Optimisation of the Philips automatic exposure control system

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14th CT Users Group
4th October 2012

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Hull and East Yorkshire Hospitals NHS Trust

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  - ACS optimisation
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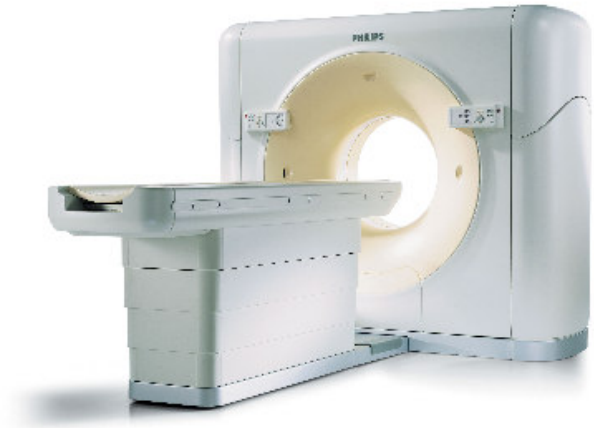
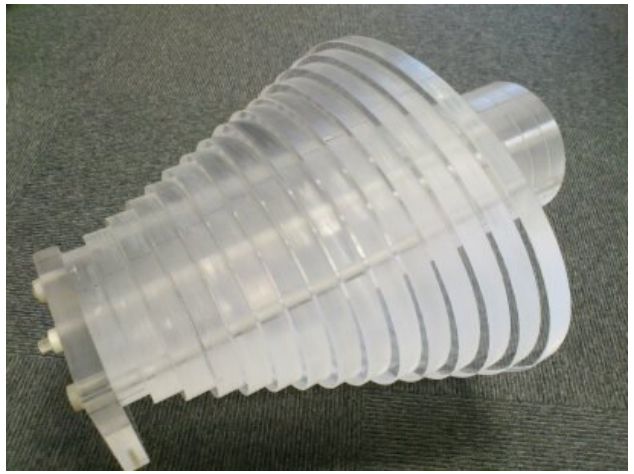




Introduction

Introduction

- We are all acutely aware of the need for, and use of automatic tube current modulation in CT
  - Optimise and reduce patient doses
  - Maintain consistent image quality throughout the scan volume
- Hull and East Yorkshire Hospitals NHS Trust have 5 Philips CT scanners (lucky me!), and one Toshiba
  - 1 x Philips Brilliance 40
  - 2 x Philips Brilliance 16
  - 2 x Philips Brilliance 16 Big Bore (Radiotherapy)
  - 1 x Toshiba Aquilion 64
- The motivation of this work followed a routine dose audit of CT examinations that use the AEC

Philips DoseRight

- The Philips DoseRight system is composed of three independent parts;

Automatic Current Selection (ACS)

Z-DOM (longitudinal modulation)

D-DOM (angular modulation)

Automatic Current Selection (ACS)

- Automatically suggests the **maximum** mAs for each patient in order to achieve a constant image noise level (between patients, not throughout the scan)
- This can be set to;
  - **Auto:**

    With automatic patient size averaging, the system measures the average body size of all patients scanned with a specific protocol, and uses this as the ‘standard’ size for that protocol
  - **Manual:**

    A ‘user determined image noise reference’ can be defined by setting the current scan as the reference image
  - **Off:**

    The user has to set appropriate mAs for each individual
- The mAs set during protocol setup also has an effect

ACS

- ‘Issues’ with ACS;
  - With automatic patient size averaging, the standard size will be constantly changing, especially if large/small patients scanned
    - Observed on repeat scans of Rando phantom over several days
  - Automatic mode involves the system ‘learning’ what the correct mAs is – the operator has to override the recommended mAs until it starts to suggest sensible values
    - How do you optimise patient dose?
  - Manual mode requires an appropriate subject for the reference image set
    - Which patient? What about phantoms?
  - In both modes of operation, it is not possible to transfer the reference image set between systems
    - Automatic mode may tend to drift apart from each other due to inter-patient variations, even if set up the same at commissioning
    - Manual mode requires the reference image to be acquired on each individual scanner – can’t use the same patient!

Z-DOM

- Dose saving by adjusting the mAs along the longitudinal direction, based upon the Surview image
- Aim is to achieve the same image quality in each slice
- Can be used with or without ACS, but **cannot** be used in conjunction with D-DOM
- ACS (or the operator) determines the **maximum** mAs to be used in the scan
  - Also displays the minimum and average mAs through the scan volume
  - The minimum is usually limited to about 40% of the maximum
  - Maximum mAs only limited by the maximum mA of the tube
    - Can be increased by increasing rotation time
    - Warning given by the system if this is going to be a problem (operator has to decide whether to allow the higher dose, or proceed with maximum tube mA or user defined value)

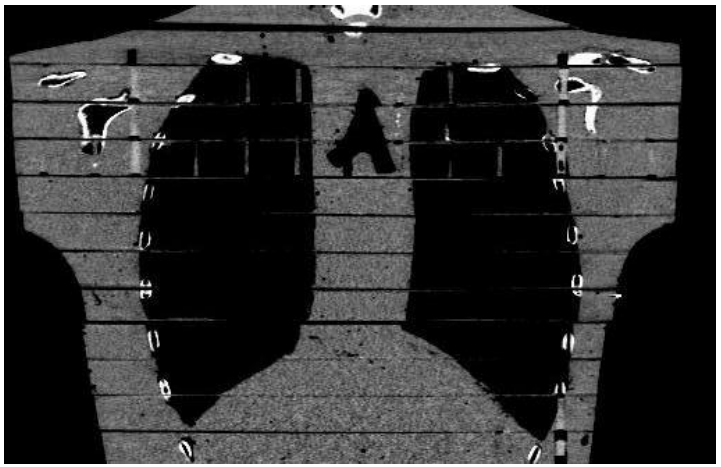
D-DOM

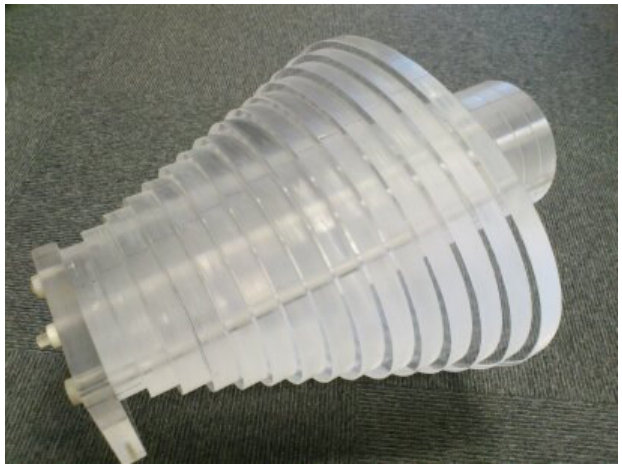
- Rotational modulator varies mAs due to asymmetry
  - Lower signals (e.g. lateral) contribute high noise, whilst high signals (A-P) make minor contributions to total noise
- Modulation is carried out online during the scan
  - Uses the data from the previous rotation to determine what to do on the next
  - Only applied if at least 10% reduction in mAs possible
- mAs displayed on image is actual mAs used for that part of the scan
- D-DOM **cannot** be used in conjunction with Z-DOM
- D-DOM should not be used for;
  - Head scans (symmetrical)
  - Single axial scans
  - Pelvic scans (Philips recommendation, but not in the manual!)

