDA (NVIDIA)
  - CTM/Brook+ (AMD)
  - OpenCL

A wide range of GPU applications

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- 3D image analysis
- Adaptive radiation therapy
- Acoustics
- Astronomy
- Audio
- Automobile vision
- Bioinfomatics
- Biological simulation
- Broadcast
- Cellular automata
- Fluid dynamics
- Computer vision
- Cryptography
- CT reconstruction
- Data mining
- Digital cinema / projections
- Electromagnetic simulation
- Equity training
- Film
- Financial
- Languages
- GIS
- Holographics cinema
- Machine learning
- Mathematics research
- Military
- Mine planning
- Molecular dynamics
- MRI reconstruction
- Multispectral imaging
- N-body simulation
- Network processing
- Neural network
- Oceanographic research
- Optical inspection
- Particle physics
- Protein folding
- Quantum chemistry
- Ray tracing
- Radar
- Reservoir simulation
- Robotic vision / AI
- Robotic surgery
- Satellite data analysis
- Seismic imaging
- Surgery simulation
- Surveillance
- Ultrasound
- Video conferencing
- Telescope
- Video
- Visualization
- Wireless
- X-Ray

Developing a suite of Biomedical Image Reconstruction Libraries – CUDA/OpenCL

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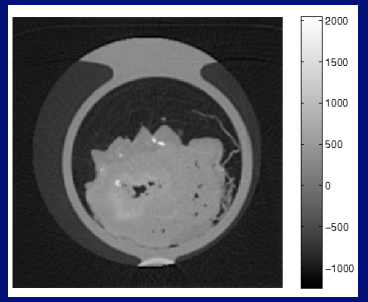
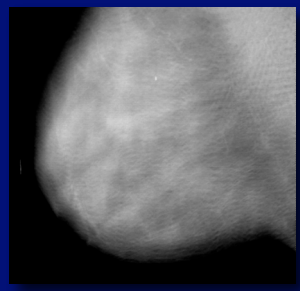
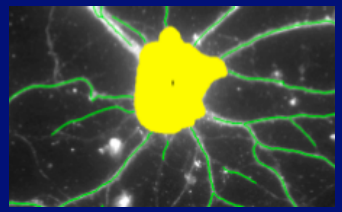
- Target applications:
  - Deformable registration - radiation oncology
  - 3-D Iterative reconstruction – cardio-vascular imaging
  - Maximum likelihood estimation – Digital Breast Tomosynthesis
  - Motion compensation in PET/CT images - cardiovascular imaging
  - Hyperspectral imaging – skin cancer screening
  - Image segmentation – brain imaging







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Performance of Two Imaging Applications on a GPU

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- 3-D Tomosynthesis Image Reconstruction
  - Reduces false-positive rates during breast cancer screening
  - Utilizes a limited angle tomography approach using many 2-D images to generate a 3-D image
  - Performs an iterative Maximum Likelihood Estimation for 3-D image reconstruction
  - Performance is a barrier to image-guided biopsy
- 3-D Spiral Cone-Beam Cardiac Image Reconstruction
  - Key new approach for identifying blockage in coronary arteries
  - Performs a least squares image reconstruction
  - Involves a forward and backward projection
  - Performance is a barrier to improve image quality

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Conventional 2-D Mammography

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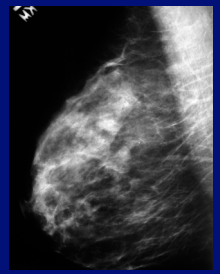
Nature of breast cancer screening work:

- For each 1000 women screened with mammography:
  - ~80 (varies from 50 to 130) are called back for additional imaging - (X-ray, US, MRI)
  - ~20 are recommended for some form of biopsy
  - ~3-7 cancers will be discovered on pathology from these biopsies

- **Overall this yields:**
  - Reduction in US breast cancer mortality: 30%
  - Sensitivity: 85% of all breast cancers will be detected by mammography
  - Specificity: 80 false positives in 1000 screenings
  - Positive predictive value (biopsy): ~25%



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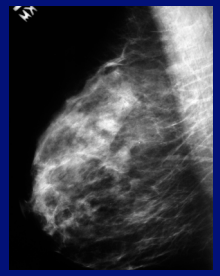
Conventional 2-D Mammography

- **Is this good enough?**
  - Positive predictive value: (~25%) 3 of 4 biopsies are benign which carries a high emotional load and additional cost
- **Problems are caused by superimposed tissue (structure noise)**
  - Missed cancers (false-negatives)
  - A cancer is obscured by superimposed breast tissue
  - Unnecessary callbacks (false-positives)
  - Superimposed normal breast tissue may look like a tumor in a 2-D mammogram



Digital Breast Tomosynthesis (DBT) — 2nd generation GE prototype

Detector:
- 300msec readout time
- 23cm × 19.2 cm area
- 100 micron pixel size

Acquisition:
- 15 projections
- 40° arc
- 15s acquisition
- Mo and Rh anodes
- same dose as CC+MLO
- 360° gantry rotation

