CONNECTING LIFE AND SCIENCE

Alternative Strategies for Linac Beam Verification or Beam Data Collection Without Using a 3D Water Tank: Linac Beam Data Collection from 1-D to 3-D

Nels C Knutson[1,2]

[1]Washington University School of Medicine, St Louis, MO

[2]University of Massachusetts Lowell, Lowell MA

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Disclosures

- Nels C Knutson[1,2]
  - [1]Washington University School of Medicine, St Louis, MO
  - [2]University of Massachusetts Lowell, Lowell, MA
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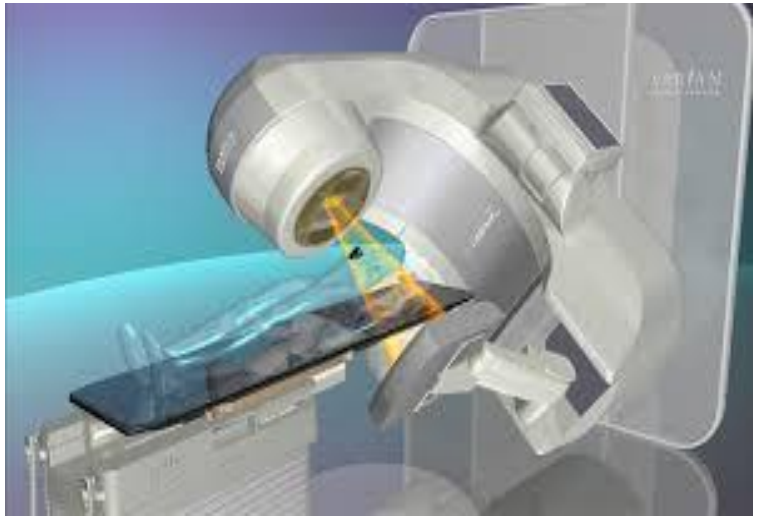
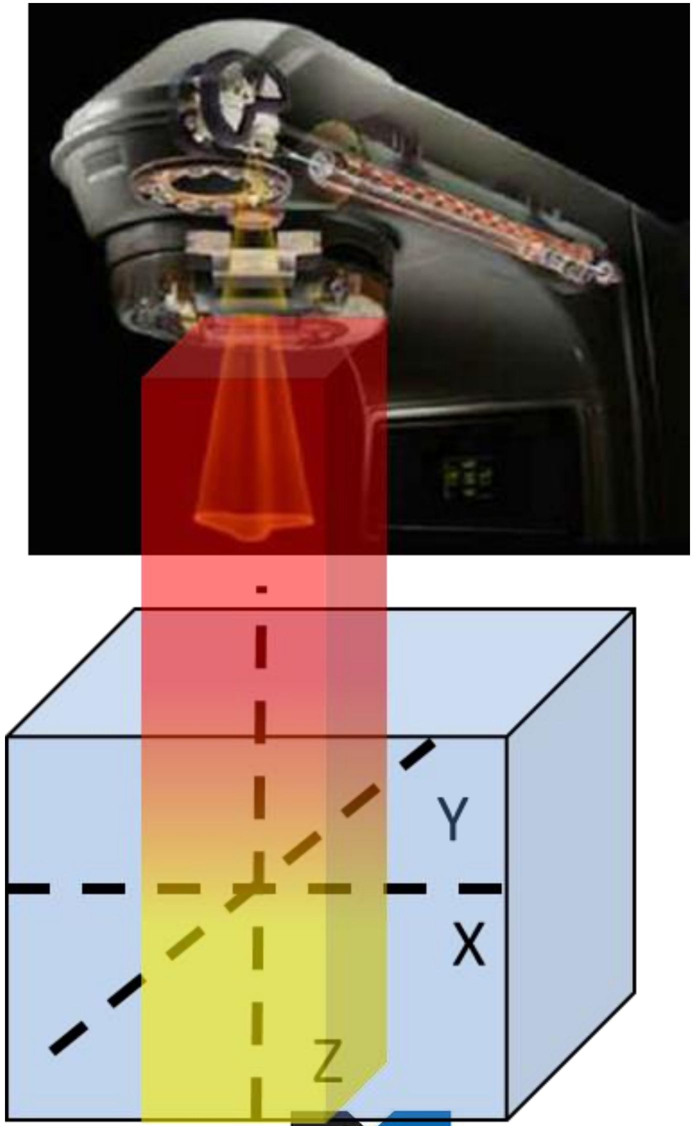
- I receive research funding and consulting income from Varian Medical Systems

Introduction-The Problem

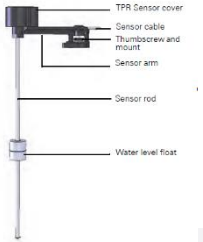
- Commissioning
  - The collection of 3D radiation beam data
  - Used to model the treatment fields we used to treat patients
  - Typically collected with a water tank that can move a detector in the 3 Cartesian directions
    - 3D water tank

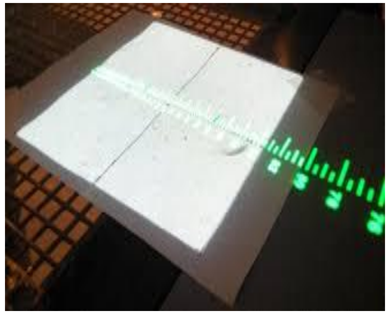




Introduction-The Problem

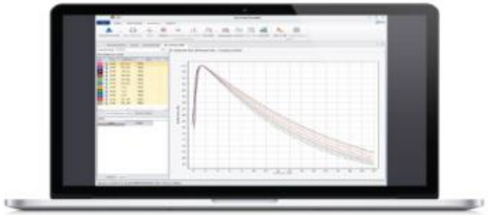
- Commissioning
  - Mistakes here affect all patients
  - A lot of equipment required
  - Expensive (~70-100k)
  - Where do you store
  - Difficult to transport
  - Takes skill to setup and use

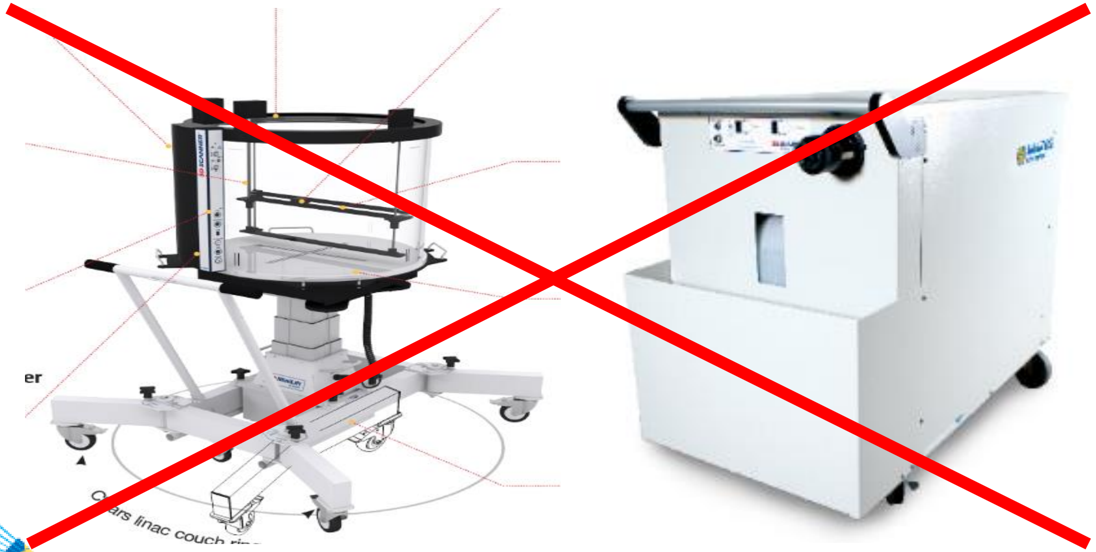




Introduction-The Problem

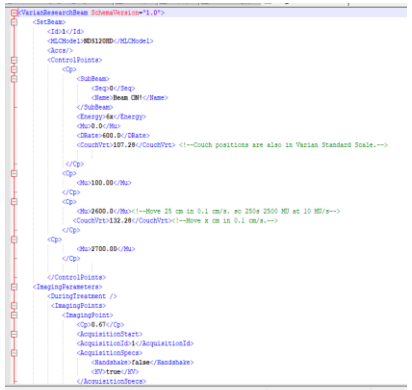
- Commissioning
  - Can this be simplified?
  - Made less expensive?
  - Could we do it with just the equipment in say checked luggage?
  - Could we utilize the linac to scan its self?





