

Enhancing Evaluations with Realistic CT Simulations

CT Simulations Frameworks and XCIST (formerly CatSim)

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Physics in Medicine & Biology



PAPER

XCIST—an open access x-ray/CT simulation toolkit

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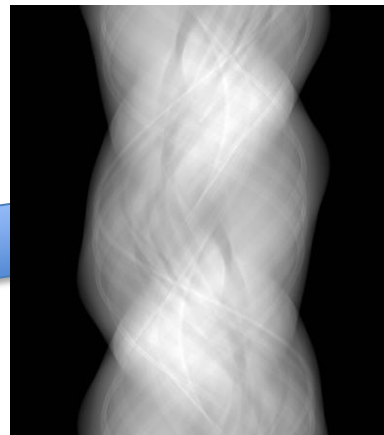
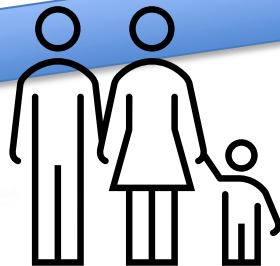
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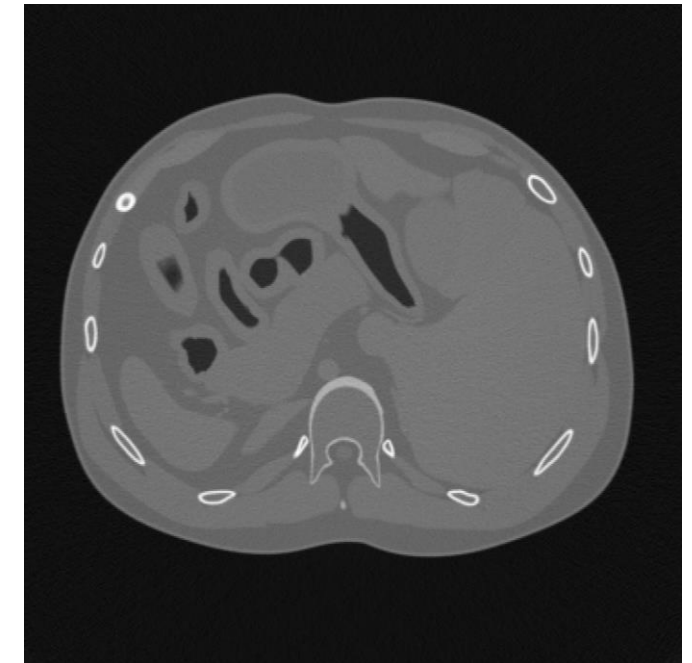
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DLIR Meeting 03/29/2023