permits all standard views

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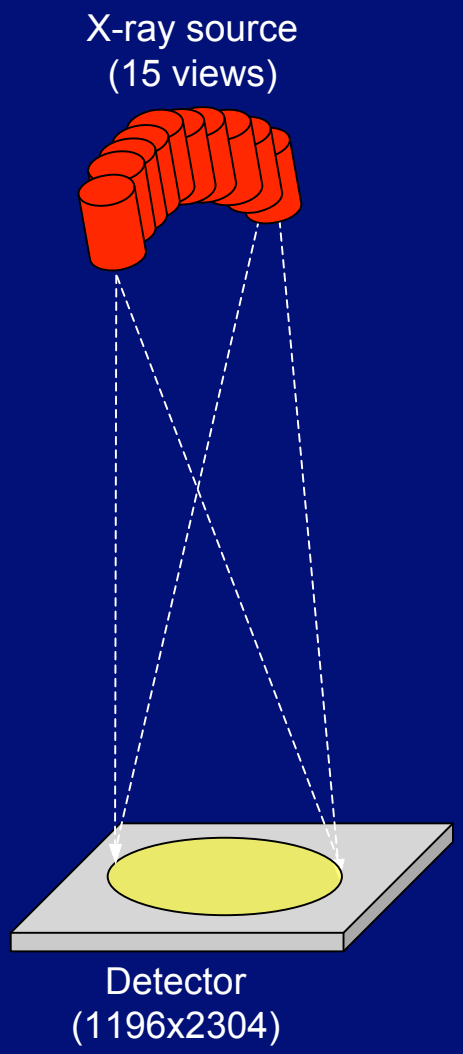
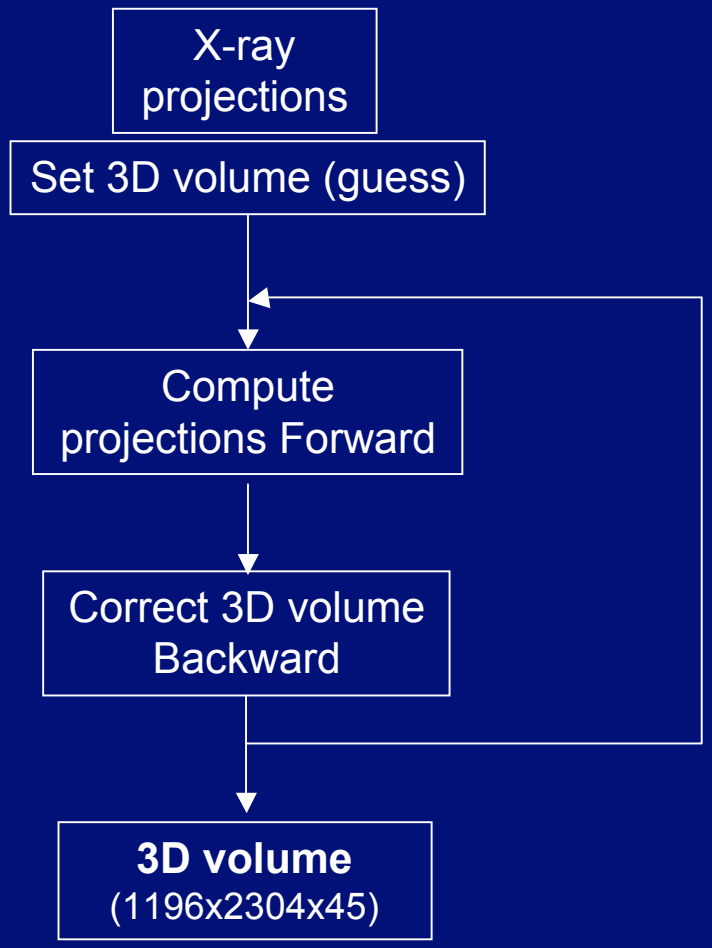
Tomosynthesis Image Reconstruction





Tomosynthesis Acceleration Study

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1. Workstation
   - Single Intel quad-core Xeon 3.2 GHz
   - Multithreaded implementation
   - 4 GB of RAM
2. Cluster A – Teracluster
   - 2.0 GHz Xeon Pentium M
   - 2 CPUs per server, dual core CPUs
   - 8 GB of RAM per server
   - Gigabit ethernet switch
3. Cluster B – Opportunity Cluster
   - 3.2 GHz Xeon EMT 64 processors
   - 2 CPUs per server
   - 4 GB of RAM per server
   - Gigabit ethernet switch
4. NVIDIA 8800 GTX GPU
   - CUDA 2.0

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Tomosynthesis acceleration on a GPU

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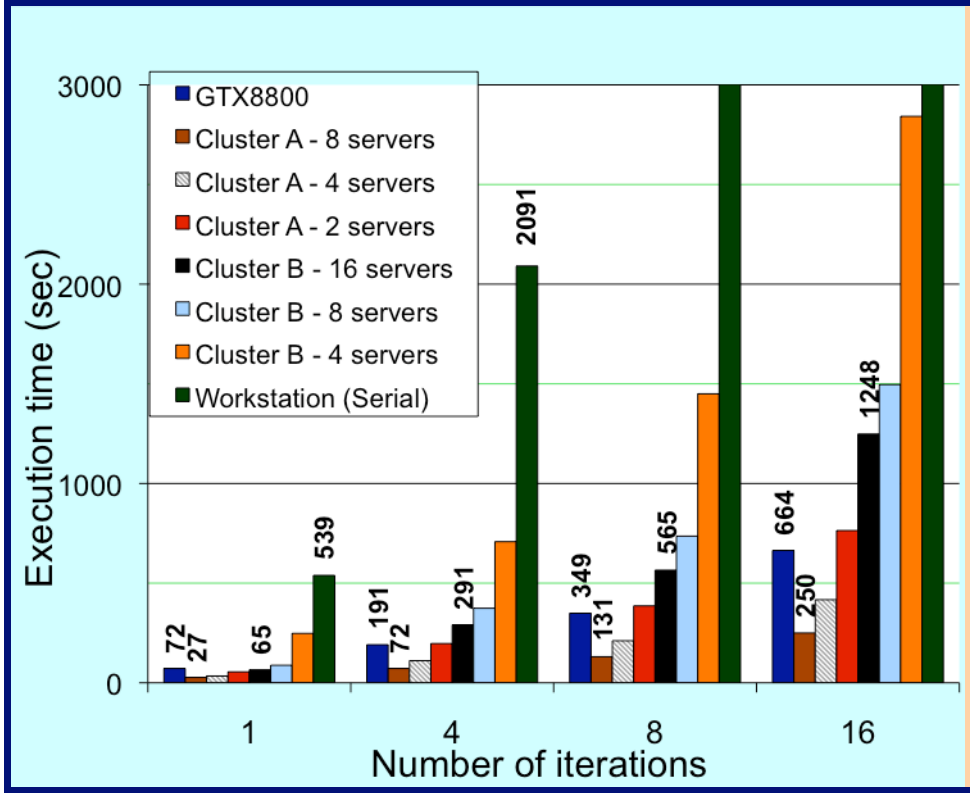
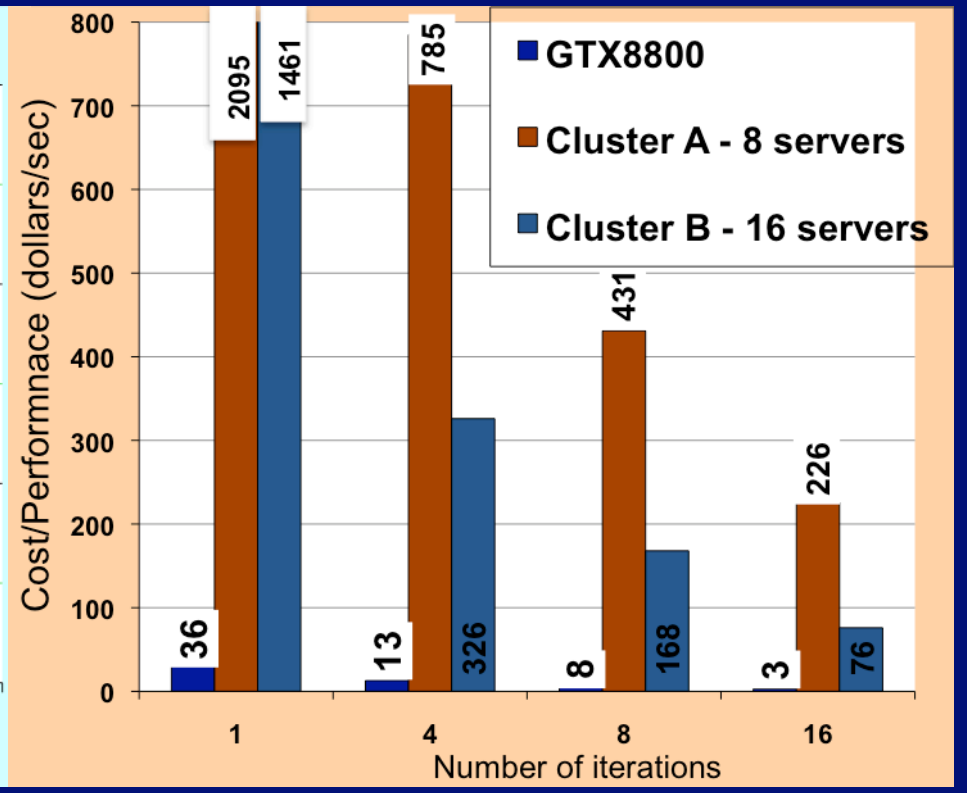
Speedup and $/sec of Breast Tomosynthesis Reconstruction* on a NVIDIA GTX8800