Introduction-Controlling the Linac-Speak the Language

- Extensible Mark Up Language (XML) used to control modern Varian linear accelerators (Halcyon, TrueBeam, VitalBeam)
- Dicom files converted internally to XML
- Developer Mode allows users to give XML directly to Linac
- This can be done in service mode as well with hardware key



- Can precisely control TrueBeam
- Can be used to program machine QA! (See MPC)

Quality control procedures for dynamic treatment delivery techniques involving couch motion

Victoria Y. Yu, Benjamin P. Fahimian, Lei Xing, and Dimitre H. Hristov[a)]

Department of Radiation Oncology, Stanford University School of Medicine, Stanford, California 94305-5847

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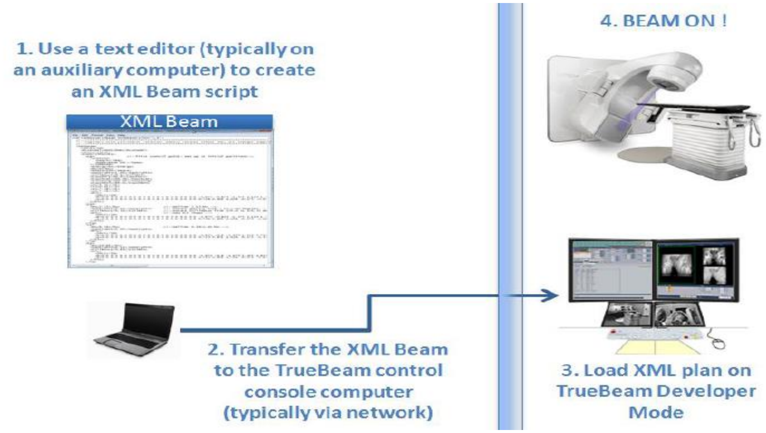
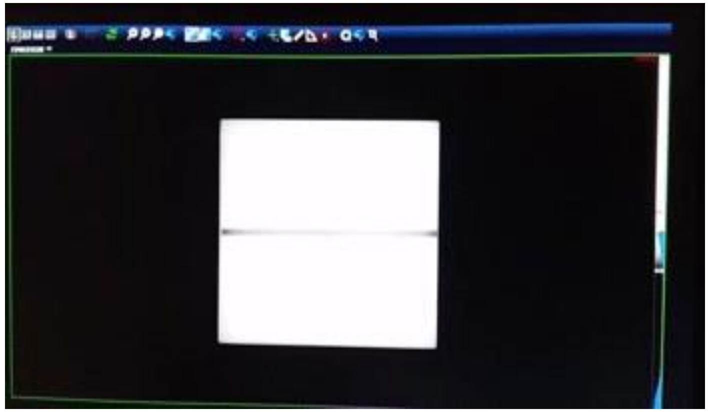
In this study, the authors introduce and demonstrate quality control procedures for evaluating the geometric and dosimetric fidelity of dynamic treatment delivery techniques involving treatment couch motion synchronous with gantry and multileaf collimator (MLC). Tests were designed to evaluate positional accuracy, velocity constancy and accuracy for dynamic couch motion under a realistic weight load. A test evaluating the geometric accuracy of the system in delivering treatments over complex dynamic trajectories was also devised. Custom XML scripts that control the Varian TrueBeam™ STx (Serial #3) axes in Developer Mode were written to implement the delivery sequences for the tests. Delivered dose patterns were captured with radiographic film or the electronic portal imaging device. The couch translational accuracy in dynamic treatment mode was 0.01 cm. Rotational accuracy was within 0.3°, with 0.04 cm displacement of the rotational axis. Dose intensity profiles capturing the velocity constancy and accuracy for translations and rotation exhibited standard deviation and maximum deviations below 3%. For complex delivery involving MLC and couch motions, the overall translational accuracy for reproducing programmed patterns was within 0.06 cm. The authors conclude that in Developer Mode, TrueBeam™ is capable of delivering dynamic treatment delivery techniques involving couch motion with good geometric and dosimetric fidelity. © *2014 American Association of Physicists in Medicine*. [http://dx.doi.org/10.1118/1.4886757]



-Varian Developer Mode Reference Guide

"Automation of Linear Accelerator Star Shot Measurement with Advanced XML Scripting and Electronic Portal Imaging Device"

-**Ngoc Nguyen**, Nels Knutson, Matthew Schmidt, Michael Price AAPM 2016 Meeting

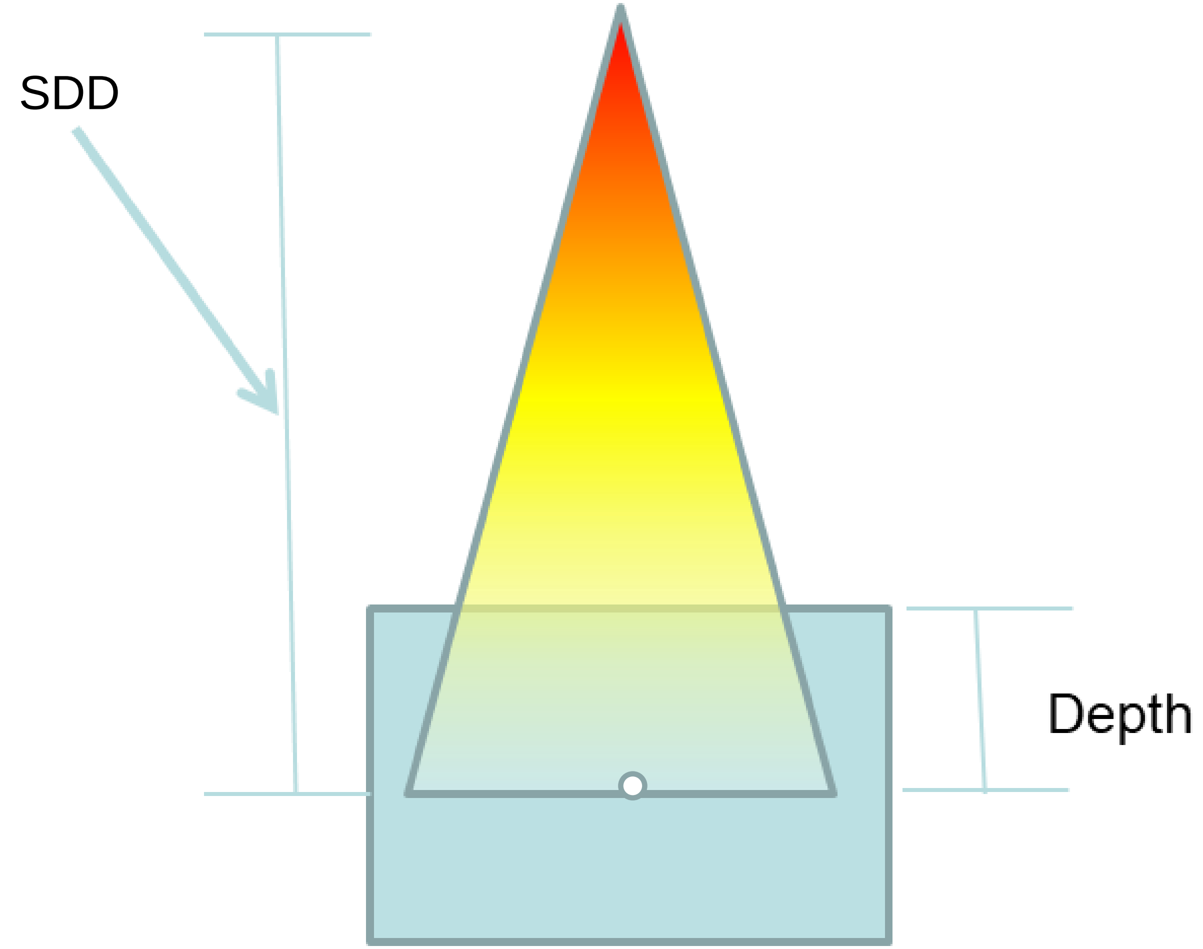


Introduction-Can We Use XML?