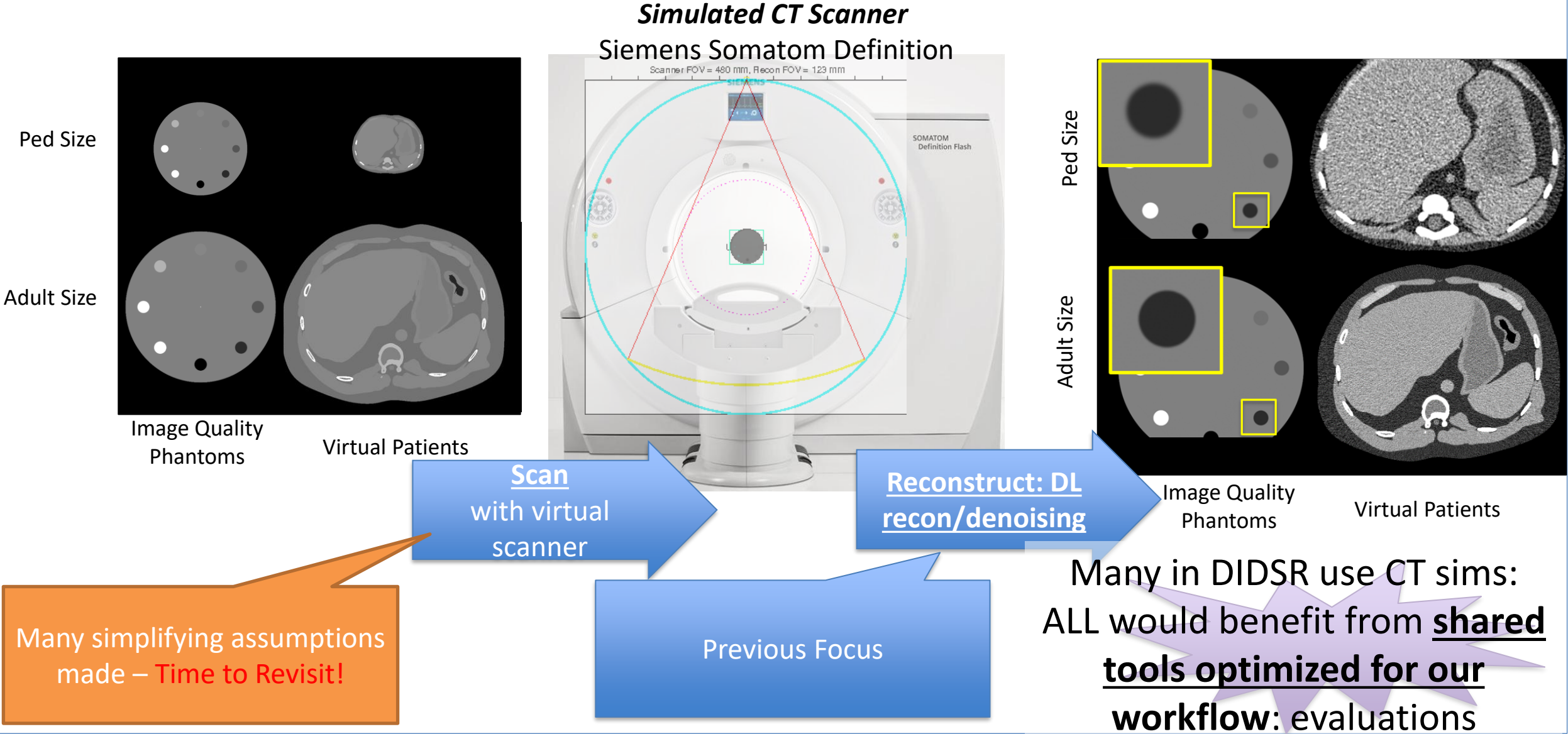
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Objectives