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Reconstruction Computing Performance

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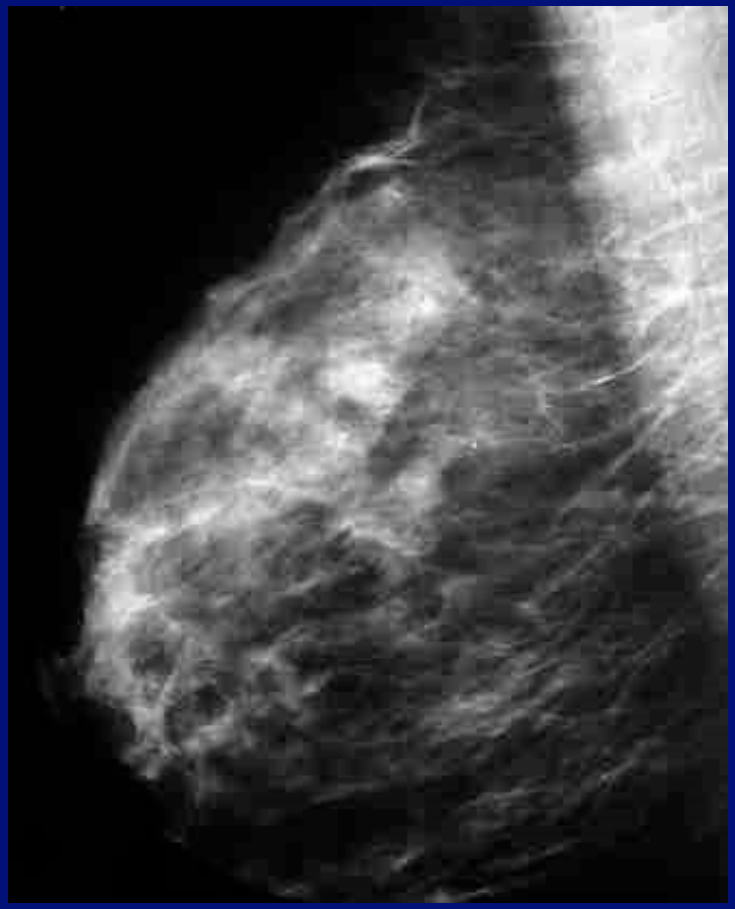
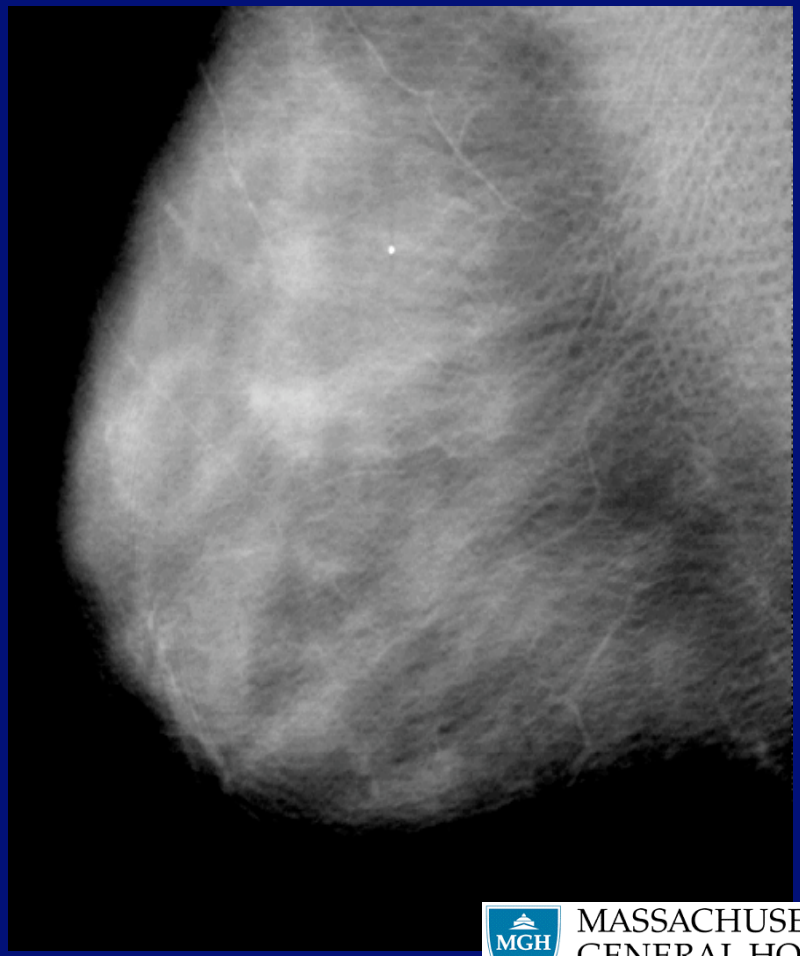
What can a GPU buy you?