Method

Method – the phantoms

- Rando phantom
  - Anthropomorphic (enough) for this study
  - Used to look at AEC performance in pseudo clinical situations
  - Used to setup the AEC for clinical use
- Uniform AEC phantom
  - Several elliptical PMMA sections based on dimensions of ImPACT phantom (3:2 ratio)
  - Modular with head section for looking at sudden transitions





Method – the scanners

- Philips Brilliance 40 (CHH)
- Philips Brilliance 16 (CHH)
- Philips Brilliance 16 Big Bore (CHH)
- Standard settings for Chest only, CTPA and Chest-Abdo-Pelvis (chest scan);

Parameter	Brilliance 40	Brilliance 16	Brilliance 16 Big Bore
kVp	120	120	120
Rotation time (s)	0.5	0.5	0.5
Beam collimation (mm)	40 × 0.625	16 × 0.75	16 × 0.75
Pitch	0.924	0.938	0.938
Slice thickness (mm)	1	1	1
Slice increment (mm)	1	1	1
Convolution kernel	Standard (B)	Standard (B)	Standard (B)
Matrix	512 × 512	512 × 512	512 × 512
Software version	2.3.0	2.3.0	2.3.0

Method – generating protocols

- Only use ‘manual’ mode for ACS (set in Preferences → Scanner → DoseRightACS) and Z-DOM
- Determined which scanner was going to be the **reference scanner for each protocol** (usually lowest dose as image quality deemed ok)
- Scanned the Rando phantom with the **reference clinical protocol** over the appropriate range and **recorded max, min and average mAs**
- Generate a **copy** of the reference clinical protocol (this does not include the ACS settings)
  - The mAs set at this point may affect the resulting AEC performance… (more on this later)

Method – generating protocols

- Scanned Rando over same range with new protocol, using the max mAs determined for the reference clinical protocol (note, Z-DOM will not be active)
- Save the resulting image set as the reference image (Operations → Save DoseRight)
  - If there is more than one scan in the protocol (e.g. chest-abdo-pelvis), you need to save a reference image for each part i.e. you can't just scan them all then click save DoseRight once
- Rescanning Rando should then give the same max, min and average mAs as the reference clinical protocol
  - but sometimes it doesn't… (again, more on this later)
- Matched protocols created on each of the other scanners and appropriate reference images created

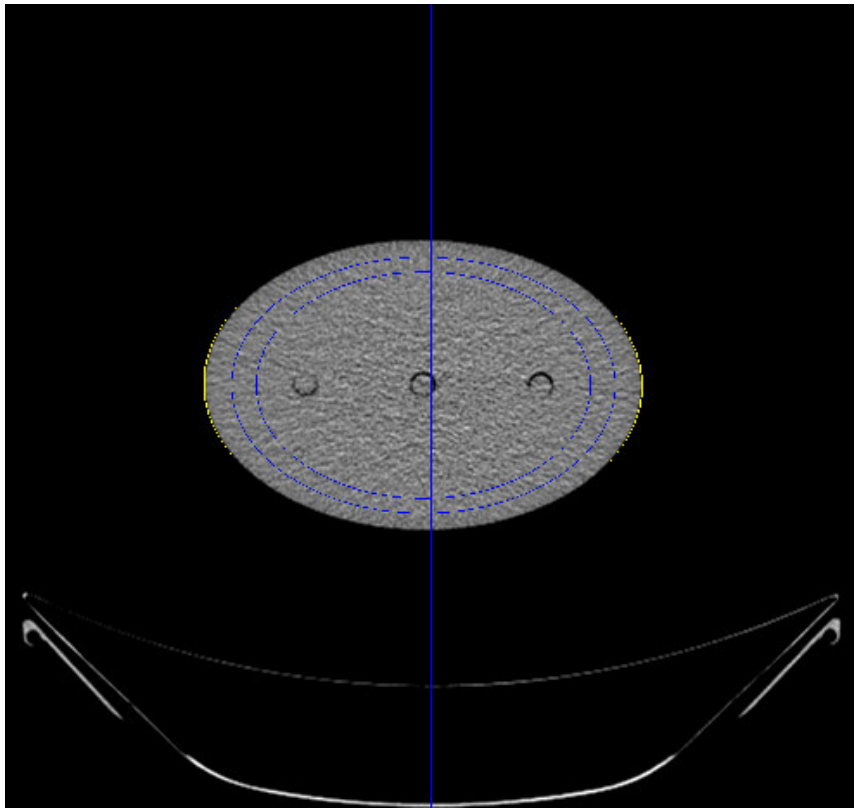
A note on default mAs settings…

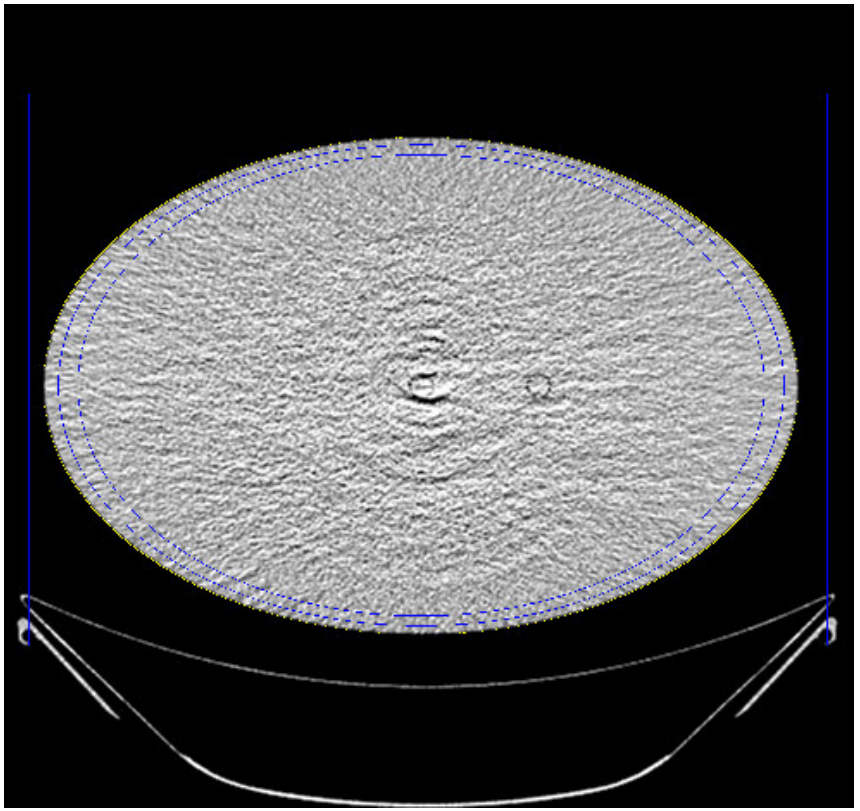
- When creating a new protocol, the operator sets a default mAs, even though it is going to be ‘trained’ to select the correct mAs on patients (be it manually or automatically)
- If this default mAs is **appreciably different** to the mAs used when creating the reference image, rescanning Rando may not give the max, min and average mAs you expect
- If the default mAs is set the same as what you intend to use for the reference image, rescanning Rando always gives the values you expect
- So need to decide;
  - If they are different for the reference clinical protocol, do you use the same for the new protocol and accept it will behave oddly, or
  - Set the default mAs the same as what you intend to use for the reference image and get predictable behaviour, but not necessarily matched performance (compared with the reference clinical protocol)!

Method – protocol characterisation

- Once protocols generated, the AEC phantom was scanned between the 22 cm and 39 cm wide sections
- Resulting image analysis performed using analysis trees in IQWorks (version 0.6)
- Expanding annular ROIs used to measure CT number and standard deviation (SD) in the central slices of each section, and the mean and SD determined
  - Expanding ROI used to avoid ring artefacts that dominate the noise measurement in thick sections
  - Consistently positioned via edge detection algorithm
- mAs and $CTDI_{vol}$ extracted from the DICOM header (routine QA demonstrated displayed $CTDI_{vol}$ within 3% of actual value)