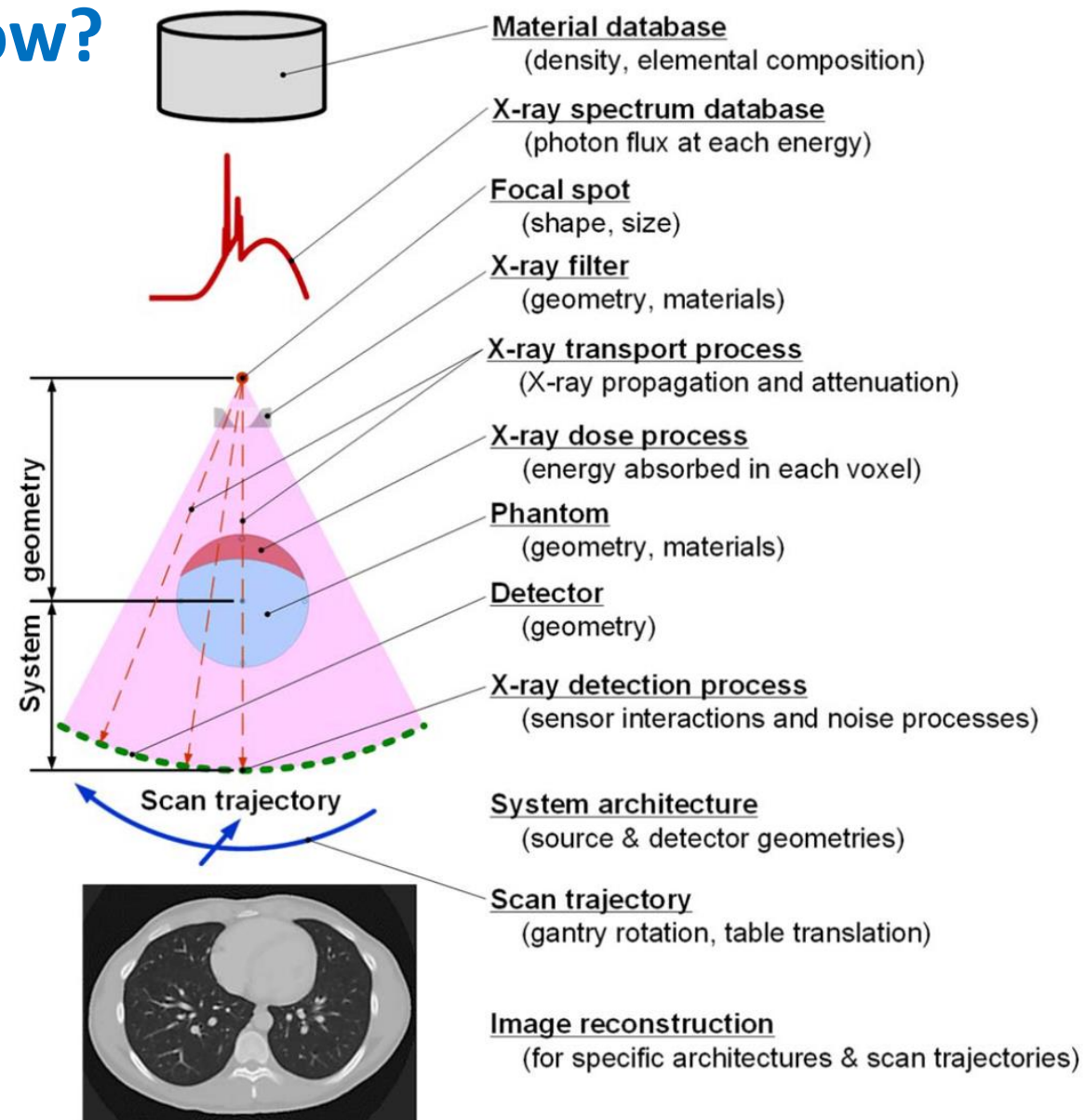
- Review current in-house use of CT Simulation Frameworks
- Introduce [XCIST](#): X-Ray Cancer Imaging Simulation Toolkit and motivate its use compared to existing frameworks
- Overview basic use and capabilities of XCIST
 - And details to incorporate into current in-house workflows/phantoms
- **Discussion and feedback on how to best develop shared in-house tools**

Where are we now?



Why change, why XCIST, and why now?

- Michigan Image Reconstruction Toolbox (MIRT)
 - Great for prototyping: fast, intuitive, low level, simple
 - Lacking in realism: monoenergetic, fan beam, ray-tracing (no scatter)
 - Not scalable: too much hand-written code for large VCT experiments (not intended use)
- XCIST: X-Ray Cancer Imaging Simulation Toolkit
 - Mature, actively maintained
 - Software engineered + industry supported (GE)