Reconstructions in 1.5 secs on 3 NVIDIA 280's





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Impacting heart disease with GPUs

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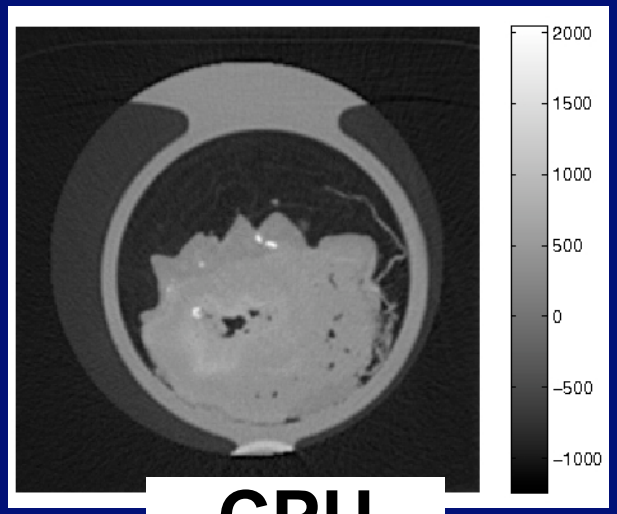
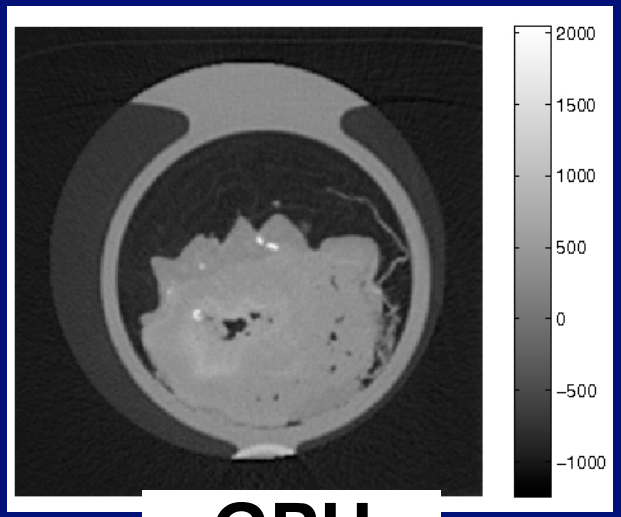
- Currently, coronary heart disease (CHD) is the single leading cause of death in America
- 3D CT imaging can be used to identify vulnerable plaque
- Forward and backward projection of 3D helical cone beam CT have been implemented on a NVIDIA Tesla S870 multi-GPU platform using CUDA



CPU



GPU

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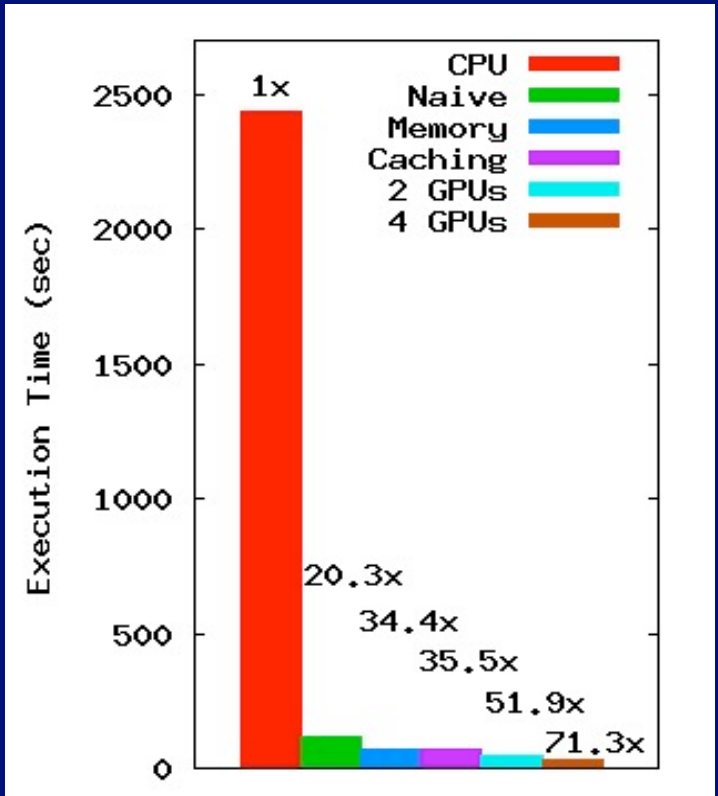
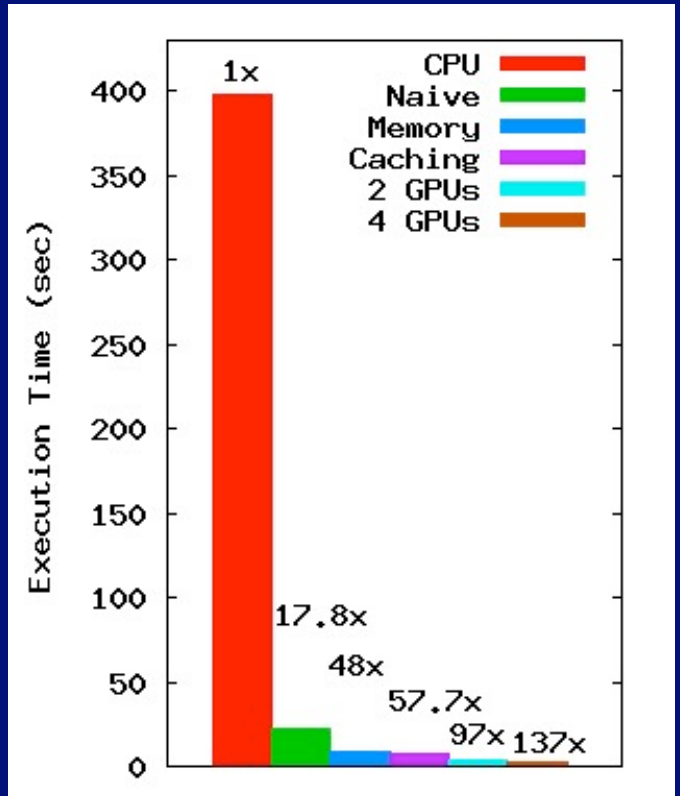
Impacting heart disease with GPUs