Method - protocol characterisation





Results

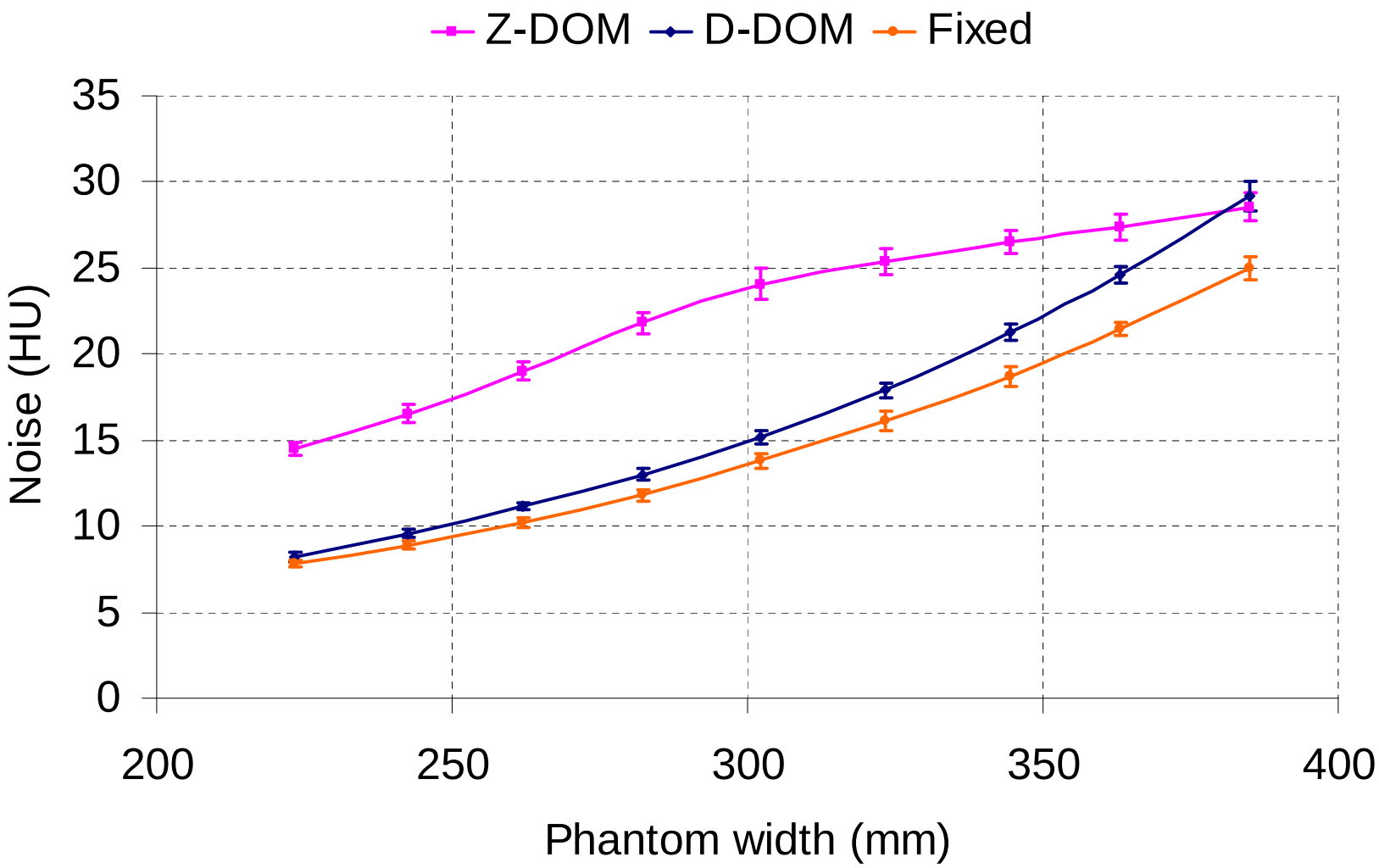
Z-DOM or D-DOM?

(but never the two together!)

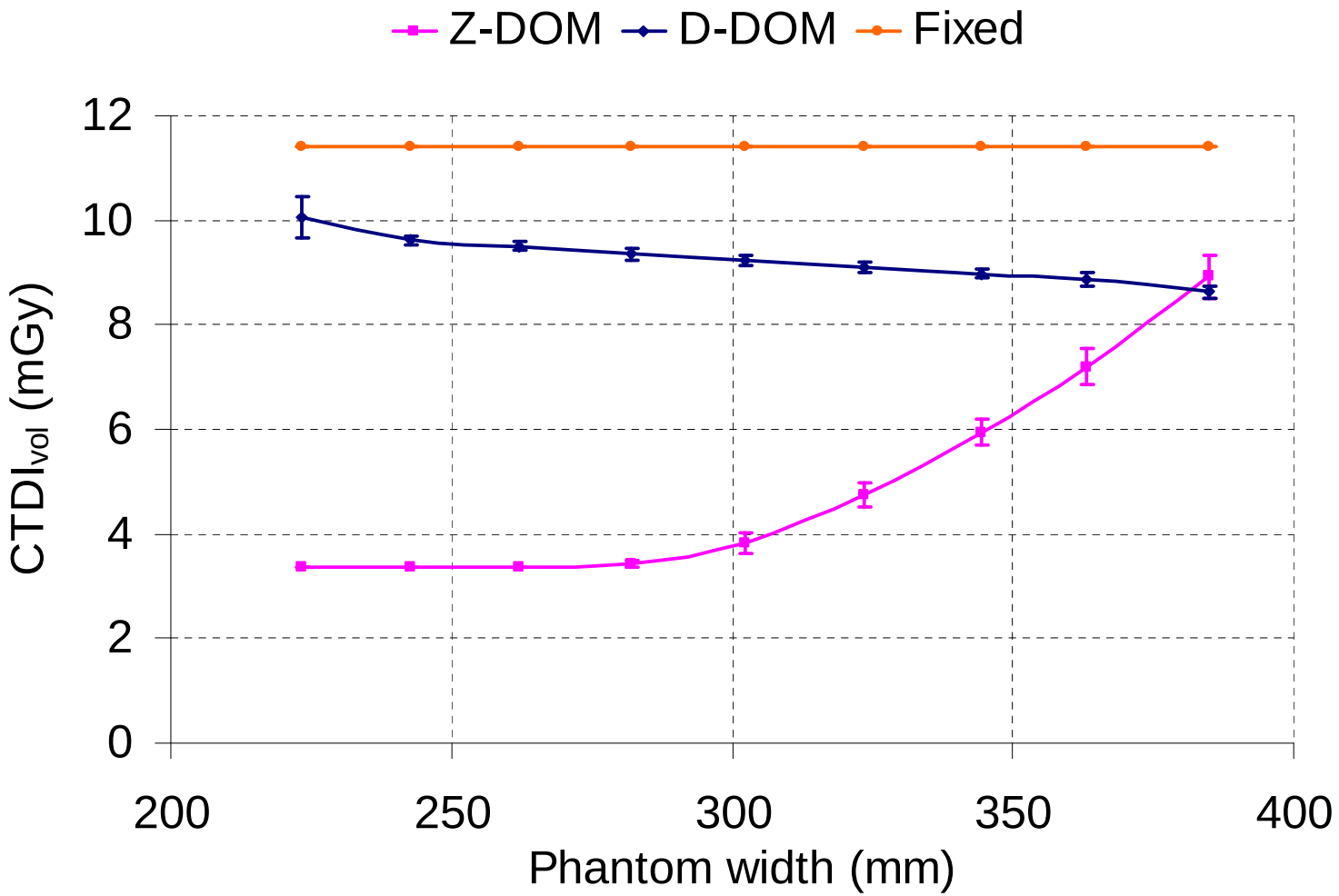
- The biggest limitation of the Philips DoseRight system is that you cannot use Z-DOM and D-DOM together
- Philips are the only manufacturer to not have a fully 3D/4D modulation system
- This makes it very difficult to optimise doses as they both have significant advantages in terms of dose reduction
- So, when setting up a new protocol, which is best?
  - There's only one way to find out…

Scan the phantoms!

Z-DOM vs D-DOM


Z-DOM
D-DOM
Fixed
Noise (HU)
35
30
25
20
15
10
5
0
200
250
300
350
400
Phantom width (mm)

Z-DOM vs D-DOM


Z-DOM
D-DOM
Fixed
12
10
8
6
4
2
0
CTDIvol (mGy)
200
250
300
350
400
Phantom width (mm)

Z-DOM vs D-DOM

- Fixed mAs yields relatively low noise for thinner sections, due to constant high dose being used
  - Noise increases rapidly with phantom width
- Z-DOM performs as expected
  - As phantom width increases, the dose increases once past the plateau at ~40% of maximum value
  - Noise increase is more moderate once the modulator kicks in (rapid increase when mAs is fixed at 40% of the maximum)
  - Overall, DLP is 54% lower than for fixed mAs
- D-DOM shows slightly higher noise than fixed mAs technique (as lower dose used in A-P projections)
  - Overall, DLP is 18% lower than for fixed mAs
- **However, $CTDI_{vol}$ actually decreases as phantom thickness increases!**

D-DOM, dose and phantom size

- Dose decreases for increased thickness of phantom due to the exponential attenuation of x-rays, and the relatively low fluence incident on the detector compared with the high detector dose for thin sections…
- Or with a bit of maths (and a few assumptions);

Assume mono-energetic; $I_x = I_{0x}\, e^{-\mu x}$ and $I_y = I_{0y}\, e^{-\mu y}$