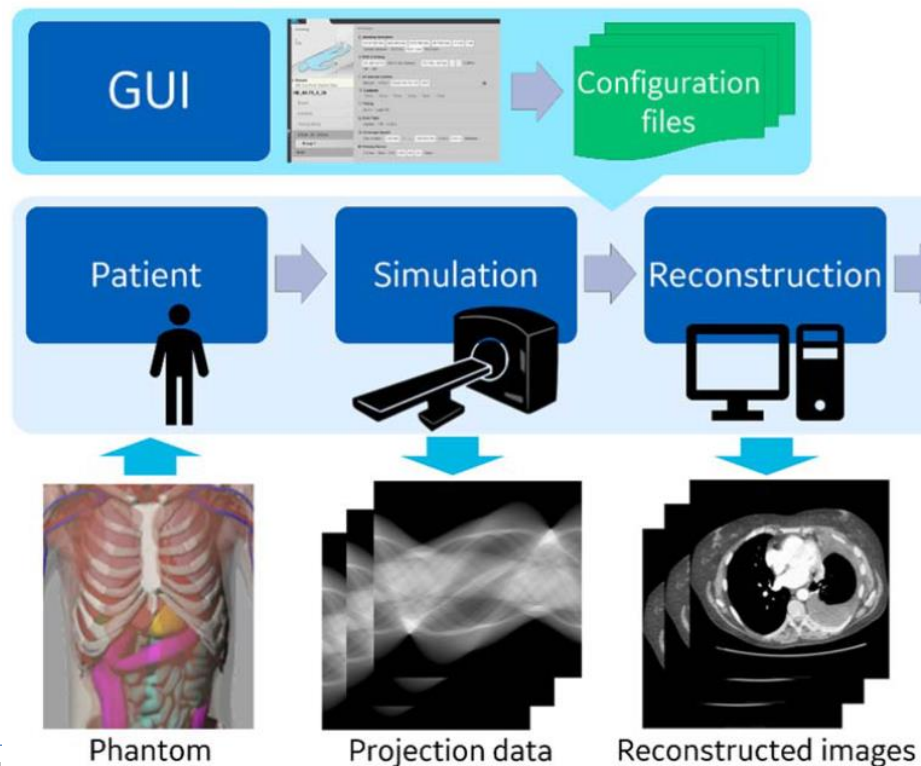
1. Wu M, FitzGerald P, Zhang J, et al. XCIST-an open access x-ray/CT simulation toolkit. *Phys Med Biol.* 2022;67(19). doi:[10.1088/1361-6560/ac9174](https://doi.org/10.1088/1361-6560/ac9174)

Comparison of X-Ray Simulation Frameworks

Framework	Physics	Beam Hardening Correction	Noise Model	Simulation Time	Benefits	Limitations
MIRT	Ray traced, monochromatic	NA	Poisson	Seconds (CPU)	Fast, optimal for developing recons	Low-level
DukeSim	Ray traced + Monte-Carlo polychromatic	Optional	Gaussian (central limit theorem, high dose assumption)	Minutes (GPU)	ease of use, well designed	Requires paid license
XCIST	Ray traced + Monte-Carlo polychromatic	Optional	Poisson + Gaussian	Minutes (CPU)	Open source, ease of use, well designed	
VICTRE	Monte-Carlo	NA	MC	Hours?	Realistic, in house	Low-level

Sample XCIST Experiment

- Config files define defaults
- High level python library for simple workflow
- Easily manage many patients, phantoms, scan/recon protocols, ...
- Lots of [documentation and examples](#)



```
# Table and gantry
protocol.scanTrajectory = "Gantry_Helical" # name of the function that d
and model
protocol.viewsPerRotation = 1000 # total numbers of view per r
protocol.viewCount = 1000 # total number of views in sc
protocol.rotationTime = 1.0 # gantry rotation period (in
protocol.rotationDirection = 1 # gantry rotation direction (
foot-end)
protocol.startAngle = 0 # relative to vertical y-axis
protocol.tableSpeed = 0 # speed of table translation
mm/sec)
protocol.startZ = 0 # start z-position of table
protocol.tiltAngle = 0 # gantry tilt angle towards n
protocol.wobbleDistance = 0.0 # focalspot wobble distance
protocol.focalspotOffset = [0, 0, 0] # focalspot position offset

# X-ray tube technique and filtration
protocol.mA = 200 # tube current (in mA)
protocol.spectrumCallback = "Spectrum" # name of function that reads
protocol.spectrumFilename = "tungsten_tar7_120_unfilt.dat" # name of the
protocol.bowtie = "small.txt" # name of the bowtie file (or
protocol.flatFilter = ['Al', 3.0] # additional filtration - mat
protocol.dutyRatio = 1.0 # tube ON time fraction (for

# recon details
recon.fov = 123.0 # diameter of the reconstruction
recon.imageSize = 512 # number of columns and rows to b
recon.sliceCount = 1 # number of slices to reconstruct
recon.sliceThickness = 1.0 # reconstruction slice thickness
recon.centerOffset = [0.0, 0.0, 0.0] # reconstruction offset relative
recon.reconType = 'fdk_equiAngle' # Name of the recon function to c
recon.kernelType = 'Bone' # 'R-L' for the Ramachandran-Lakshminarayanan f
# 'S-L' for the Shepp-Logan (S-L) filter, sinc
# 'Soft', 'Standard', 'Bone' for kernels simila
```