- Single GPU speedup versus multi-threaded dual-core CPU execution – 20.3x forward / 17.8x backward
- A series of optimizations applied, includes utilizing multiple GPUs – 71.3x forward / 137x backward



Forward projection



Backward projection

* Collaboration with Synho Do (MGH), Clem Karl (BU) and Homer Pien (MGH)

GPU Strengths

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- Supercomputing on the desktop
- Easy to program (small learning curve)
- Many demonstrated successes accelerating complex applications
- CUDA allows us to read and write data at any location in the device memory
- Memory close to the processors (registers + shared memory)

GPU Limitations

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- Porting applications to the latest-and-greatest hardware becomes a time-consuming task
  - Suggests we need to raise the abstraction level
  - OpenCL is a step in the right direction
- Many microarchitectural details are hidden
  - Performance optimization requires deep knowledge of the microarchitecture
- Better tools are needed
  - Register usage
  - Memory blocking and layout
  - Aggressive threading schemes
  - Multi-GPU exploration
- What do researchers want??
  - Semi-automatic tuning

GPU Acceleration

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- Multi-GPU acceleration
- Memory coalescing and loop vectorization
- PTX optimization
- Library optimization

How can we more effectively exploit GPUs?

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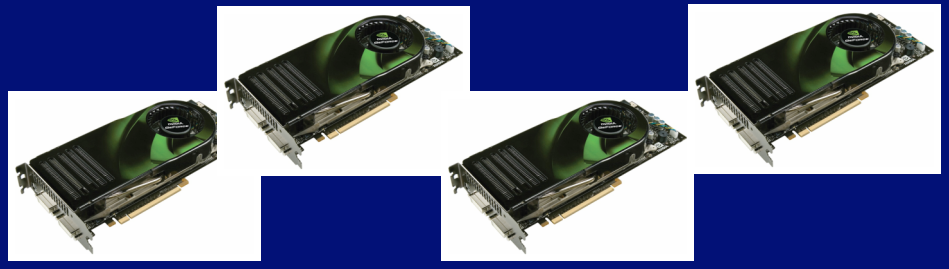
- We are developing a suite of biomedical imaging libraries specific to GPUs
  - Plan to target both CUDA (performance) and OpenCL (portability)
- We are expanding on our previous work on a profile-guided approach for CUDA code to guide users on the best target multi-GPU platform for the specific application
  - ✓ **D. Schaa and D. Kaeli, "Exploring the Multiple-GPU Design Space," *IEEE International Parallel and Distributed Processing Symposium*, Best Paper Award, May 2009.**



Multi-GPU Design Space Exploration

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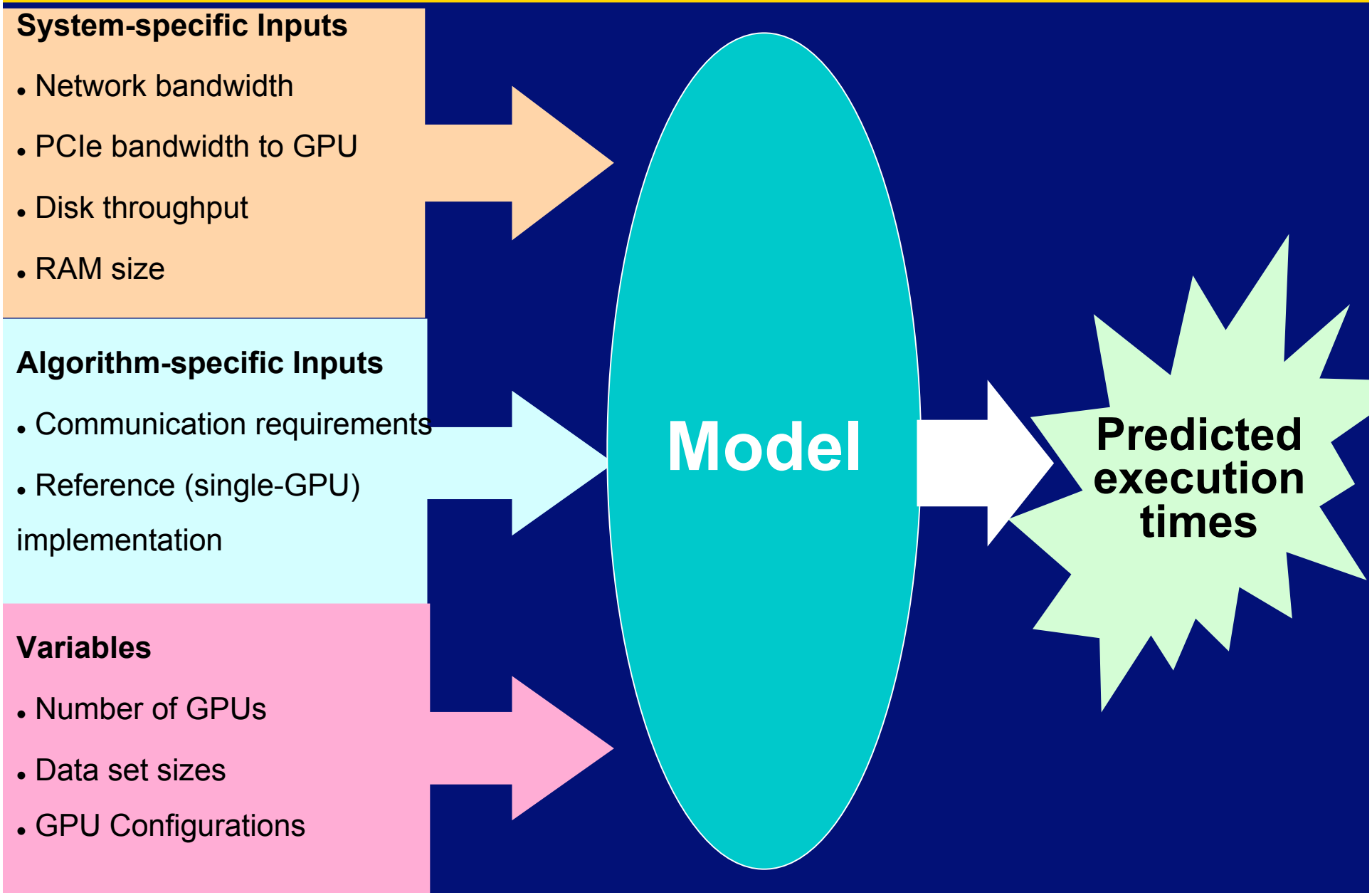
- Predict performance for GPU programs while scaling either the number of GPUs or the input data size
- Select the optimal configuration of GPUs (distributed/multi-system or shared-memory/multi-processing, and how many) without having to purchase hardware
- Avoid architecture-specific optimizations which limit scalability and portability to future generations of hardware