Assume D-DOM aims to give same detector dose for lateral and A-P projections;

$$I_y = I_x$$

Hence; $$I_{0y}\, e^{-\mu y} = I_{0x}\, e^{-\mu x}$$

Rearrange; $$I_{0y} = I_{0x}\, e^{-\mu x} / e^{-\mu y}$$

$$\mathbf{I_{0y} = I_{0x}\, e^{-\mu(x-y)}}$$

D-DOM, dose and phantom size

- We know ratio of lateral to A-P dimensions is 3:2 and I_0 α mAs, so:

$$mAs_Y = mAs_X e^{-\mu(x-2/3x)} = mAs_X e^{-\frac{\mu}{3}x}$$

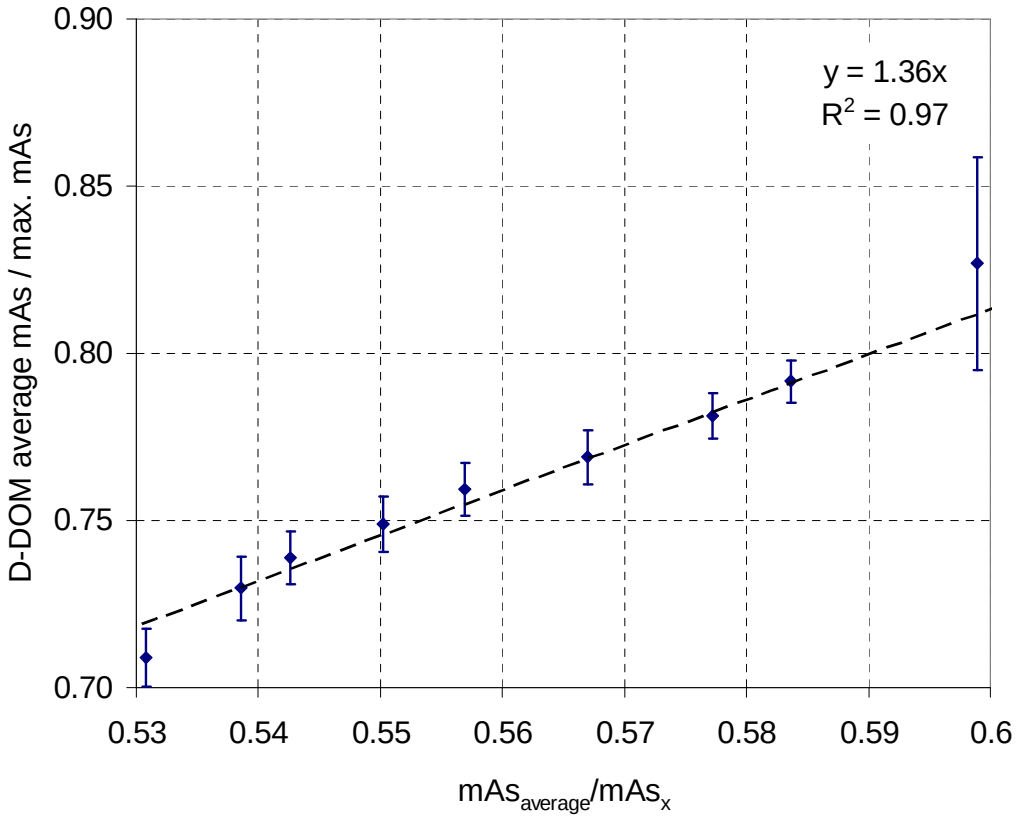
- So, the mAs used for the A-P projection shows exponential decay that is dependent on the lateral mAs and size of the phantom
- Now assume mean mAs in a slice is just the average of the lateral and A-P projections;

$$mAs_{average} = \frac{(mAs_Y + mAs_X)}{2} = \frac{(mAs_X e^{-\frac{\mu}{3}x} + mAs_X)}{2}$$

$$\frac{mAs_{average}}{mAs_X} = \frac{(e^{-\frac{\mu}{3}x} + 1)}{2}$$

D-DOM, dose and phantom size

- Or, use IPEM Report 78 spectrum processor to determine for poly-energetic beam
- Compare with the measured ratio of average mAs to maximum mAs for each phantom size…



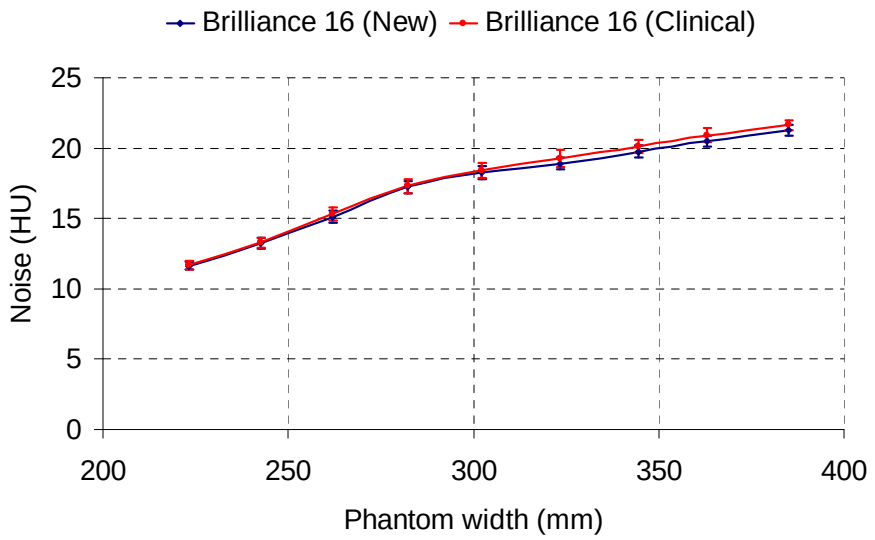
D-DOM

- Obviously, the AEC phantom does not represent a realistic clinical situation
- However, this highlights potential clinical problems;
  - In scans that have any variations in the longitudinal direction, the average mAs/slice will be lowest in the most attenuating parts
  - For a chest, the average mAs/slice will be lowest in the shoulders and highest in the lung!
  - Similar effect for abdo-pelvis protocols
- Conclusion is that **D-DOM must only be used where longitudinal variations are <u>negligible</u>**
  - How many **default** clinical protocols can be sure of this?
- In most clinical situations, Z-DOM will yield a greater dose saving than D-DOM
  - e.g. chest-abdo-pelvis scan of Rando yields 14% lower dose with Z-DOM compared with D-DOM

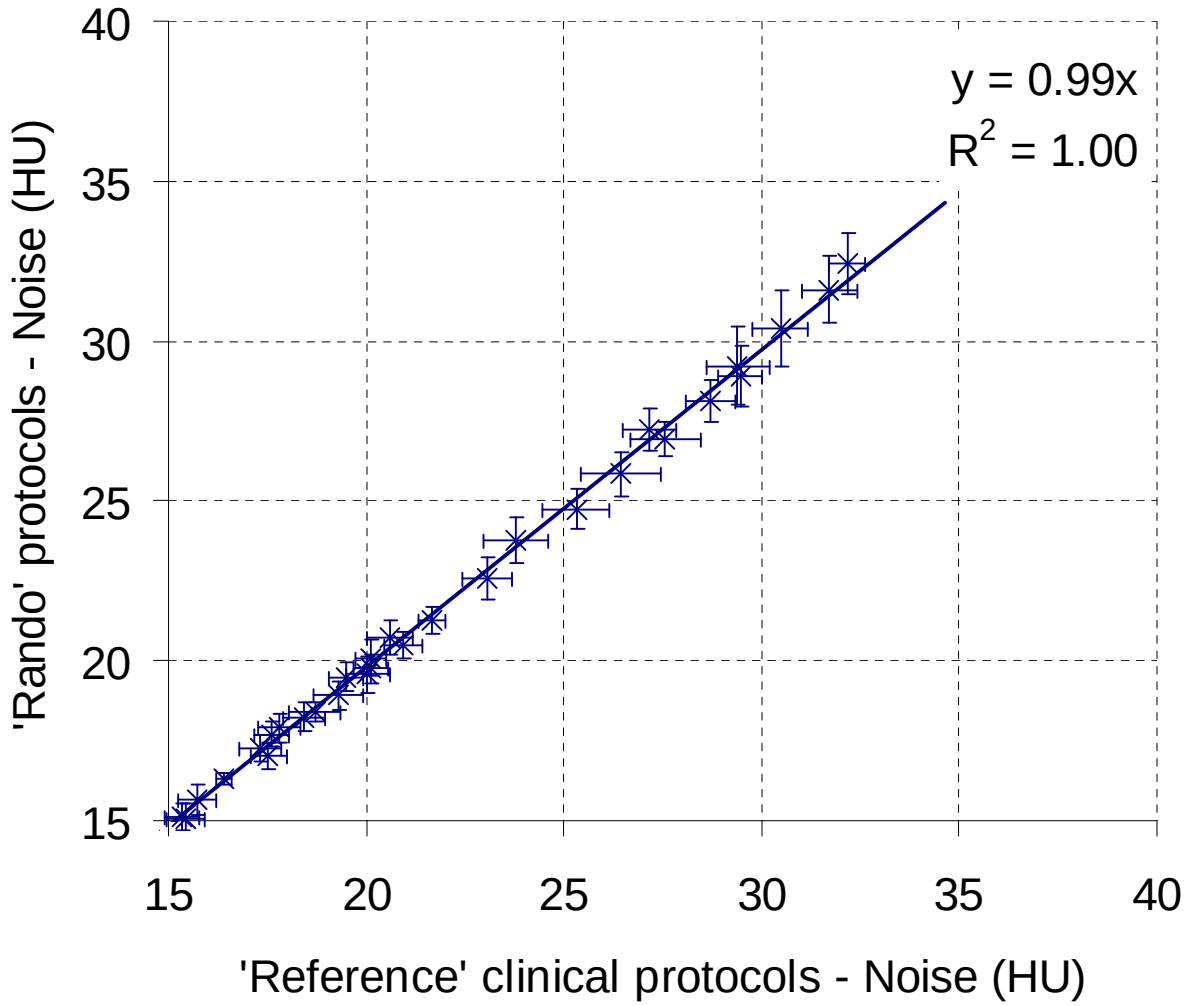
So, Z-DOM it is then…

Validation of ‘Rando Reference Images’