- Could we use automated couch motions to collect 3D (XYZ) radiotherapy data?
- My work was done in sort pieces
  - Step 1-Section A
    - Z dimension (Depth Profiles)
    - TMR
  - Step 2 – Section B
    - X&Y dimensions (Lateral Profiles)
  - Step 3 – Section C
    - Putting it all together & Lesions learned

Section A - Measurement of 1D Data, The Direct and Continuous TMR

- Tissue Maximum Ratio (TMR)
- Fixed Source to Detector Distance (SDD) with changing amounts of buildup.
- Time consuming in practice
- Traditionally measured by
  - Adding solid water
  - Changing depth of chamber in water and manually setting table height
  - Draining water
  - Converting measured PDDs



Section A – Our Method & Workflow

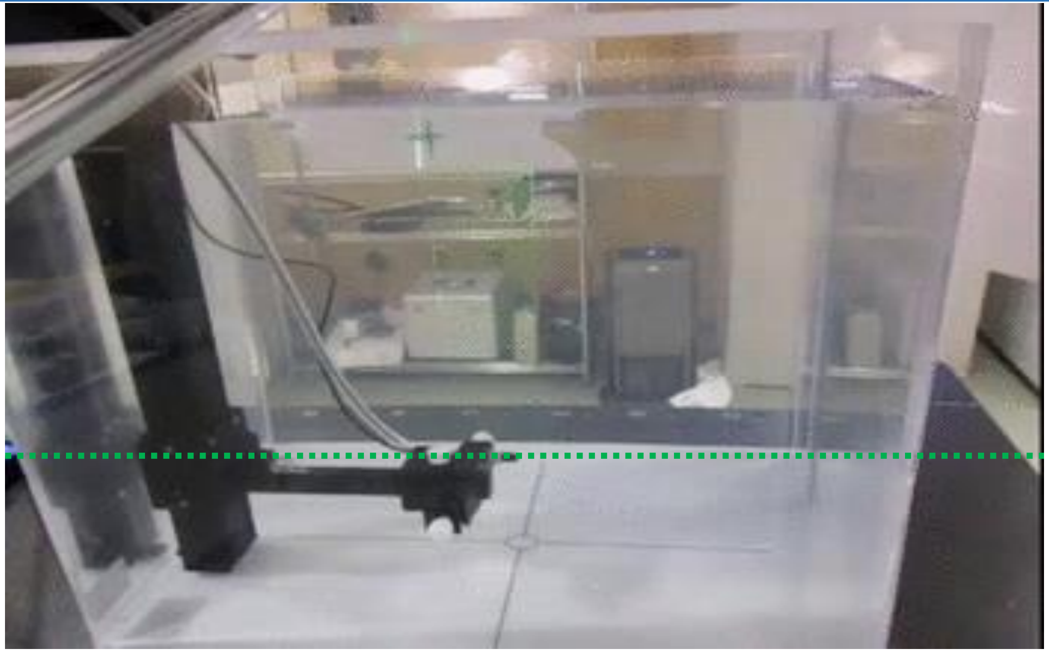
- Write XML to synchronize couch motion with scanning tank motion
- Keeping the chamber at isocenter while changing the depth.

System

Events

System				
TrueBeam	Load XML	Beam On And hold	Release Beam Hold When Scan Motion Starts	Beam Off
Water Tank/PCE Software	Initiate Tank Software	Initial scan		Scan Ends