Requirements for Performance Prediction



Current GPU Optimizations

- Loop Vectorization – targeting the vector architecture provided for on the AMD Firestream platform
- Targets linearizing data to improve the number of loops that can vectorized on AMD GPUs

```
A[0:N] [0:M]
B[0:N] [0:M]
for (i1=0;ii1<N;i1++)
For (i2=0;i2<=M;i2++)
A[i1][i2]=B[i1][M-i2]+1;
```

Transform Array B

```
A[0:N] [0:M]
B[0:N] [M:0]
for (i1=0;ii1<N;i1++)
For (i2=0;i2<=M;i2++)
A[i1][i2]=B[i1][i2]+1;
```

*To appear at PPOPP 2010

Loop vectorization

- Loop Vectorization – targeting the vector architecture provided for on the AMD Firestream platform
- Targets linearizing data to improve the number of loops that can vectorized on AMD GPUs

```
A[0:N] [0:M]
B[0:N] [0:M]
for (i1=0;ii1<N;i1++)
or (i2=0;i2<=M;i2++)
][i2]=B[i1][M-i2]+1;
```

Transform Array B

```
A[0:N] [0:M]
B[0:N] [M:0]
for (i1=0;ii1<N;i1++)
For (i2=0;i2<=M;i2++)
A[i1][i2]=B[i1][i2]+1;
```

Obtained up to 11X speedup over scalar code for Livermore Loops

*To appear at PPOPP 2010

GPU Memory Accessible in CUDA

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- Mapped host memory: up to 4GB, ~5.7GB/sec bandwidth (PCIe), accessible by multiple GPUs
- Global memory: up to 4GB, high latency (~600 clock cycles), 140GB/sec bandwidth, accessible by all threads, atomic operations (slow)
- Texture memory: read-only, cached, and interpolated/filtered access to global memory
- Constant memory: 64KB, read-only, cached, fast/low-latency if data elements are accessed in unison by peer threads
- Shared memory:16KB, low-latency, accessible among threads in the same block, fast if accessed without bank conflicts

Memory Optimizations

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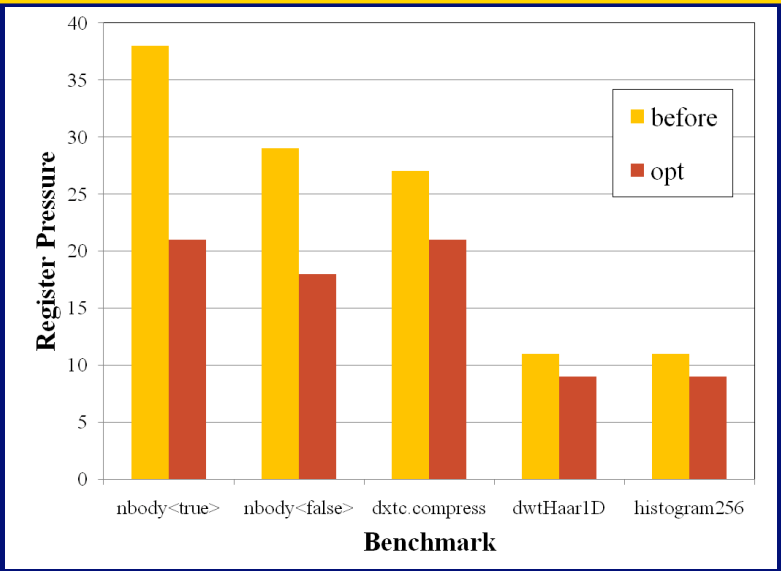
- Memory Selection and Coalescing on NVIDIA GPUs
- Multiple memory spaces are exposed to the program on NVIDIA GPUs – a remnant of graphics

Memory	Location	Cached	Access	Scope
Global	Off Chip	No	R/W	Thread Grid
Constant	Off Chip	Yes	R	Thread Grid
Texture	Off Chip	Yes	R	Thread Grid
Local	Off Chip	No	R/W	Thread
Shared	On Chip	N/A	R/W	Thread Block
Register	On Chip	N/A	R/W	Thread

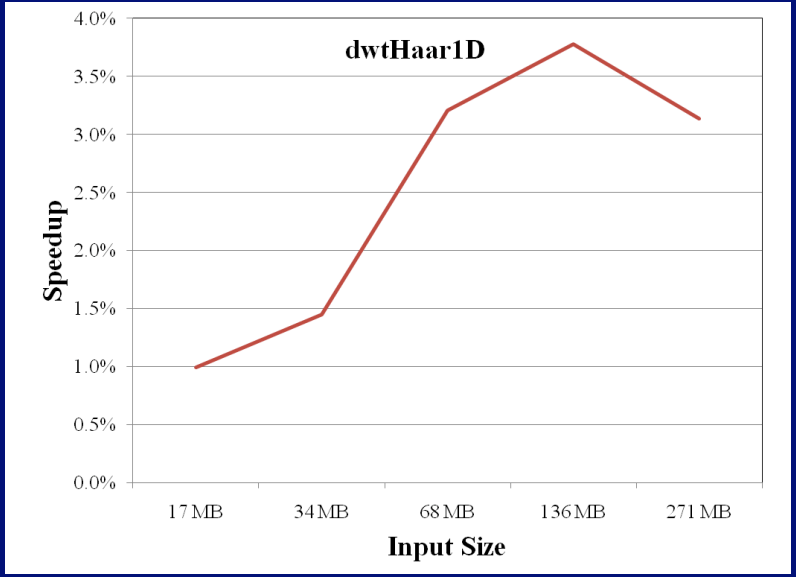
- Mathematical framework developed that characterizes loop-based array iteration spaces
- Applied mapping framework to Parboil and PhysBAM programs
- Speedups ranged from 1.3X to 15X speedup

