$$
\begin{aligned}
& \text { MIC-GPU: } \\
& \text { High-Performance Computing } \\
& \text { for Medical Imaging } \\
& \text { on Programmable Graphics } \\
& \text { Hardware (GPUs) }
\end{aligned}
$$

## Parallelism in Medical Imaging

Klaus Mueller, Ziyi Zheng, Eric Papenhausen

## Transmission CT: Data Generation

 Medical Imaging

Stony Brook University
Computer Science
Stony Brook, NY

## CT Reconstruction

SPIE •...;",
Medical Imaging

High-dose CT reconstruction usually uses FDK algorithm

- backprojection of filtered views

Low-dose CT reconstruction pipeline typically uses iterative
3D reconstruction with regularization

- projection of volume into set's views
- correction factor computation
- backprojection of correction factors (views)
- regularization




## Kernel-Centric Decomposition

SPIE Medical Imaging

SPIE Medical Imaging 2012

We can consider each of these steps to be a SIMT kernel
Iterative 3D reconstruction with regularization:

- backprojection of volume into set's views $\rightarrow$ projection kernel
- correction factor computation $\rightarrow$ correction factor kernel
- backprojection of correction factors $\rightarrow$ backprojection kernel
- regularization $\rightarrow$ regularization kernel
=- projector with interpolation
_ vector operations
_ image processing filters



## Kernel Scheduling

SIMT can only execute one kernel at a time

- this prohibits kernel overlap, even if mathematically correct
- we may merge kernels if targets are identical $\rightarrow$ this favors load balancing and the reduction of passes

First decompose the reconstruction pipeline into components

- develop an optimized kernel for each component
- overlap (=hide) the loading of data (if needed) with execution of a prior kernel (or within kernel)
- optimize what platform to run the computations (CPU, GPU), but then consider transfer of data

We shall discuss all material in terms of 3D reconstruction

- the reduction to 2D slice reconstruction is straightforward

Pixels: the basis elements (point samples) of the projection image (the photon measurements)

Voxels: the basis elements (point samples) of the reconstruction volume (the attenuation densities or the tracer photon emissions)


SPIE Medical Imaging 2012


Backprojection: Options

- voxel-driven: sample in projection space
- one write per thread



## Backprojection: Options

- voxel-driven: sample in projection space - pixel-driven, sample in volume space
- one write per thread
- multiple writes per thread (scatter)


SPIE Medical Imaging 2012
MIC-GPU
14

CUDA Memory - Backprojection
SPIE
Medical Imaging
-

| Access | Global Memory | Texture Memory |
| :---: | :---: | :---: |
| Cached | Read/Write | Read only |
| Subject to coalescing | No | Yes |
| Interpolation | No support | No |
| Dimension | arbitrary | 1D, 2D, 3D (supported |
| after CUDA 2.0) |  |  |

Medical Imaging

A 3x4 matrix $M$ transforms 3D voxel coordinates to 2D pixel coordinates on the detector

Perform perspective divide if necessary (cone-beam)

$$
\left[\begin{array}{cccc}
a_{00} & a_{01} & a_{02} & a_{0} \\
a_{10} & a_{11} & a_{12} & a_{13} \\
a_{20} & a_{21} & a_{22} & a_{23}
\end{array}\right]\left[\begin{array}{c}
x_{v} \\
y_{v} \\
z_{v} \\
1
\end{array}\right]=\left[\begin{array}{c}
x_{h} \\
y_{h} \\
w_{h}
\end{array}\right] \quad P_{\varphi}(u, v)=\left(\frac{x_{h}}{w_{h}}, \frac{y_{h}}{w_{h}}\right)
$$

## CUDA Implementation

## Incremental Computation

## SPIE <br>  <br> Medical Imaging

[Host]:
for all projections $P_{i}$, trigger kernel on device
[Device]: per thread
loop through each voxel in the thread

- obtain voxel coordinates in volume space

$$
M^{3 \times 4} \cdot\left[\begin{array}{c}
x_{v} \\
y_{v} \\
z_{v} \\
1
\end{array}\right]=\left[\begin{array}{c}
x_{h} \\
y_{h} \\
w_{h}
\end{array}\right]
$$

- compute projected coordinates on the detector using a 3x4 transformation matrix $M$
- perform perspective-divide if needed

$$
P_{\varphi}(u, v)=\left(\frac{x_{h}}{w_{h}}, \frac{y_{h}}{w_{h}}\right)
$$

- depth weighting if needed
- interpolate pixel values on the detector (bilinear)
- accumulate sampled values on voxel


## Example:

Feldkamp Cone-Beam Reconstruction
360 projections ( $1024^{2}$, general position), $512^{3}$ volume


CPU


GPU

tumor profiles
SPIE Medical Imaging 2012 MIC-GPU
performance in seconds


## Expressed in Projections/Sec.

360 projections, $512^{3}$ volume


Original


GPU-recon

SPIE Medical Imaging 2012

## Forward Projection

Sample in volume space (pixel-driven / ray-driven)


CUDA Memory - Forward Projection $\begin{aligned} & \text { SPIE } \\ & \text { Medcal lizain }\end{aligned}$

|  | Global Memory | Texture Memory |
| :---: | :---: | :---: |
| Access | Read/Write | Read only |
| Cached | No | Yes |
| Subject to coalescing | Yes | No |
| Interpolation | No support | Hardwired |
| Dimension | arbitrary | 1D, 2D, 3D (supported <br> after CUDA 2.0) |
|  |  |  |
|  | projections | volume |

## Forward Projection: Memory

```
SPIE ?.a{",om
Medical Imaging
```

Ray-driven: sampling in volume space (trilinear interpolation)
Volume can be represented as either