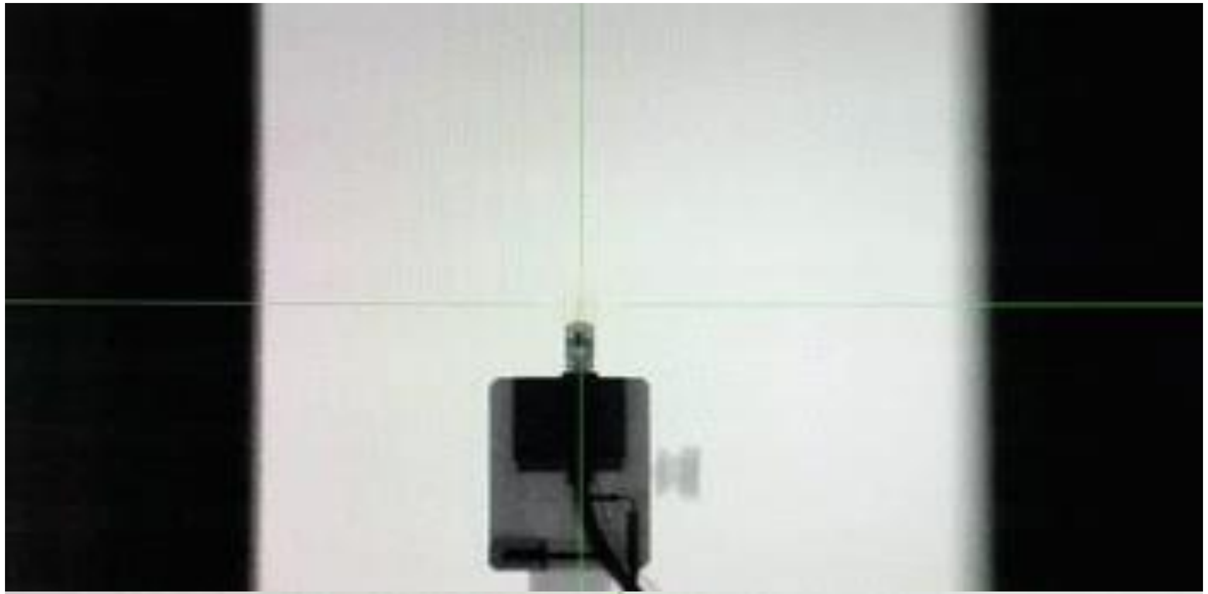
Time

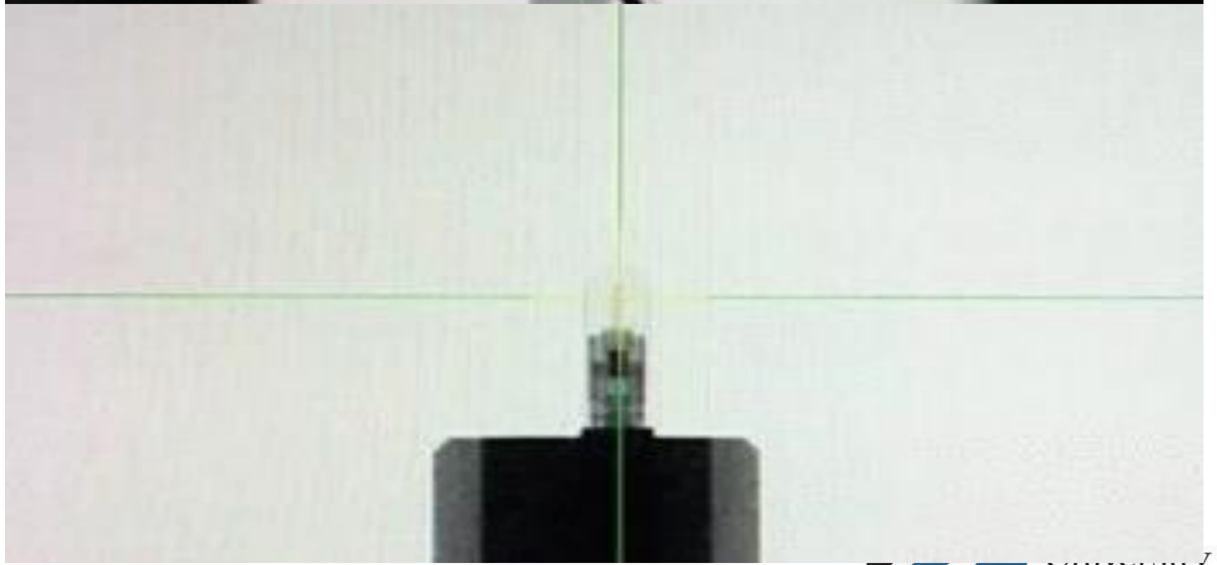


Section A – Use of Imaging

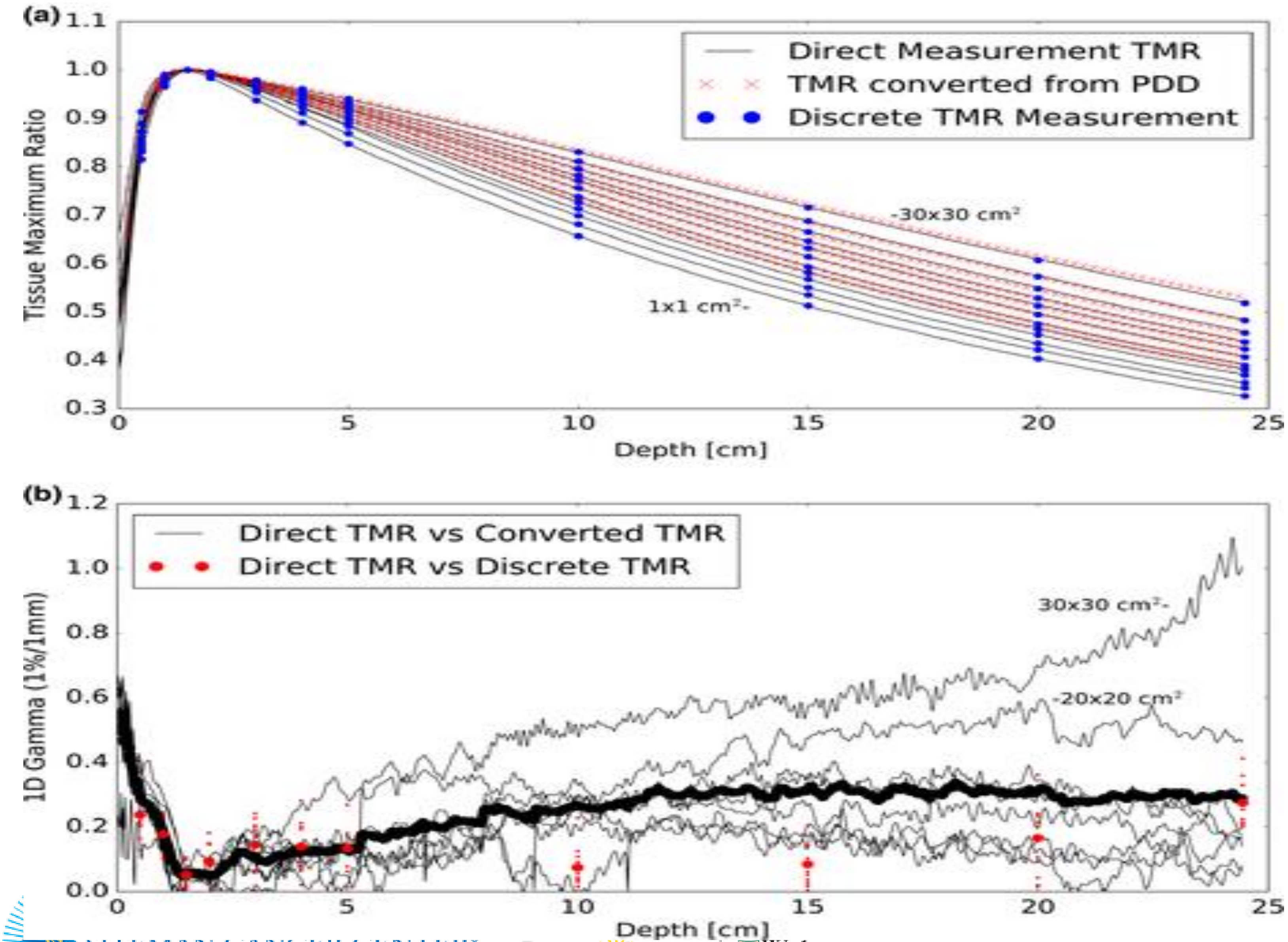
Fluoroscopy during delivery to confirm setup

With some skill we found we can keep SDD within 1mm of 100 cm





Section A – Results



- Continuous TMR matches Discrete TMR
- Converted TMRs are not within 1% of measurement

Comparison vs. discrete TMR data

Field size [cm²]	Max Γ	Mean Γ	Max Abs diff in TMR	Mean Abs diff. in TMR
1 × 1	0.605	0.061	0.009	0.001
2 × 2	0.600	0.169	0.006	0.002
3 × 3	0.600	0.062	0.007	0.001
4 × 4	0.622	0.138	0.015	0.003
5 × 5	0.683	0.142	0.013	0.002
6 × 6	0.702	0.183	0.013	0.003
8 × 8	0.650	0.142	0.011	0.002
10 × 10	0.657	0.131	0.012	0.002
12 × 12	0.643	0.103	0.006	0.002
15 × 15	0.741	0.149	0.006	0.002
20 × 20	0.658	0.108	0.009	0.002
30 × 30	0.653	0.124	0.007	0.002
All field sizes	0.741	0.126	0.015	0.002

N.C. Knutson *et al.*, "Technical Note: Direct Measurement of Continuous TMR Data with a 1D Tank and Automated Couch Movements," Med. Phys. (2017).

Section A – Conclusions

- Continuous TMR matches discrete TMR
- Converted TMRs are not within 1% of directly measured TMRs
- This method provides convenient and accurate method for direct measurement of TMRs

Technical Note: Direct measurement of continuous TMR data with a 1D tank and automated couch movements

Nels C. Knutson[a)]
Medical Physics Program, University of Massachusetts Lowell, Lowell, MA 01852, USA
Department of Radiation Oncology, Rhode Island Hospital, The Alpert Medical School of Brown University, Providence, RI 02903, USA
Department of Physics, University of Rhode Island, Kingston, RI 02881, USA
Department of Radiation Oncology, Washington University School of Medicine, St. Louis, MO 63110, USA

Matthew C. Schmidt
Medical Physics Program, University of Massachusetts Lowell, Lowell, MA 01852, USA
Department of Radiation Oncology, Rhode Island Hospital, The Alpert Medical School of Brown University, Providence, RI 02903, USA
Varian Medical Systems, Education Department, Las Vegas, NV 89119, USA

Matthew D. Belley and Ngoc B. Nguyen
Department of Radiation Oncology, Rhode Island Hospital, Providence, RI 02903, USA
Department of Radiation Oncology, Rhode Island Hospital, The Alpert Medical School of Brown University, Providence, RI 02903, USA

H. Harold Li
Department of Radiation Oncology, Washington University School of Medicine, St. Louis, MO 63110, USA

Erno Sajo
Medical Physics Program, University of Massachusetts Lowell, Lowell, MA 01852, USA

Michael J. Price
Department of Radiation Oncology, Rhode Island Hospital, Providence, RI 02903, USA
Department of Radiation Oncology, Rhode Island Hospital, The Alpert Medical School of Brown University, Providence, RI 02903, USA

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N.C. Knutson *et al.*, Med. Phys. (2017).

Section B – 2D Data, Lateral Profiles

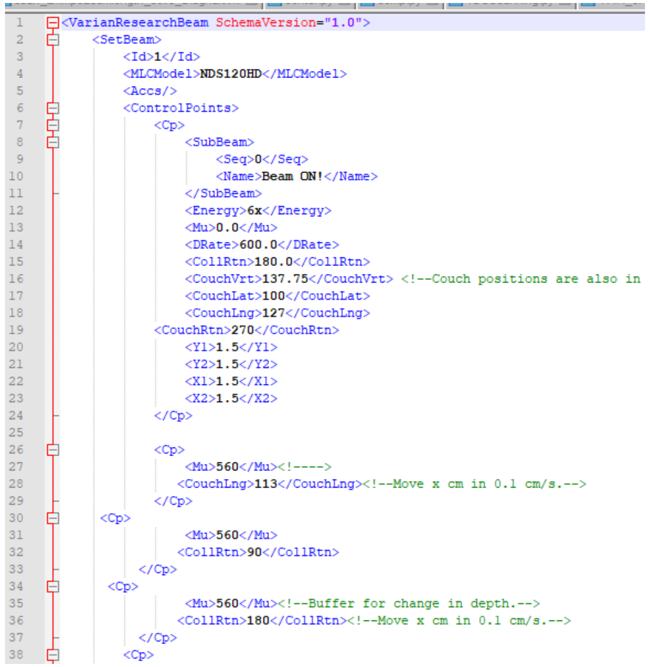
- 1D motion along Z axis worked well!
- Why not X and Y axis of the couch.
- Could we make a clinically equivalent beam model with just this equipment


```xml
<VarianResearchBeam SchemaVersion="1.0">
    <SetBeam>
        <Id>1</Id>
        <MLCModel>NDS120HD</MLCModel>
        <Accs/>
        <ControlPoints>
            <Cp>
                <SubBeam>
                    <Seq>0</Seq>
                    <Name>Beam ON!</Name>
                </SubBeam>
                <Energy>6x</Energy>
                <Mu>0.0</Mu>
                <DRate>600.0</DRate>
                <CollRtn>180.0</CollRtn>
                <CouchVrt>137.75</CouchVrt> <!--Couch positions are also in Varian Standard Scale.-->
                <CouchLat>100</CouchLat>
                <CouchLng>127</CouchLng>
            <CouchRtn>270</CouchRtn>
                <Y1>1.5</Y1>
                <Y2>1.5</Y2>
                <X1>1.5</X1>
                <X2>1.5</X2>
            </Cp>

            <Cp>
                <Mu>560</Mu><!---->
               <CouchLng>113</CouchLng><!--Move x cm in 0.1 cm/s.-->
            </Cp>
     <Cp>
                <Mu>560</Mu>
               <CollRtn>90</CollRtn>
          </Cp>
      <Cp>
                <Mu>560</Mu><!--Buffer for change in depth.-->
               <CollRtn>180</CollRtn><!--Move x cm in 0.1 cm/s.-->
          </Cp>
        <Cp>
```