GPU Optimizations – Rematerialization in PTX

- Goal: Reduce register pressure in PTX code which should improve performance on NVIDIA GPU
- Implemented a backward list scheduler that arranges instructions within a basic block
- Performs liveness analysis and builds a data dependence graph
- The scheduler iterates through the ready list evaluating a cost function depending on the set of registers live and the use-defs of each instruction
- We rematerialize selected registers based on lifetimes and register pressure



***Presented at NVISIONS 2009**



SC09 - Joint work with J. Cavazos, U. Delaware and M. Smith, NVIDIA

Library Construction for GPUs

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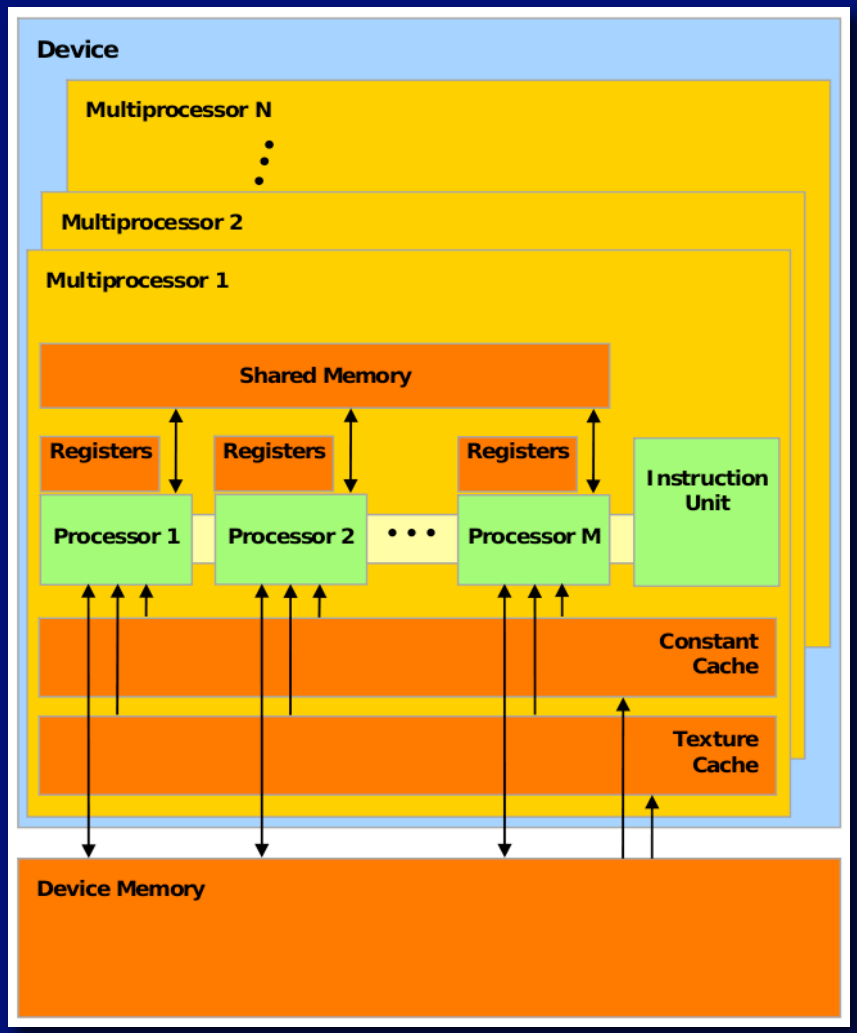
- System-wide mapping: different parts of an application may run better on the CPU or GPU
- Developing general GPU solutions for multiple problem instances is difficult
- Matching the architecture is important
  - Select a thread hierarchy with limited shared resources (shared memory, registers)
  - Exploit the characteristics of the memory hierarchy



MATLAB OpenCL API (MOCA)

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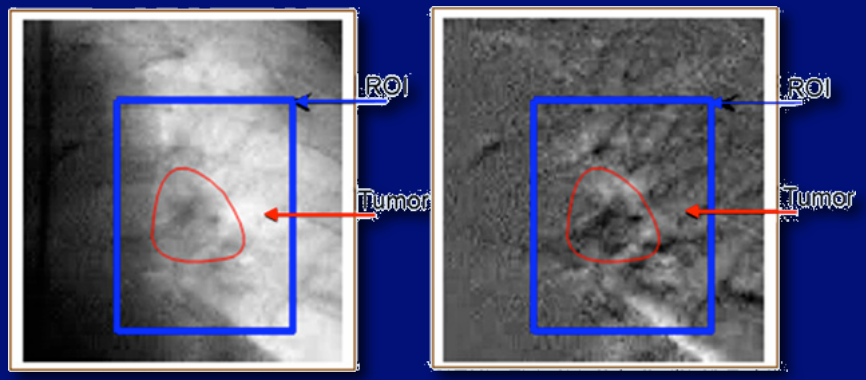
- MOCA aids implementation space exploration
  - Currently binds to CUDA, but designed to work with OpenCL
- Raises the level of abstraction for faster and easier development
  - Data structures track multiple aspects of host and GPU resources
  - Functions wrap up numerous API calls into larger tasks
  - Front end catches some errors producing useful diagnostics
  - Hides different code for different memory types
  - Concentrates CUDA code for a given activity in one location
- Goal: use MOCA functionality to explore proper parameterization of GPU libraries for adaptability

Case Study: Lung Tumor Tracking

- Based on a MATLAB lung tumor tracking application by Cui, et al.
- Matches a tumor template with incoming imagery using 2D correlations – corr2() in MATLAB
- Application handles variation during respiration by using multiple tumor templates and searching a region of interest around the original template location
- Results in greater computational requirements – a 2D correlation for each template for each position in the ROI for each video frame

$$corr2(A,B)=\frac{\sum_M\sum_N (A_{MN}-\bar{A})(B_{MN}-\bar{B})}{\sqrt{(\sum_M\sum_N (A_{MN}-\bar{A})^2)(\sum_M\sum_N (B_{MN}-\bar{B})^2)}}$$



Y. Cui, J. G. Dy, G. C. Sharp, B. Alexander, and S. B. Jiang, "Multiple template-based fluoroscopic tracking of lung tumor mass without implanted fiducial markers." Physics in medicine and biology, vol. 52, no. 20, pp. 6229–42, 2007.