Small details for those wanting to get started

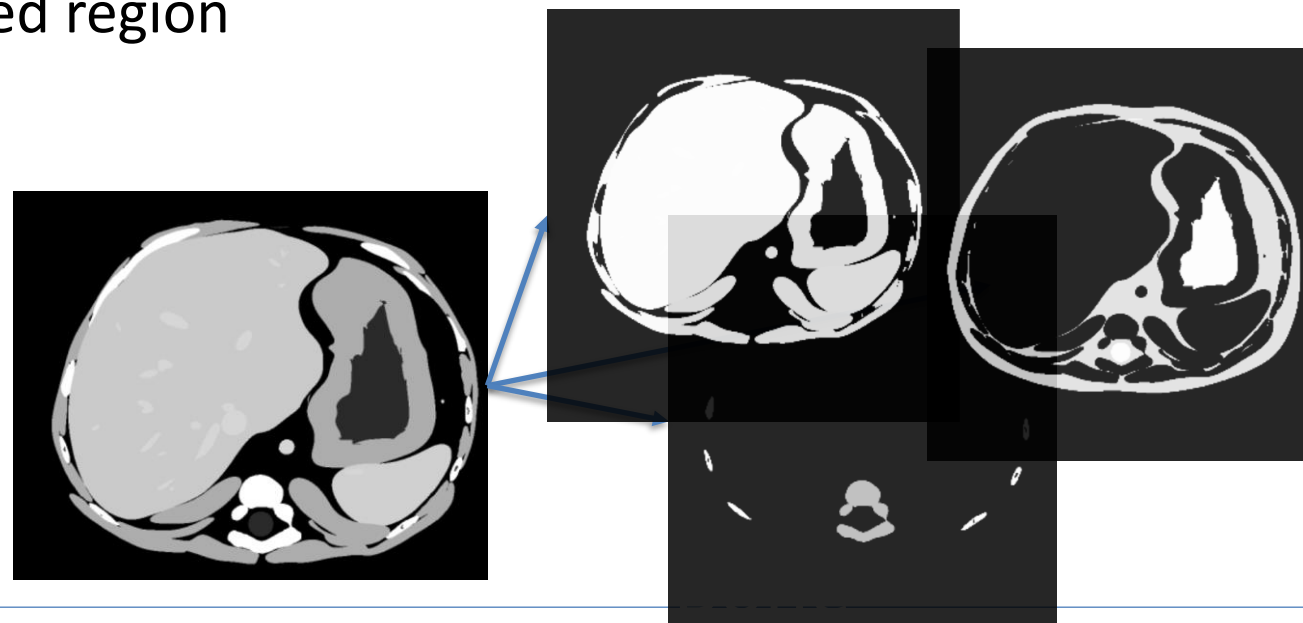
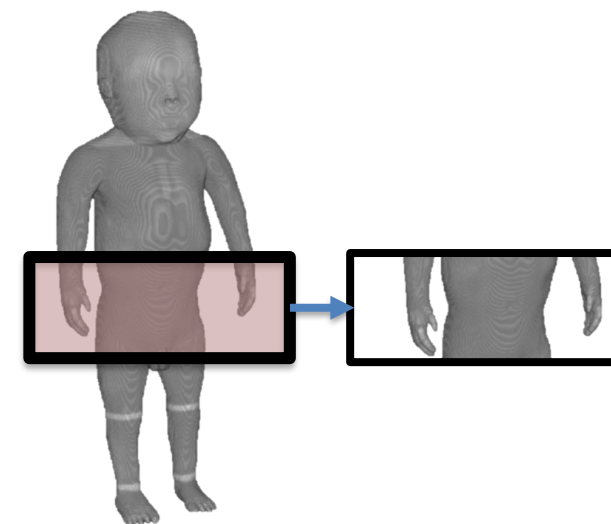
Possible Inputs:

- Non-Uniform Rational B-Splines – NURBS
→ XCAT format (see [Andreu's 2022 AAPM talk for more](#))*