Section B – Methods

- Compare dosimetry data for 6MV photons
  - Collected using a 3D water tank (3DS)
  - Collected using a 1D tank with automated couch motions (1DS)
- All data collected with IBA CC13 chambers
  - (2.5 mm/s 1.25 mm pt spacing)
- PDDs & profiles
  - 3x3, 4x4, 5x5 6x6, 10x10, 20x20, 30x30, and 40x40 cm^2
- Two beams models created with the two data sets and compare the two outputs



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                <DRate>600.0</DRate>
                <CollRtn>180.0</CollRtn>
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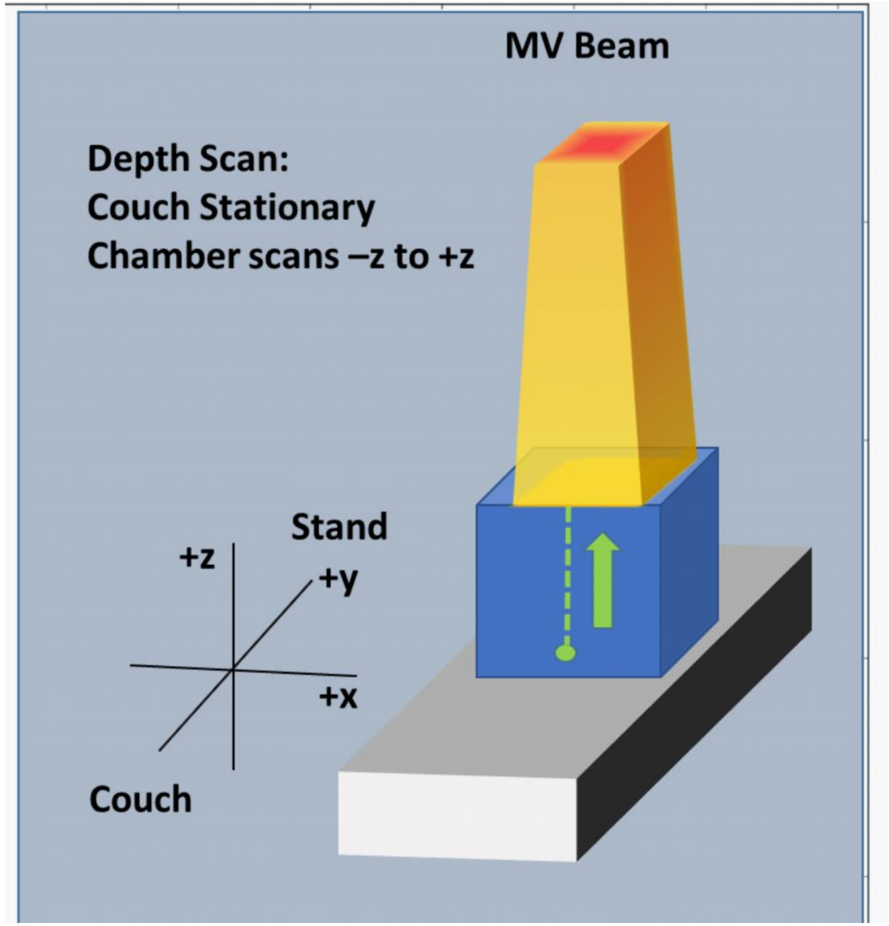
                <CouchLng>127</CouchLng>
            <CouchRtn>270</CouchRtn>
                <Y1>1.5</Y1>
                <Y2>1.5</Y2>
                <X1>1.5</X1>
                <X2>1.5</X2>
            </Cp>