Data Set Parameters

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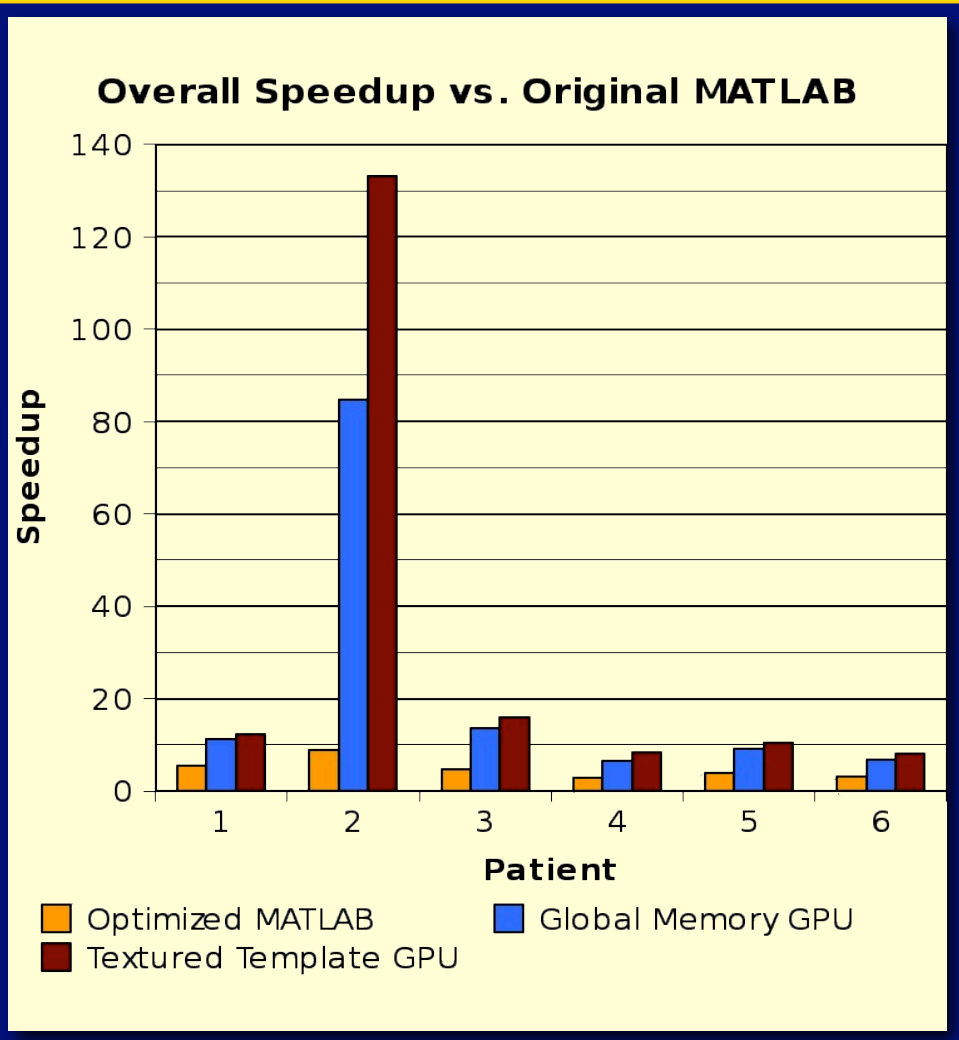
Patient	Frames	Templates	Template Dimensions	Shift V/H	corr2() Calls
1	442	12	53x54	18/9	3532464
2	348	13	23x21	11/5	1144572
3	259	10	76x45	9/4	442890
4	290	11	116x175	9/3	424270
5	293	12	78x109	11/6	979524
6	210	14	107x159	9/2	279300

- Data set includes parameters that are not powers of two
  - Total computational requirements vary on corr2() calls and template sizes
- GPU implementation launches all of the 2D correlations in parallel
  - Six individual GPU kernel are used to implement the parallel corr2()
  - Current kernels can be improved: no shared memory usage and uncoalesced global memory accesses

Explored Memory Mappings

- MOCA was used to move application data into different GPU memory types
  - Frame and template data in global or texture memory
- Runtime compared to a second MATLAB implementation optimized with knowledge from studying the application
- Textured template data improved the average GPU speedup from 22 to 31 (85 to 133 max.)
  - Data locality in template accesses allows the cached texture memory to offer improved performance



Summary of MOCA

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- MOCA is useful for exploring CUDA implementation space
  - Memory type selection can be an important factor
- MOCA abstractions don't hinder (but help!) performance
  - Implementation choices/optimizations are exposed to the user
  - Optimal GPU/CPU mapping is often not 1:1
    - MOCA allows implementing functionality across the CPU/GPU boundary
- Future work: data reorganization to improve GPU memory hierarchy performance, other GPU vendors, general MOCA improvements
- Focus on the optimal dimensions for parameterization and representation within a library
- Parameterized library code applicable to a range of uses and scenarios -- focus on memory as well as kernels

Ongoing Work on GPU Acceleration

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- Physics-based simulation (PHYSBAM) acceleration
  - Surgery simulator – Simquest
- Machine learning algorithms
  - Medical image analysis
  - Security
- GPU@Home
  - Utilize idle GPUs

Summary and Future Work

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- GPUs are revolutionizing biomedical computing
- Biomedical imaging applications need to be developed in portable languages and libraries
- We can quickly determine the best GPU configuration from our estimation without purchasing hardware
  - Programmer does not need to focus on low-level optimization – instead, exploit another GPU
  - Programmer can move more easily between different versions of hardware – libraries
- Future work
  - Deliver new modeling and biomedical GPU library
  - Develop libraries based on OpenCL
  - Consider a wider range of GPU/CPU configurations

For more info on GPGPUs

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- Workshop on GPU Computing for Biomedical Research– 10/22 @ Harvard Medical School
  - *http://nebiogrid.org/biomed-gpu-workshop-2009*
- GPGPU3 - 3rd workshop focused on utilizing GPUs for general purpose computing - to be held at ASPLOS 2010
- First Workshop on Language, Compiler and Architecture Support for GPGPU - to be held at HPCA 2010 in Bangalore
- IEEE Transactions on Parallel and Distributed System special issues on Hardware Accelerators – focused on GPUs

- Also check out: *http://www.gpgpu.org*

Questions?


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AMD


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