- a single 3D texture (supported after CUDA 2.0)
- stacks of 2D textures
- A $3^{\text {rd }}$ interpolation between adjacent 2D slices


## Projection Algorithm

Raycasting methods [Krueger'03]

- [Host]:
- generate volume bounding box (aligned with axis $\mathrm{X} / \mathrm{Y} / \mathrm{Z}$ )
generate threads for each pixel (ray), trigger kernel on device


## Raycasting methods [Krueger'03]

- [Host]:
- generate volume bounding box (aligned with axis $\mathrm{X} / \mathrm{Y} / \mathrm{Z}$ )
- generate threads for each pixel (ray), trigger kernel on device
- [Device]: in each thread
- obtain ray entry \& exit points using volume bounding box info - get ray directions using entry \& exit points



## Projection Algorithm

Raycasting methods [Krueger'03]

- [Host]:
generate volume bounding box (aligned with axis $\mathrm{X} / \mathrm{Y} / \mathrm{Z}$ )
generate threads for each pixel (ray), trigger kernel on device
- [Device]: in each thread
obtain ray entry \& exit points using volume bounding box info get ray directions using entry \& exit points cast rays, inside the loop:
- sample in volume space
- accumulate values
- step forward equidistantly



## Projection Accuracy

Investigated various schemes in terms of accuracy:


It was shown that the convenient grid-interpolated (trilinear) scheme is qualitatively competitive to the more involved ones listed here.

- see Xu / Mueller, "A comparative study of popular interpolation and integration methods for use in computed tomography," "IEEE 2006 International Symposium on Biomedical Imaging (ISB'I '06)

SPIE Medical Imaging 2012

## Sync






## Regularization

SPIE 는
Medical Imaging

Overall goal: make the reconstruction conform to expectations

- reconstruction is not noisy
- reconstruction has sharp edges


## Various techniques

- Total Variation Minimization (TVM)
- bilateral filter (BLF)
- non-local means filter (NLM)


## TVM

- motivated by compressive sensing (sparseness) theory


## BLF, NLM

- popular in image processing and computer vision


## SPIE -, untor' Medical Imaging

Want to remove low-dose CT artifacts:


20 projections CT with low dose data

$\uparrow$
high-dose data CT

Total Variation Minimization (TVM)
Medical Imaging

What we want to achieve - ideally:


20 projections

SNR=10

CT + regularization

$\uparrow$
high-dose CT

## Relaxation Parameters (TVM)

Gradient step size $\beta$ :

- $\ll 1$, usually 0.2

Fidelity term $\lambda$ :

- initially set to 0
- next iterations:

$$
\lambda=\frac{1}{\sigma^{2}|\Omega|} \int_{\Omega} d i v\left(\frac{\nabla I}{|\nabla I|}\right)\left(I-I_{0}\right) d x d y
$$

- assuming:

$$
\min _{I} \int_{\Omega}|\nabla I| d x d y \quad \text { subject to } \frac{1}{|\Omega|} \int_{\Omega}\left(I-I_{0}\right)^{2} d x d y=\sigma^{2}
$$

## Non-linear Neighborhood Filters

Minimize using the steepest descent method

- for each voxel $\mathrm{v}_{\mathrm{i}}$ do iteratively:

$$
\begin{gathered}
v_{i}^{k+1}=v_{i}^{k}-\beta \cdot\left(\operatorname{div}\left(\frac{\nabla v_{i}^{k}}{\left|\nabla v_{i}^{k}\right|}\right)+\lambda\left(v_{i}^{k}-v_{i}^{0}\right)\right. \\
\text { original voxel value }
\end{gathered}
$$

- Generalization of discrete convolution


Computation
Based on Neighborhood values


SPIE Medical Imaging 2012

## Bilateral Filter (BLF)

- Edge-preserving non-linear filter:

original edge

bilateral filter


Replaces a pixel at $x$ with the mean of the pixels $y$ with similar Gaussian-weighted neighborhood:

(search) window $W$
patch with updated pixel $x$
Gaussian-weighted neighborhood patches with pixels $y$
(only highly-weighted shown)

## Bilateral Filter (BLF)

Medical Imaging

- Edge-preserving non-linear filter:

$$
u(x)=\frac{\int_{-\infty}^{\infty} \int_{-\infty}^{\infty} f(\xi) c(\xi-x) s(f(\xi)-f(x)) d \xi}{\int_{-\infty}^{\infty} \int_{-\infty}^{\infty} c(\xi-x) s(f(\xi)-f(x)) d \xi}
$$

## Non-Local Means Filter

Replaces a pixel at $x$ with the mean of the pixels $y$ with similar Gaussian-weighted neighborhood:

$$
N L M(x)=\frac{\sum_{y \in W} e^{-\frac{\sum_{t \in N} G_{a}(t)|\operatorname{img}(x+t)-\operatorname{img}(y+t)|^{2}}{h^{2}}} \operatorname{img}(y)}{\sum_{y \in W} e^{-\frac{\sum_{t \in N} G_{a}(t)|\operatorname{img}(x+t)-\operatorname{img}(y+t)|^{2}}{h^{2}}}}
$$

$x, y, t$ : spatial variables
W: window centered at $x$
$N$ : neighborhood centered at $x, y \quad G_{a}$ : Gaussian kernel $h$ : filtering weight controls the influence of dissimilar pixels

## NLM vs. TVM: Quality

NLM is as good (often better) than TVM

input
TVM, $\lambda=40$
NLM, h=15

## Bilateral vs. NLM

## Course Schedule

Faster than NLM, but quality is lower