            <Cp>
                <Mu>560</Mu><!---->
               <CouchLng>113</CouchLng><!--Move x cm in 0.1 cm/s.-->
            </Cp>
       <Cp>
                <Mu>560</Mu>
               <CollRtn>90</CollRtn>
           </Cp>
        <Cp>
                <Mu>560</Mu><!--Buffer for change in depth.-->
               <CollRtn>180</CollRtn><!--Move x cm in 0.1 cm/s.-->
           </Cp>
         <Cp>
```

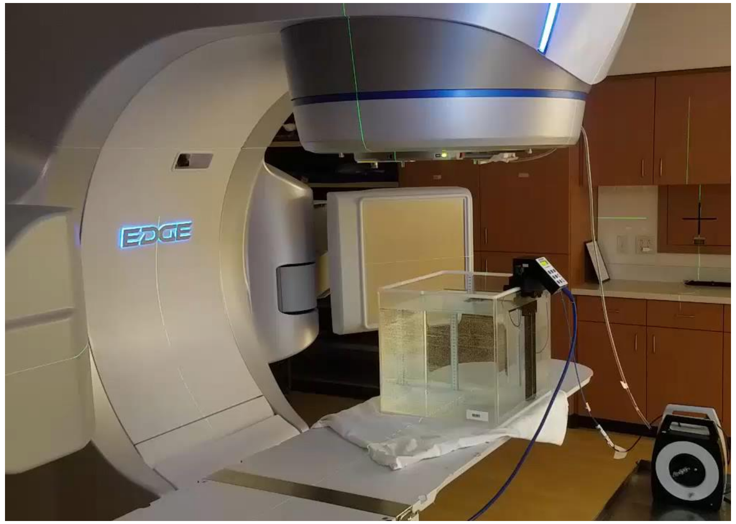

Section B – 1DS Method-Depth Profiles



- Standard method for PDD collection.
- Scan the chamber from deep depth to surface.
- Fixed SSD.

N.C. Knutson *et al.*, "Equivalency of beam scan data collection using a 1D tank and automated couch movements to traditional 3D tank measurements," J. Appl. Clin. Med. Phys. (2018).

Section B – 1DS Method X, Y, and XY



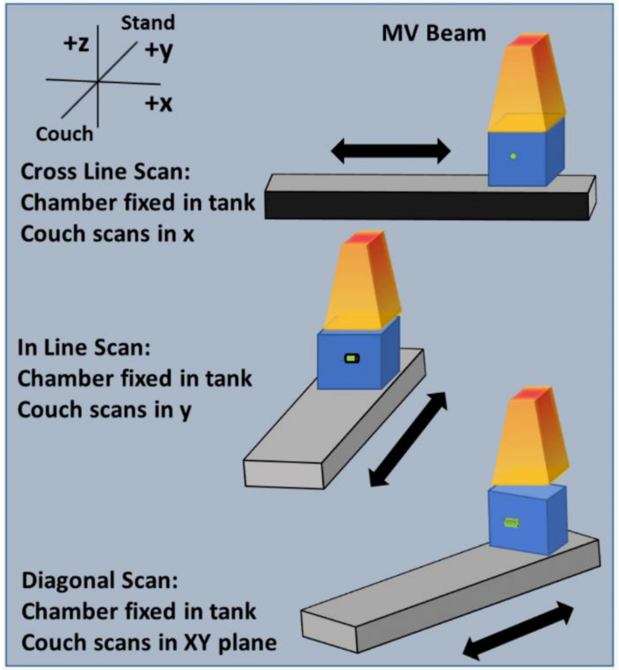
System

Events

TrueBeam	Load XML	Beam On XML runs with programmed pauses to change depth	Beam Off

Water Tank/PCE Software	Initiate Electrometer Measurement and Data Logging	Set Initial Tank Depth	Change Depth At Each Pause In Beam Programed in XML	Stop Measurement and Data Logging Save Data for Analysis

Time



N.C. Knutson *et al.*, "Equivalency of beam scan data collection using a 1D tank and automated couch movements to traditional 3D tank measurements," J. Appl. Clin. Med. Phys. (2018).

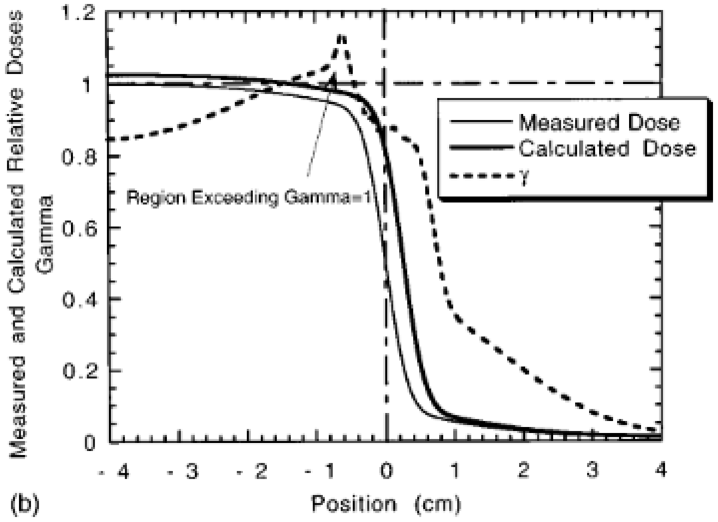
Section B – Data Comparison Method

- **Post hoc**: convert saved electrometer data to profiles using Python
- Utilized 1D gamma for all profiles.
- Depth profiles data was normalized to maximum dose
- Lateral profiles were centered and normalized to CAX
- For calculated comparisons a 3D gamma was used to compare calculated volumes normalized to the max dose in the TPS

$$\gamma(\mathbf{r}_m) = \min\{\Gamma(\mathbf{r}_m, \mathbf{r}_c)\} \forall \{\mathbf{r}_c\},$$

where

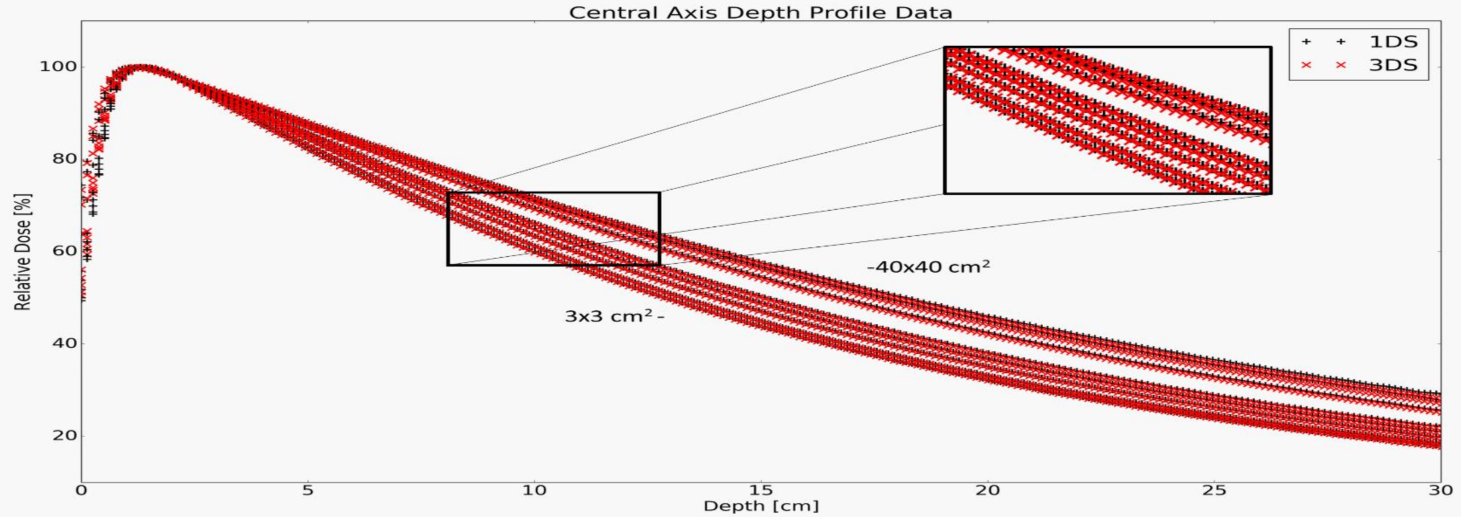
$$\Gamma(\mathbf{r}_m, \mathbf{r}_c) = \sqrt{\frac{r^2(\mathbf{r}_m, \mathbf{r}_c)}{\Delta d_M^2} + \frac{\delta^2(\mathbf{r}_m, \mathbf{r}_c)}{\Delta D_M^2}},$$



Low, Daniel A., et al. MedPhys (1998): 656-661.

Section B – Results- Measured PDDs

1a)



1b)

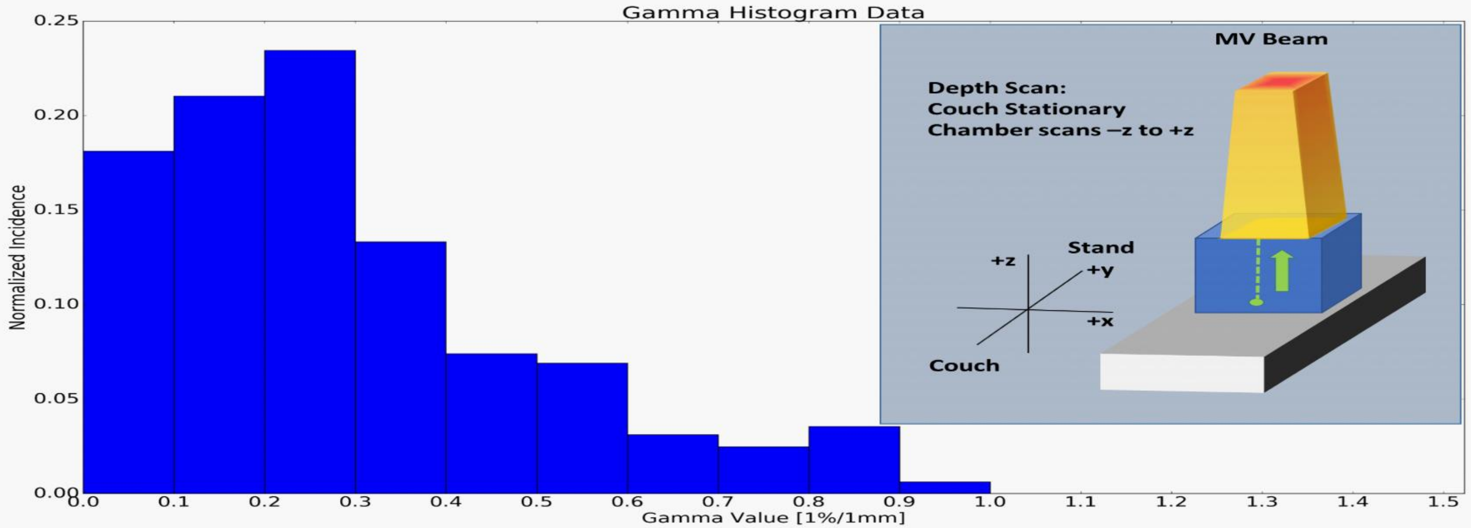


Table 1 1D gamma comparison of 1DS PDD data to 3DS central axis depth profile data (Γ: 1%/1 mm).

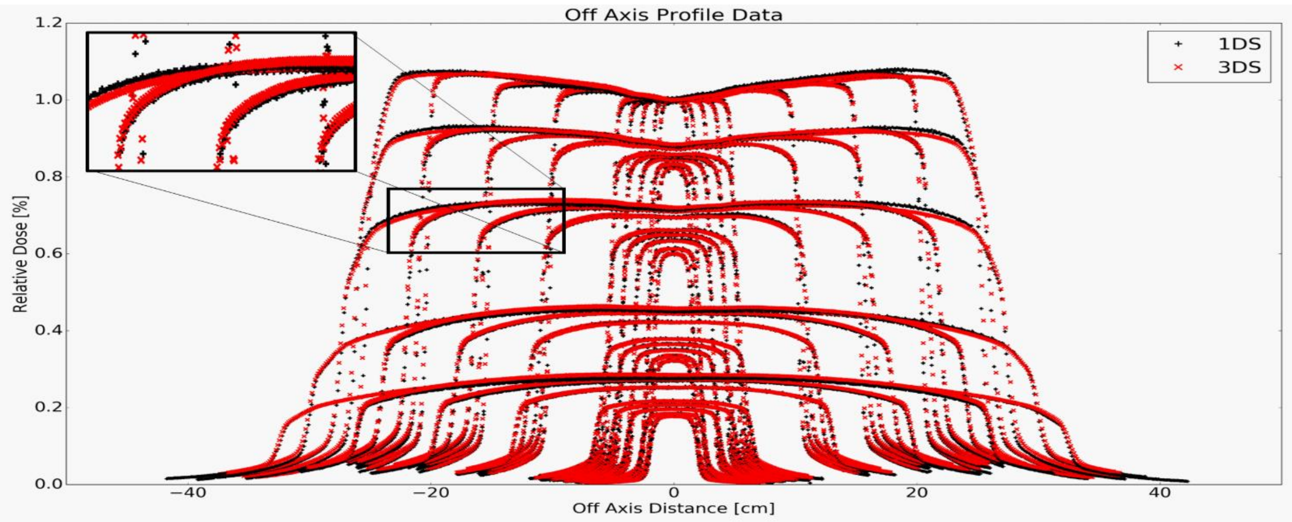
	1DS vs 3DS		
Field size (cm^2)	% points $\Gamma < 1$	Mean Γ	Max Γ
3 × 3	100	0.101	0.916
4 × 4	100	0.174	0.916
6 × 6	100	0.195	0.822
8 × 8	100	0.259	0.815
10 × 10	100	0.266	0.810
20 × 20	100	0.395	0.704
30 × 30	99.9	0.539	1.523
40 × 40	100	0.386	0.992
All field sizes	99.9	0.290	1.523

- 1D tank reproduces 3D tank PDDs
- Not a surprise

N.C. Knutson *et al.*, “Equivalency of beam scan data collection using a 1D tank and automated couch movements to traditional 3D tank measurements,” J. Appl. Clin. Med. Phys. (2018).

Section B – Results-Measured Profiles