- The new clinical protocols were initially checked by rescanning Rando over the same region, and ensuring the same exposure factors were selected
- AEC response curves compared for the reference clinical protocol and the new one
  - e.g. CTPA
- Chest only protocols now used clinically without problems



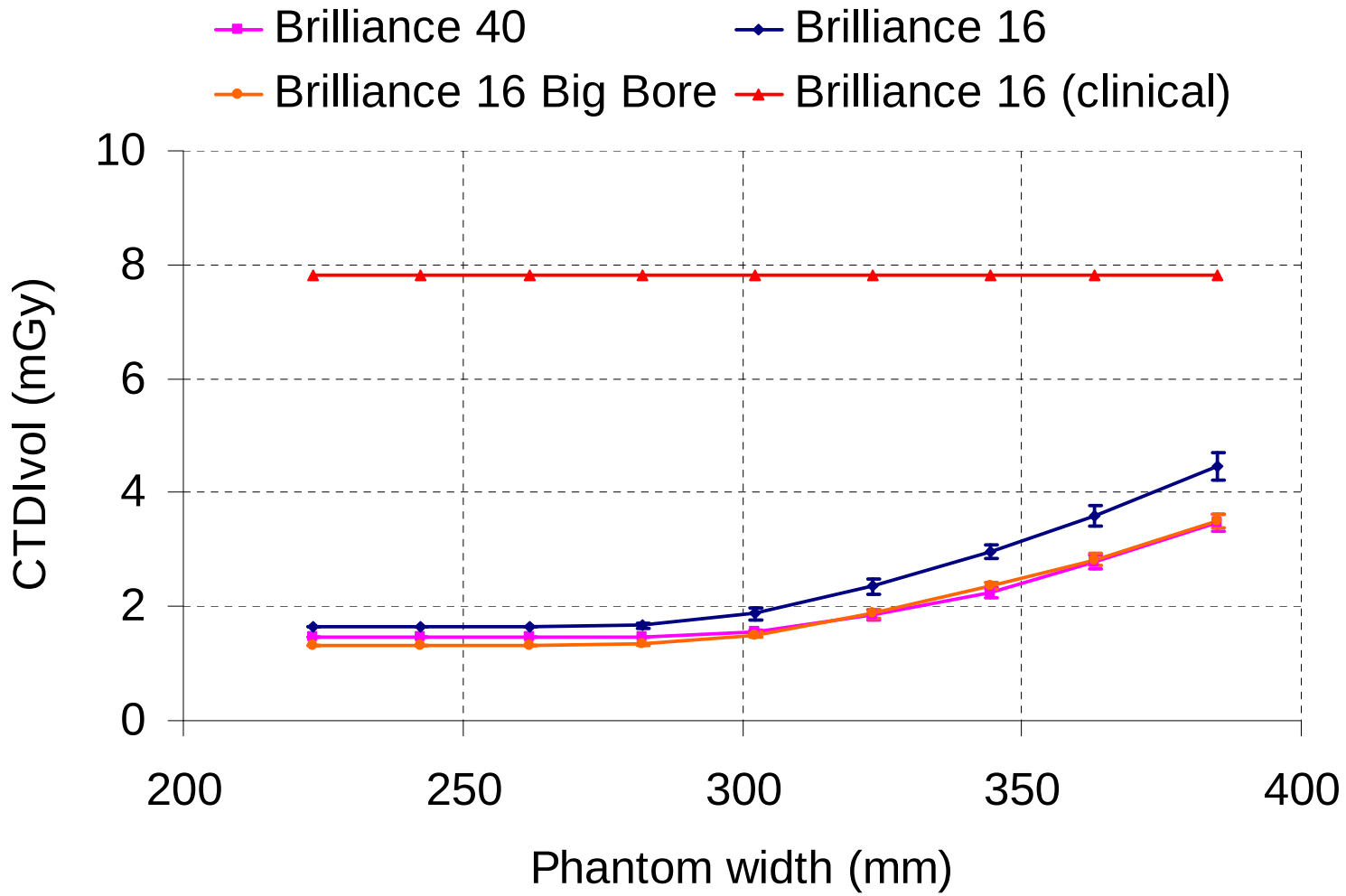
Validation of ‘Rando Reference Images’



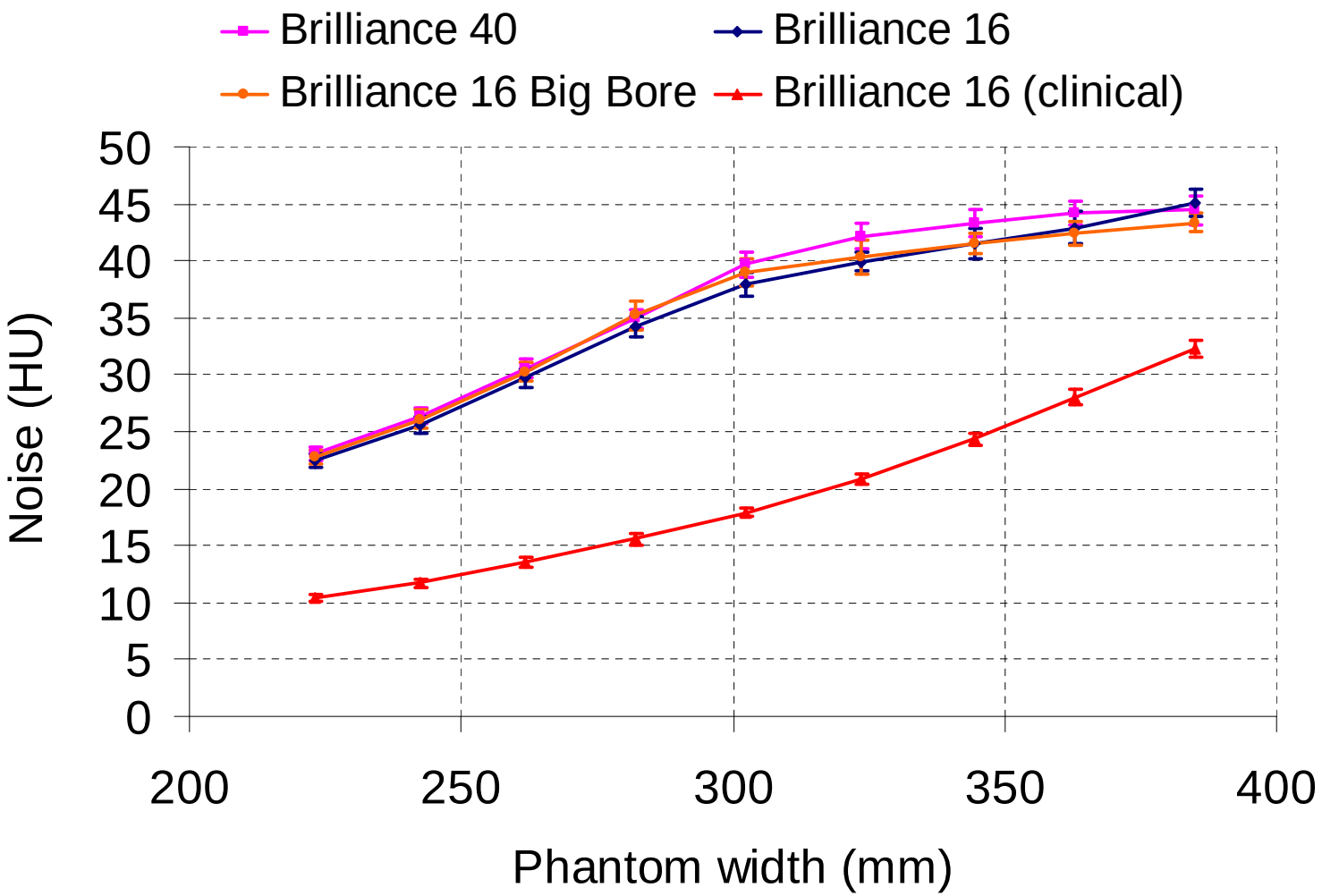
Matching protocols

- The combination of Rando and AEC phantom scans were used to check that protocols created on the different scanners were matched in terms of dose and image quality
- mAs used for Rando scans of clinically relevant region on each system checked for agreement
- Full characterisation of AEC performance with uniform elliptical phantom for more detailed analysis…