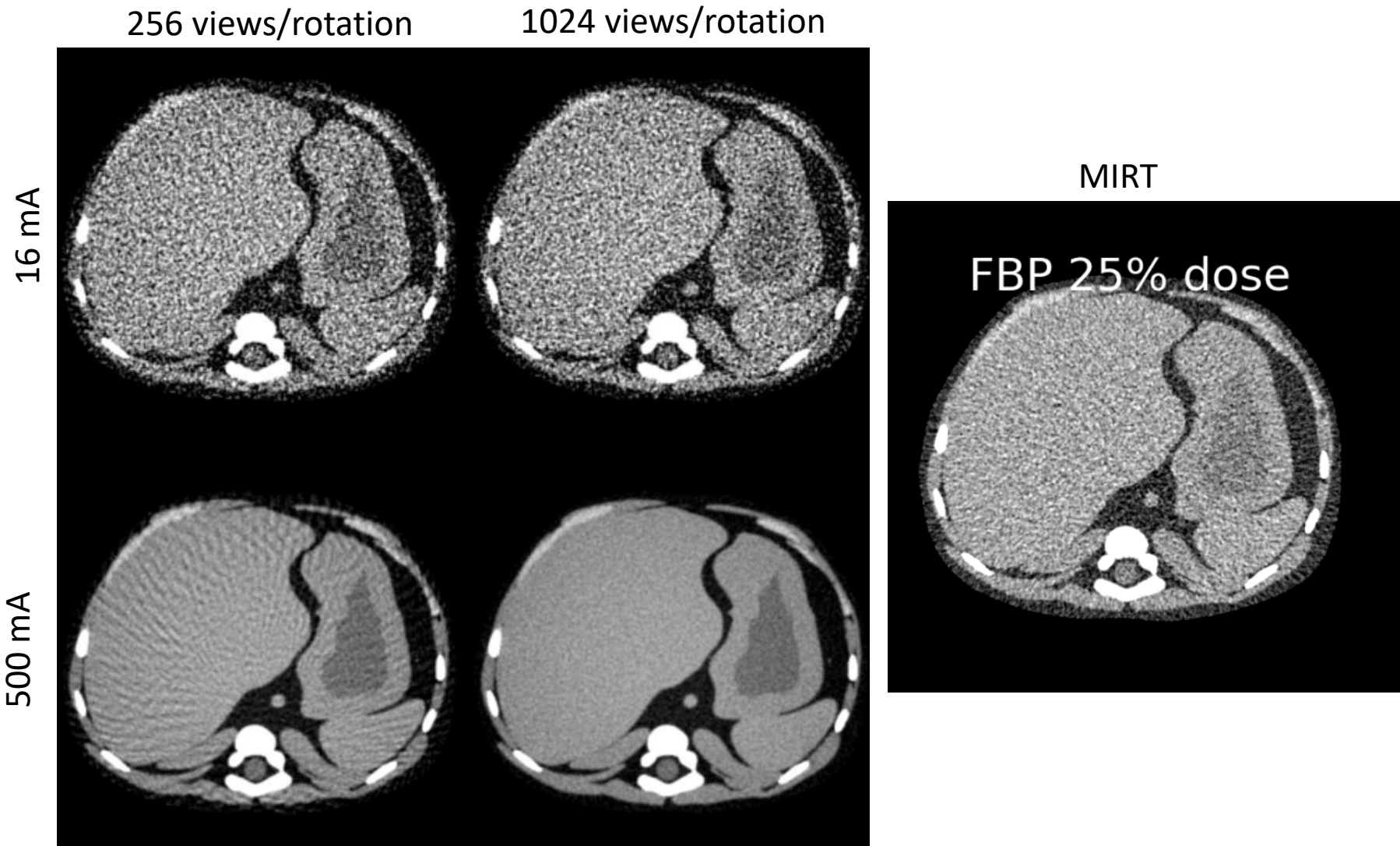
- *Cannot feed in whole XCAT patient → Need NURBS editing software (e.g. [Rhino3D](#), AutoDesk, SolidWorks) crop to desired region

- **Voxelized Phantoms****

- **Requires segmented volumes of each tissue type
- Raw_to_DICOM.py →
DICOM_to_Voxelized.py →
XCIST.py