2a)



2b)

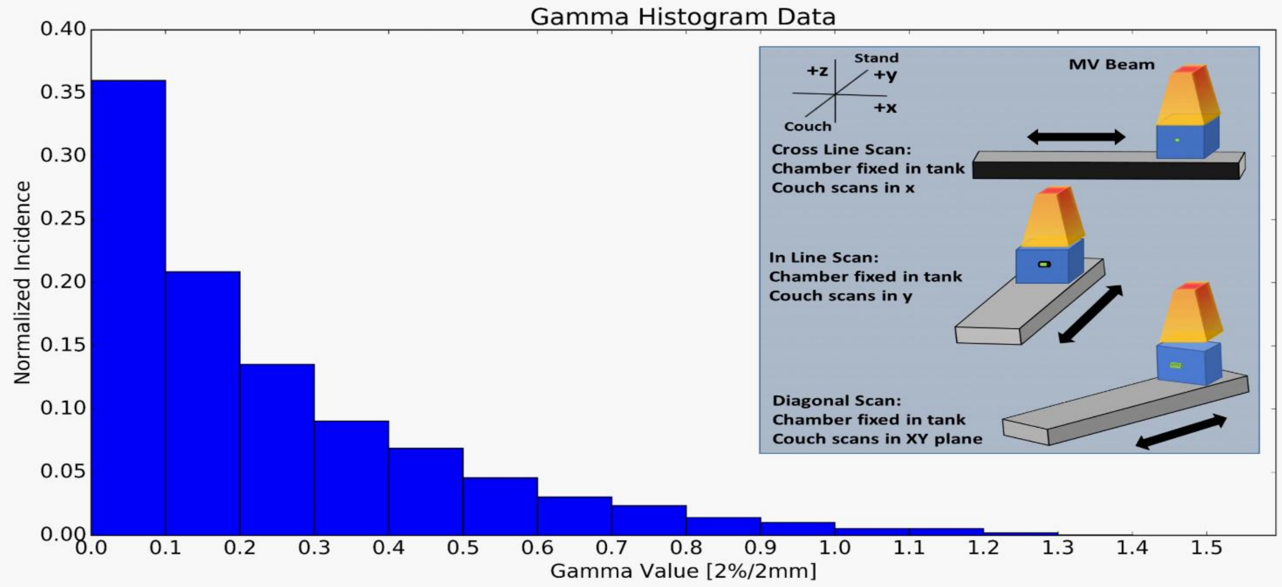


TABLE 2 1D gamma comparison (2%/2 mm) of 1DS lateral profile data to 3DS lateral profile data.

	(Γ: 2%/2 mm)		
Field size (cm^2)	% points Γ < 1	Mean Γ	Max Γ
3 × 3	100	0.102	0.668
4 × 4	100	0.084	0.617
6 × 6	100	0.092	0.655
8 × 8	100	0.107	0.660
10 × 10	100	0.125	0.715
20 × 20	99.9	0.256	1.040
30 × 30	96.6	0.312	1.284
40 × 40[a]	98.0	0.329	1.593
All field sizes	98.7	0.241	1.593

[a]Includes diagonal profiles.

- Profiles generally with 2%/2mm
- All within 3%/3mm
- Within 1%/1mm for field sizes < 20x20

N.C. Knutson *et al.*, "Equivalency of beam scan data collection using a 1D tank and automated couch movements to traditional 3D tank measurements," J. Appl. Clin. Med. Phys. (2018).

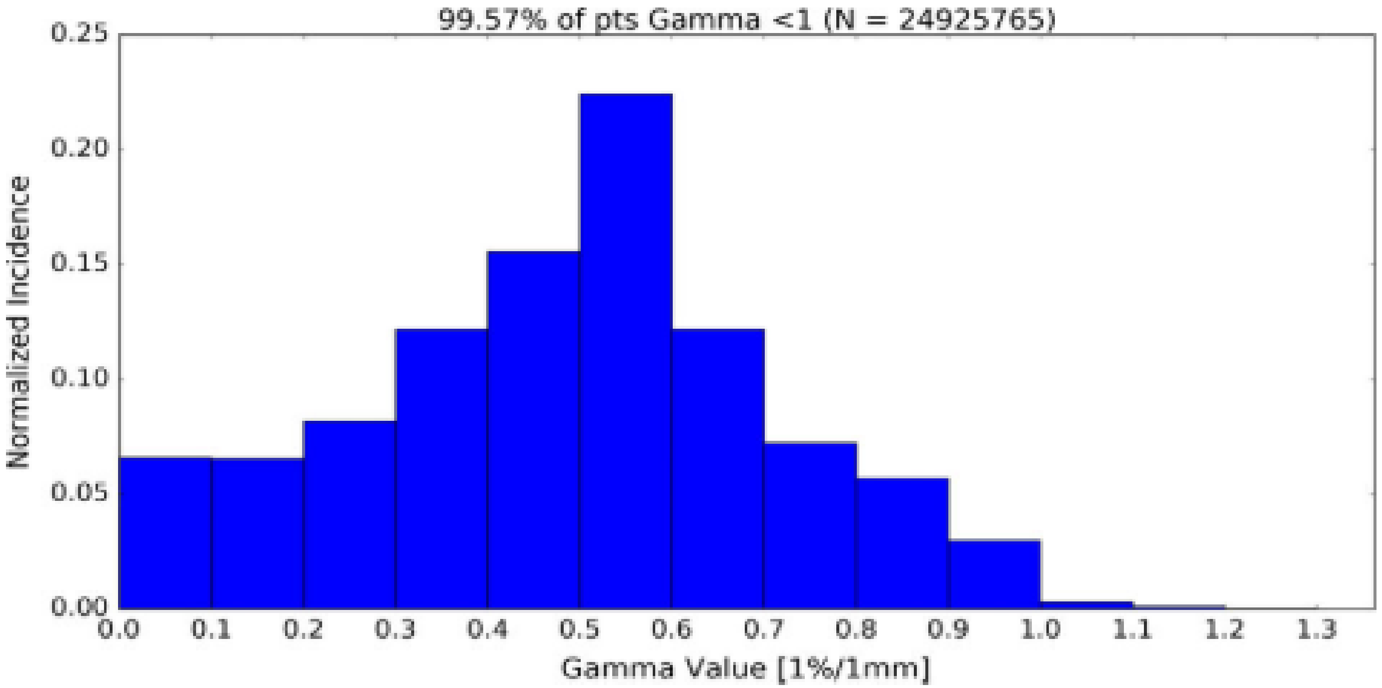
Section B – Results-Beam Models

Table 3 3D gamma comparison (1%/1 mm 5% threshold) of dose distributions calculated from the BM_{1DS} and BM_{3DS} beam models.

	(Γ: 1%/1 mm)			
Field size X × Y (cm^2)	# of data points	% points $\Gamma < 1$	Mean Γ	Max Γ
2 × 2	3.95×10^4	100.00	0.241	0.706
3 × 30	8.25×10^5	99.99	0.333	1.363
4 × 16	5.77×10^5	99.99	0.318	1.145
5 × 5	2.27×10^5	100.00	0.299	0.908
5 × 10	4.47×10^5	100.00	0.330	0.889
7 × 7	4.36×10^5	100.00	0.322	0.917
10 × 5	4.47×10^5	100.00	0.319	0.787
10 × 10	8.77×10^5	99.99	0.354	1.044
15 × 15	1.95×10^6	99.99	0.376	1.123
16 × 4	5.76×10^5	100.00	0.327	0.937
25 × 25	5.36×10^6	99.20	0.522	1.215
30 × 3	8.17×10^5	99.99	0.335	1.109
35 × 35	1.05×10^7	99.41	0.570	1.356
Dynamic chair (12 × 20)[a]	1.20×10^6	99.97	0.401	1.171
Pyramid field (12 × 25)[a]	6.64×10^5	99.66	0.482	1.254
All fields	2.49×10^7	99.57	0.483	1.363

[a]Dynamic MLC fields.

- Resultant calculation comparisons for numerous field sizes
- 1%/1mm gamma normalized to max dose



N.C. Knutson *et al.*, “Equivalency of beam scan data collection using a 1D tank and automated couch movements to traditional 3D tank measurements,” J. Appl. Clin. Med. Phys. (2018).

Section B – Conclusions

- PDDs within 1%/1mm
- Small fields agree with 1%/1mm criterion
- Large fields generally within 2%/2mm with small percentage exceeding gamma value of 1
- Resultant beam models generally within 1%/1mm

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RADIATION ONCOLOGY PHYSICS

WILEY

Equivalency of beam scan data collection using a 1D tank and automated couch movements to traditional 3D tank measurements

Nels C. Knutson[1,2,3] | Matthew C. Schmidt[2,3,4] | Matthew D. Belley[3,5] | Ngoc Nguyen[3,5] | Michael Price[3,5] | Sasa Mutic[1] | Erno Sajo[2] | H. Harold Li[1]

[1]Department of Radiation Oncology, Washington University School of Medicine, St. Louis, MO 63110, USA
[2]Medical Physics Program, University of Massachusetts Lowell, Lowell, MA 01852, USA
[3]Department of Radiation Oncology, Rhode Island Hospital, The Alpert Medical School of Brown University, Providence, RI 02903, USA