Matching protocols – Chest only



Matching protocols – Chest only



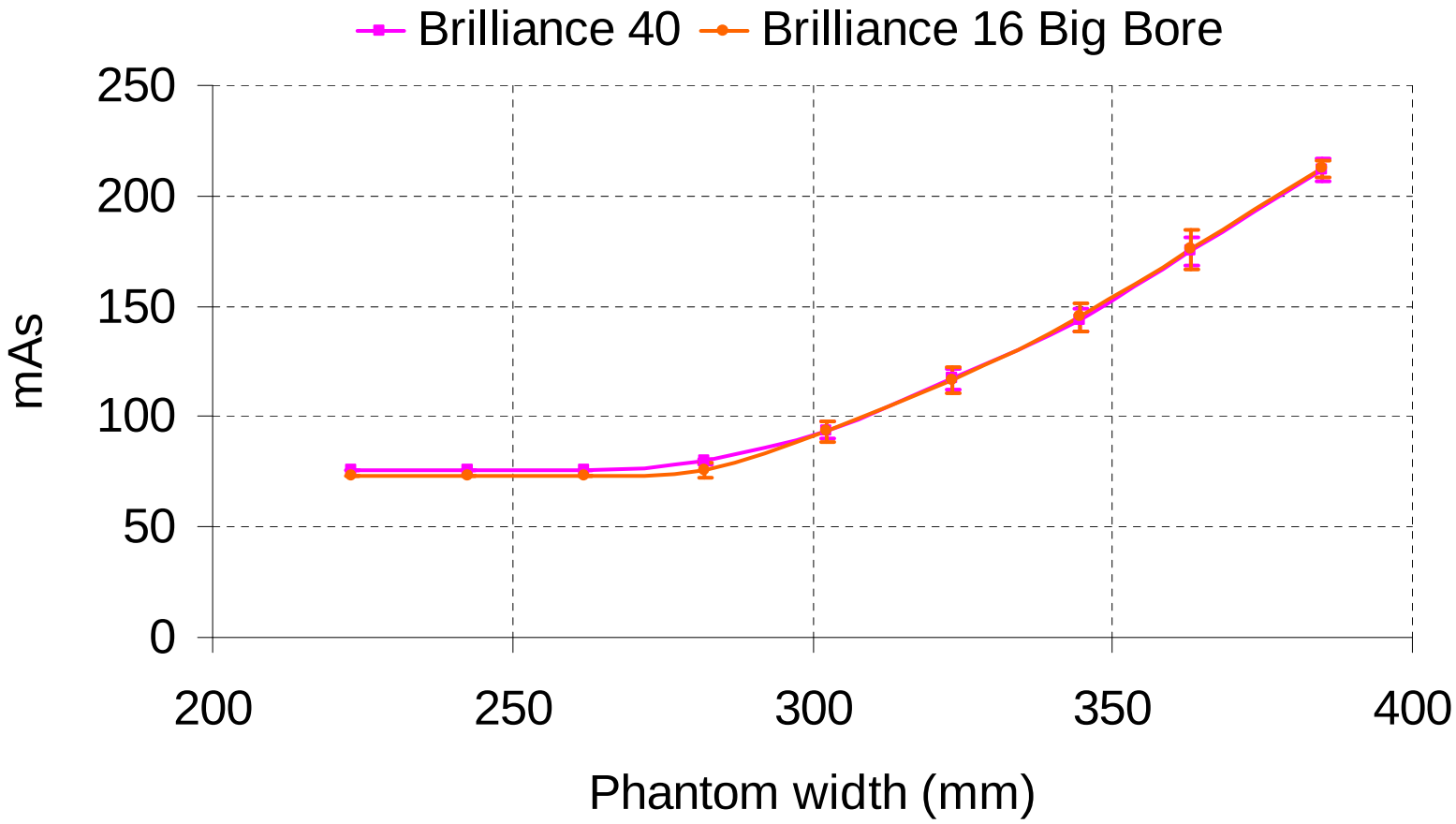
CT Chest only (non-contrast)

- This protocol is now being used **clinically** on the Brilliance 40 and 16 scanners
  - Brilliance 40 ~ 6 months
  - Brilliance 16 < 1 month
- No issues with image quality identified (as expected)
- Not had sufficient time for collection of dose audit data to compare performance