Sample Results on Ped XCAT Data



Sample Results from XCIST Paper

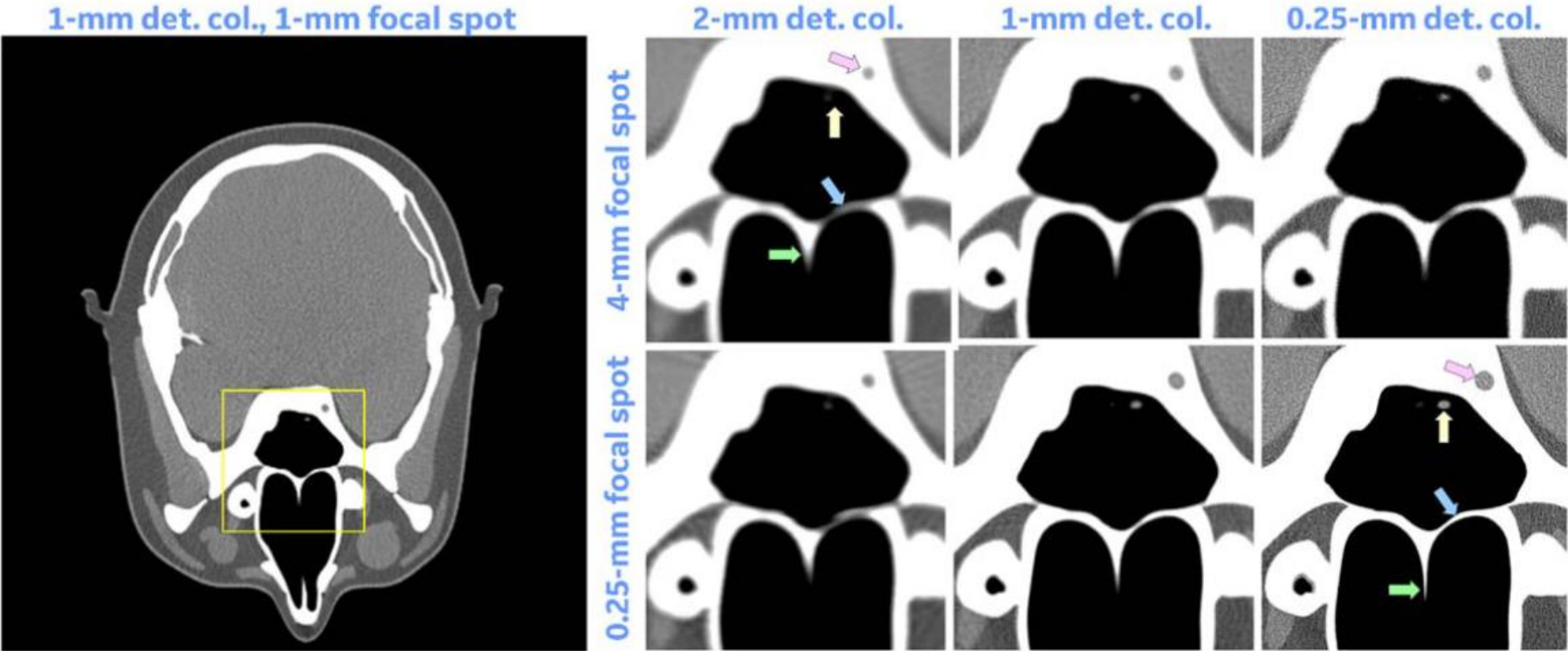
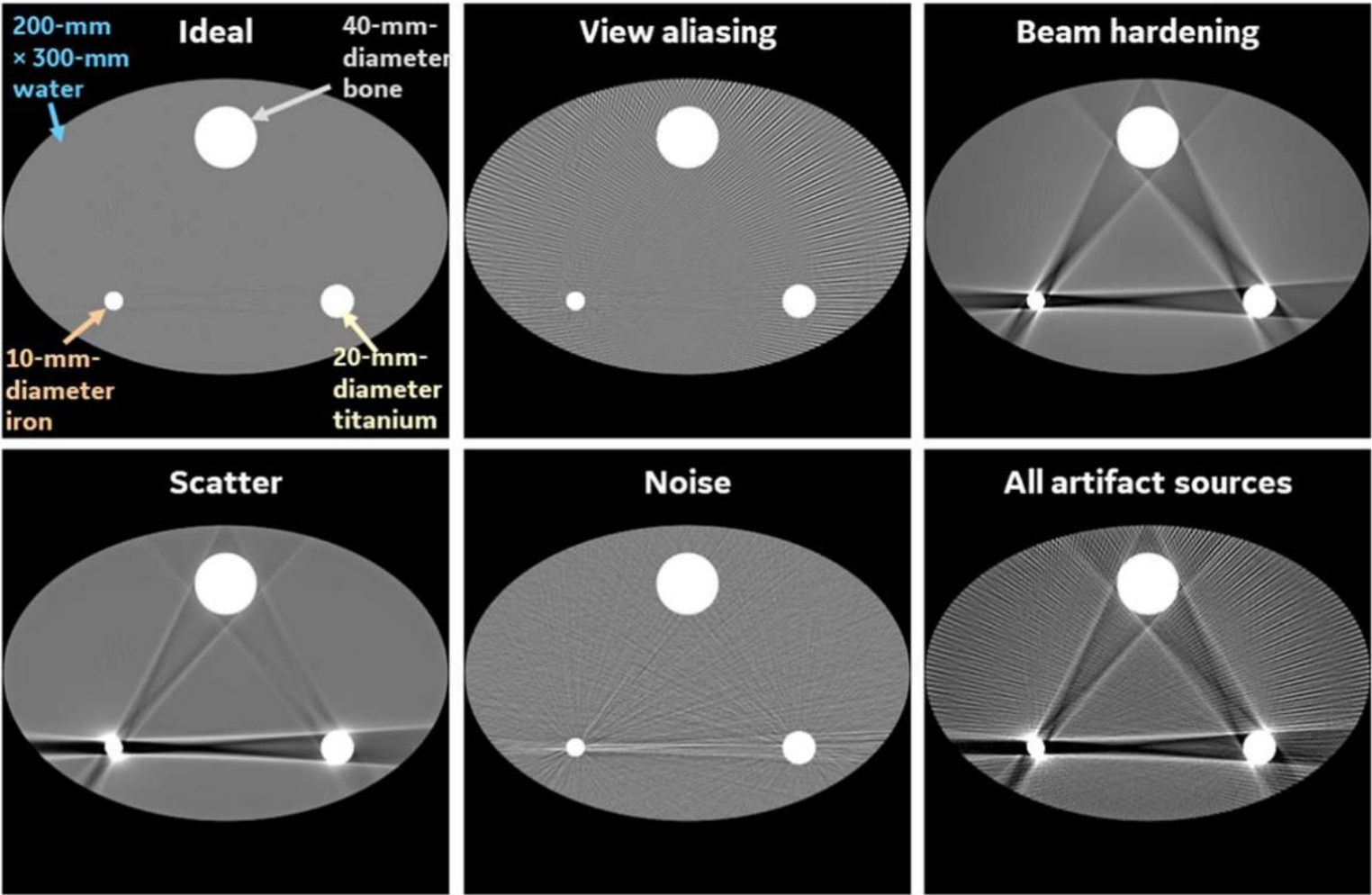


Figure 10. Experiment 3 results. A head section of an XCAT phantom is used to demonstrate the impact of the x-ray source’s focal spot width and the x-ray detector’s column width on spatial resolution. Left, a 260 mm FOV reconstruction shows the entire head cross-section. The yellow box indicates a 60 mm region of interest. Right, 60 mm FOV reconstructions using two x-ray source focal spot sizes and three detector column widths. Arrows indicate features that become sharper, with more well-defined dimensions, as the focal size and detector column widths are reduced. All images are displayed with window width = 1000 HU, window level = 0 HU.

Sample Results from XCIST Paper



Discussion on shared in house tools Dev

- XCIST (and other high-level frameworks: DukeSim) simplify complex VCT experiments
 - More time for science, less on writing boiler plate code
- Use of common tools in-house enables improved collaboration
- How best to do this? (Discussion welcomed!)
 - Common shared install location e.g. /gpfs_projects/<tool name here>
 - Docker/Docker files for less setup time?
 - Github Forks
 - ...