But a word of warning…

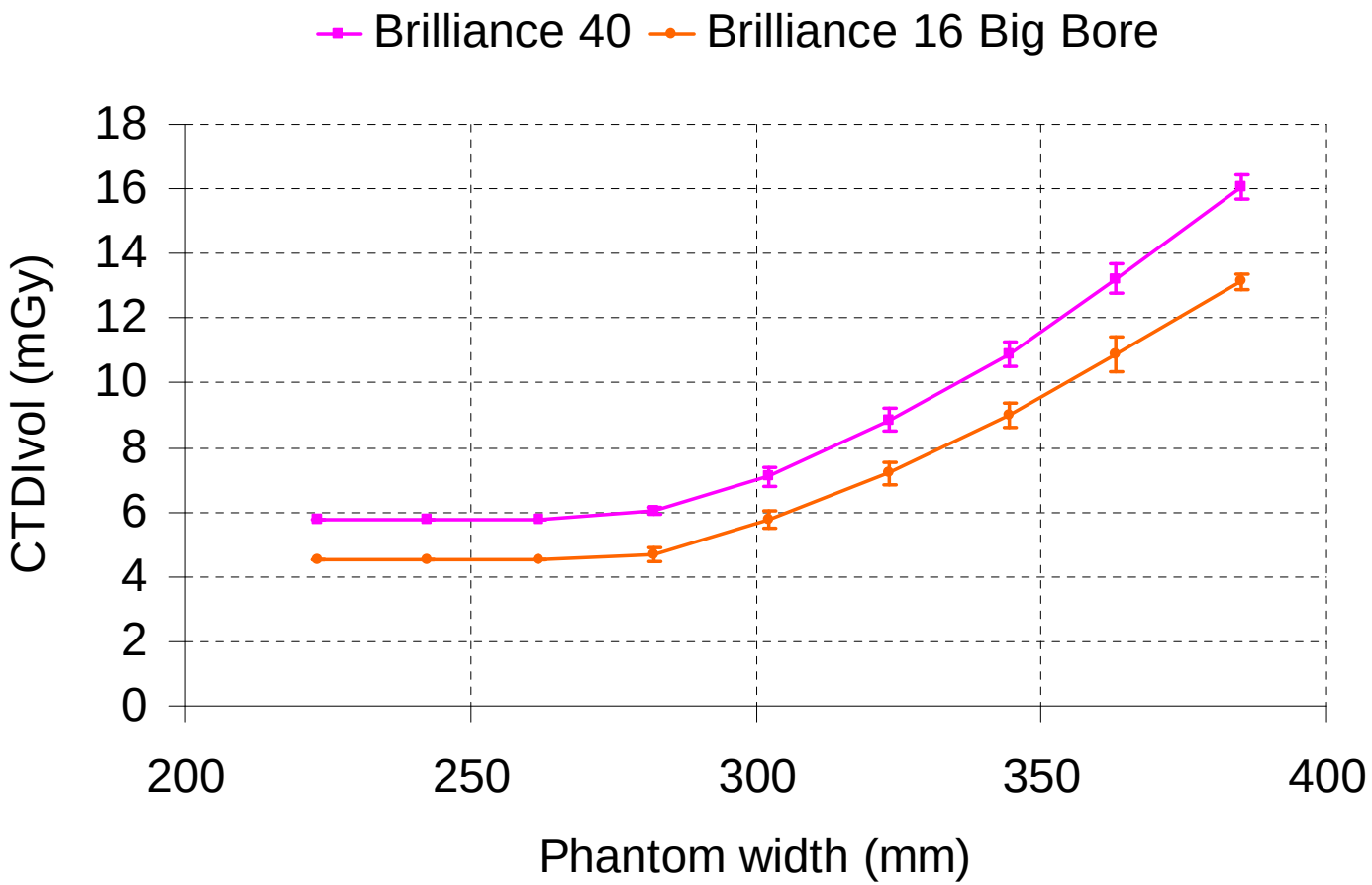
Matching protocols – CTPA

Protocols are easily matched in terms of max/min/average mAs…

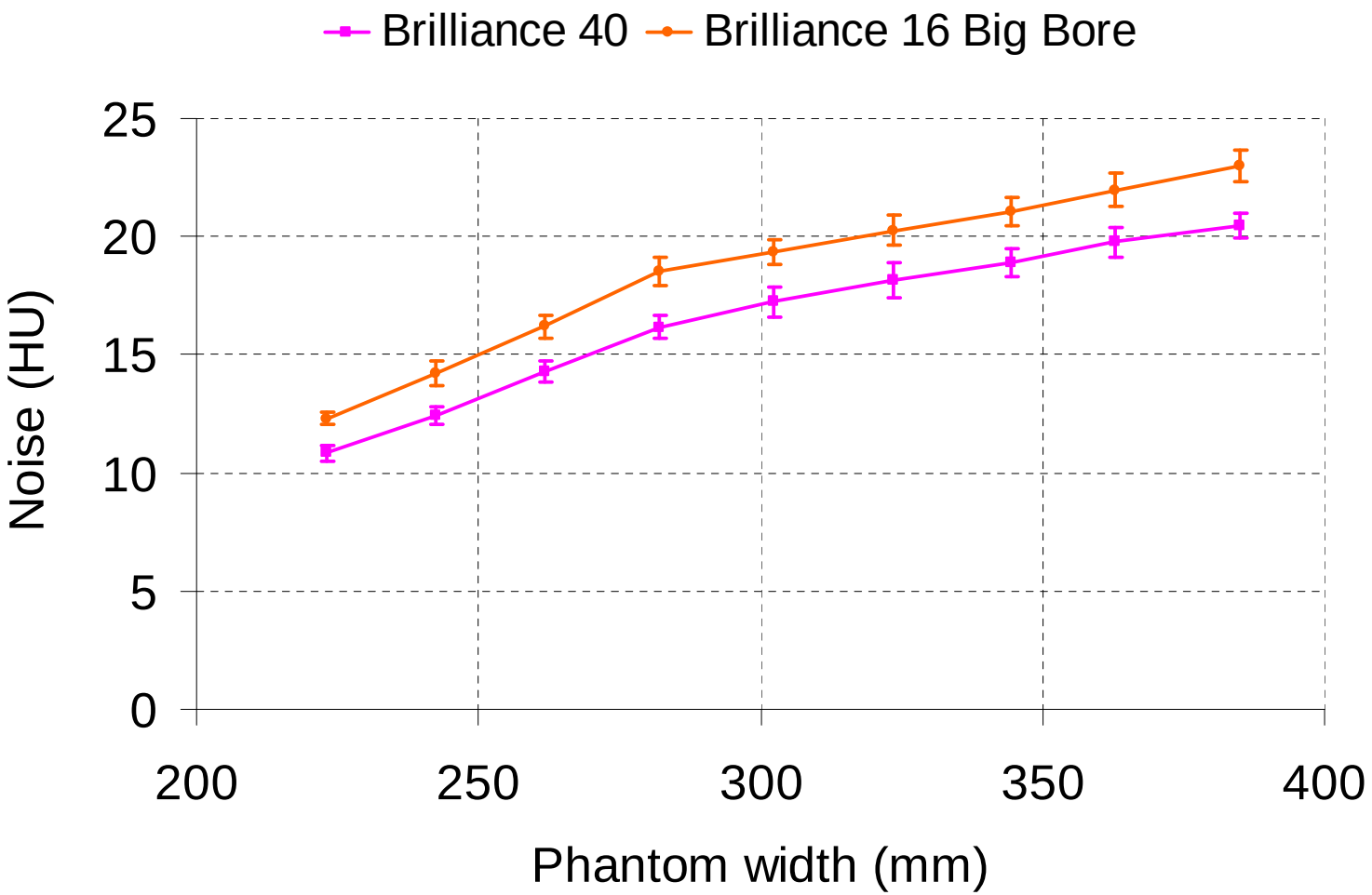


Matching protocols – CTPA

…but the Big Bore has greater focus-to-isocentre distance, so…

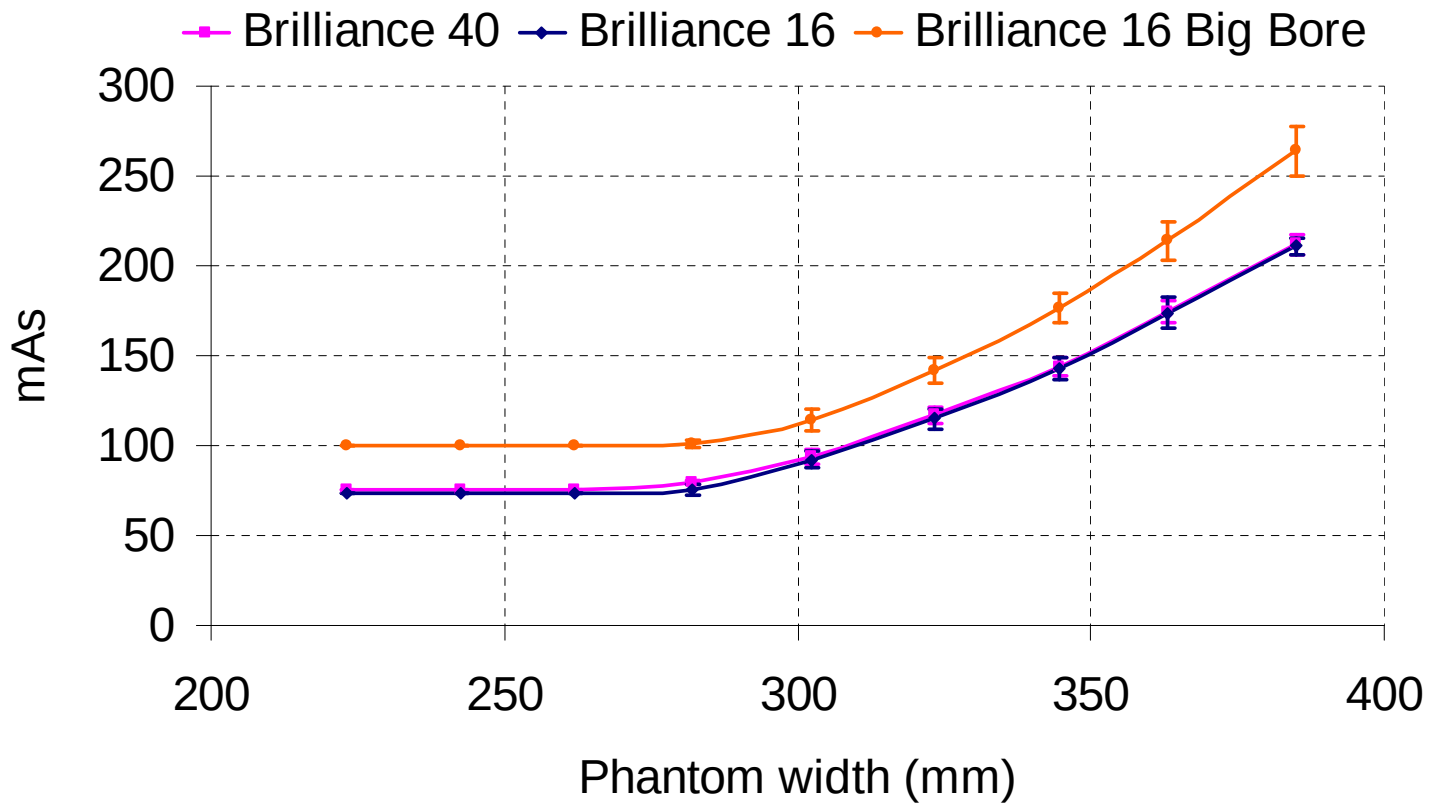


Matching protocols – CTPA



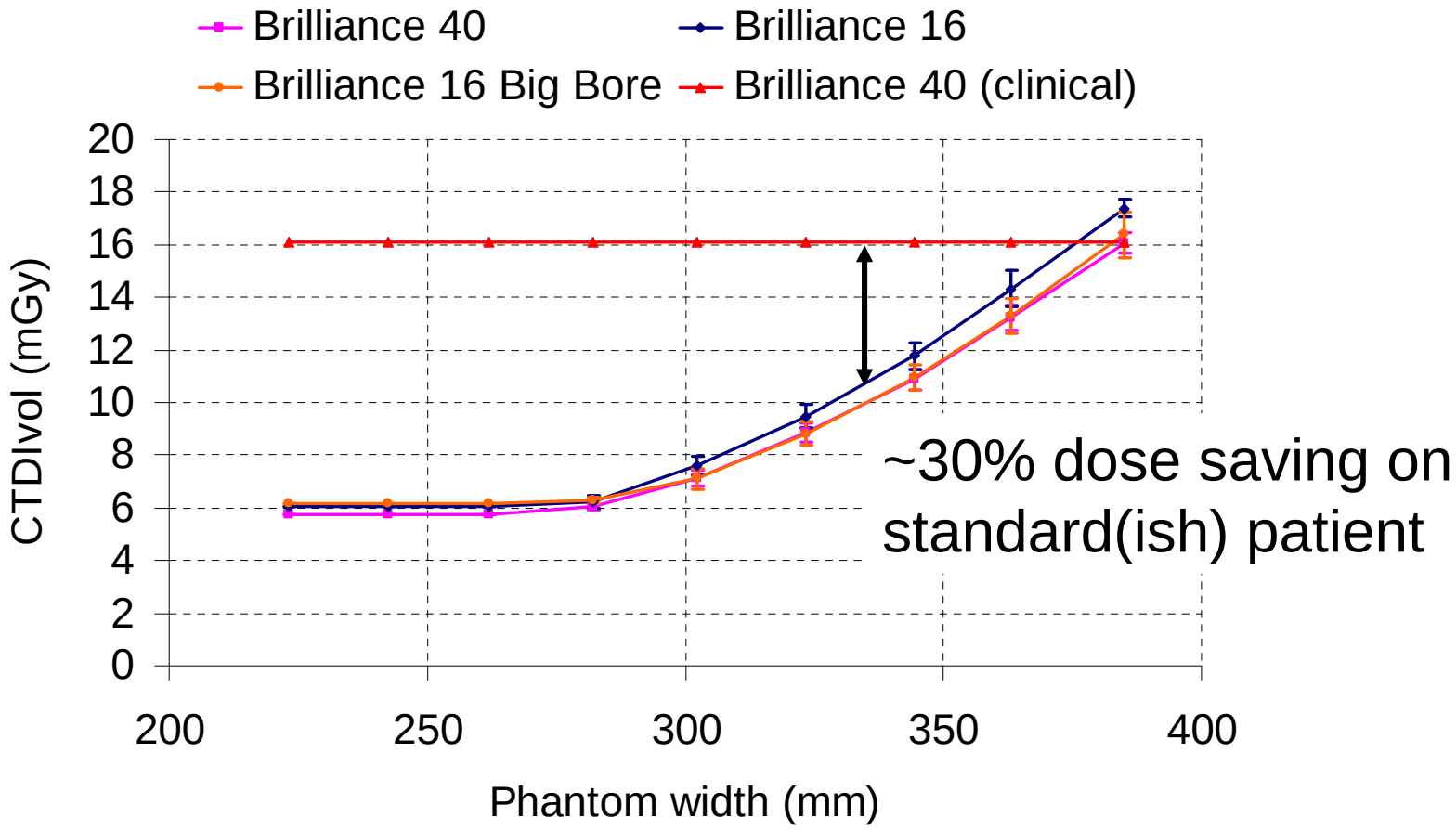
Matching protocols – CTPA

But if maximum mAs used for reference image is corrected for the ratio of $CTDI_{vol}$/mAs measured during routine QA (~1.21)…



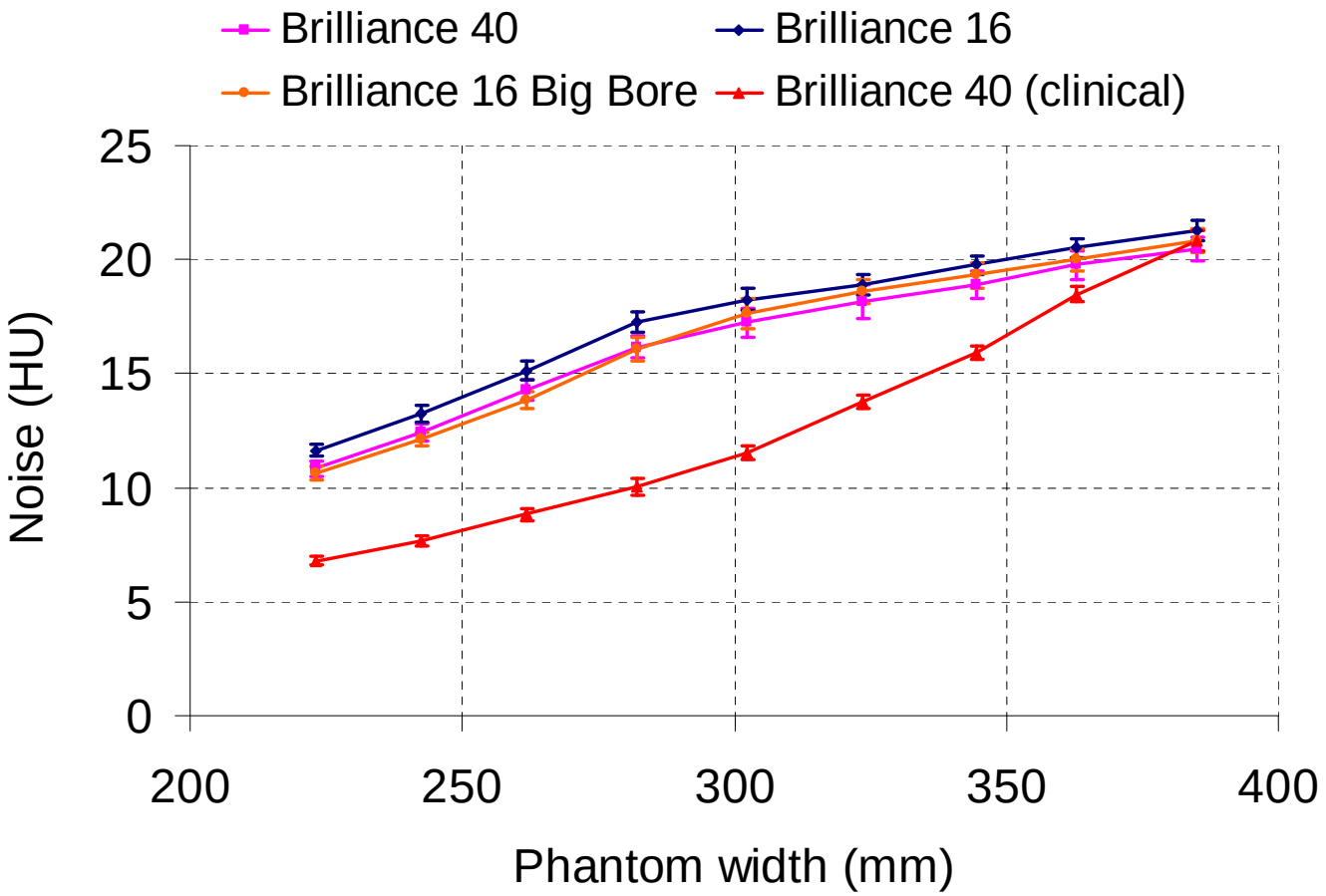
Matching protocols – CTPA

… doses are well matched...



Matching protocols – CTPA

…as is image noise!



ACS optimisation

- First stage in optimisation is nearing completion
  - Scan protocols on each system will be matched in terms of AEC performance
  - The performance of each scanner should not change over time (provided no-one changes the protocol settings)
- When happy that patient doses are matched (need all protocols to go clinical, and time for dose audit), will start investigating whether there is any scope for further dose optimisation
  - All that will be necessary is to rescan Rando with new mAs value and save as DoseRight (system will warn whether doses will go up or down as a result)

CT AEC QA?

- Acquired lots of data as part of this project
- Can be extremely time consuming if looking at every protocol on a scanner!
- So what about QA?
  - Routine?
    - Scan nominated test protocol every year and compare response curves? What about picking up changes in clinical setup (particularly problematic with Philips scanners)?
  - Reactive?
    - When a (frequently used) protocol is created, acquire baseline response curves
    - Routinely monitor patient doses
    - If changes in patient doses detected, test AEC against the baseline performance for that protocol?
  - Do nothing?...

Conclusions

- What started as a small project looking into the optimisation of the ‘unique’ Philips DoseRight system has revealed how important it is to actually understand the way in which the AEC works (or as far as possible)!
- A technique has been developed for setting up reference images on a number of different scanners that ensures protocols are well matched in terms of dose and imaging performance
  - Avoid giving much higher doses just because of the way the AEC is setup!
- The D-DOM system is extremely limited for the purposes of dose optimisation
  - This should be the default protocol option when it is known that longitudinal variations will be negligible
- A full 3D/4D AEC system from Philips is long overdue!

Acknowledgements

- Radiation Physics Department, Hull and East Yorkshire Hospitals NHS Trust
  - Dr Craig Moore
  - Paul Credland

- Radiology Department, Hull and East Yorkshire Hospitals NHS Trust
  - Andrew Stephens
  - CT Radiographers