[4]Education Department, Varian Medical Systems, Las Vegas, NV 89119, USA
[5]Department of Physics, University of Rhode Island, Kingston, RI 02881, USA

Author to whom correspondence should be addressed. Nels C. Knutson
E-mail: nknutson@wustl.edu; Telephone: 314-273-1497; Fax: 314-747-9557.

Abstract

This work shows the feasibility of collecting linear accelerator beam data using just a 1-D water tank and automated couch movements with the goal to maximize the cost effectiveness in resource-limited clinical settings. Two commissioning datasets were acquired: (a) using a standard of practice 3D water tank scanning system (3DS) and (b) using a novel technique to translate a commercial TG-51 complaint 1D water tank via automated couch movements (1DS). The Extensible Markup Language (XML) was used to dynamically move the linear accelerator couch position (and thus the 1D tank) during radiation delivery for the acquisition of inline, cross-line, and diagonal profiles. Both the 1DS and 3DS datasets were used to generate beam models (BM_{1DS} and BM_{3DS}) in a commercial treatment planning system (TPS). 98.7% of 1DS measured points had a gamma value (2%/2 mm) < 1 when compared with the 3DS. Static jaw defined field and dynamic MLC field dose distribution comparisons for the TPS beam models BM_{1DS} and BM_{3DS} had 3D gamma values (2%/2 mm) < 1 for all 24,900,000 data points tested and >99.5% pass rate with gamma value (1%/1 mm) < 1. In conclusion, automated couch motions and a 1D scanning tank were used to collect commissioning beam data with accuracy comparable to traditionally acquired data using a 3D scanning system. TPS beam models generated directly from 1DS measured data were clinically equivalent to a model derived from 3DS data.

PACS
87.56.-v

N.C. Knutson *et al.*, JACMP. (2018).

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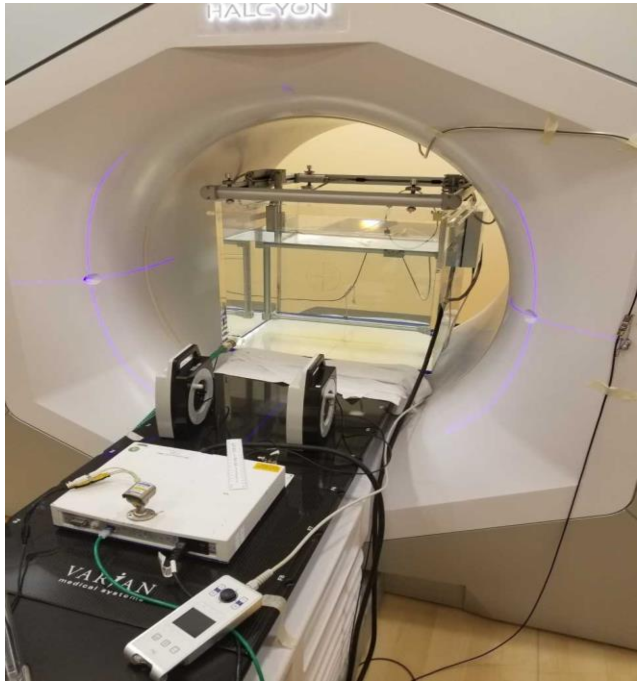
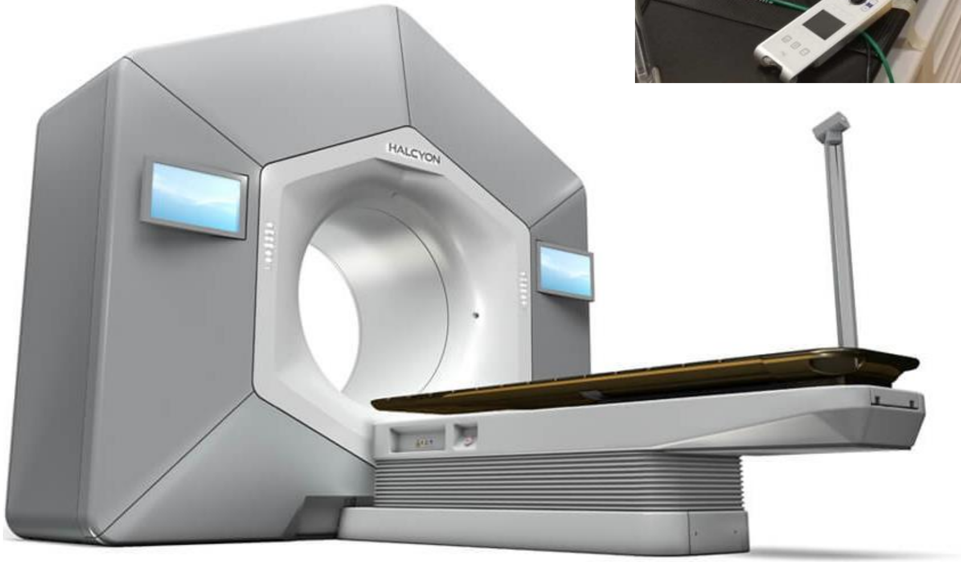
Section C – Lesions learned and work to do

- Sections A & B: showed a very strong proof of principal
- But still work to be done to bring all this together and optimize
  - Why were a few points > 2%/2mm?
  - Characterize the uncertainties associated with the measurement and minimize them where possible
  - Can we improve the workflow for increased efficiency and be more user friendly
  - Can we simulate the 1DS & 3DS using analytical calculation to see the expected difference between the two due to the different geometries
  - Could we calculate a correction for phantom size to allow for a more direct comparison between the two with increased accuracy
  - Can we do this on a non TrueBeam linac with no developer mode.

Section C – Halcyon Research Linac

- Varian Halcyon pre-clinical research linac:
  - Pre-clinical system installed at Wash U
  - No time for the details but the answer to the questions on the previous slide is yes (ePoster Discussion yesterday has these)



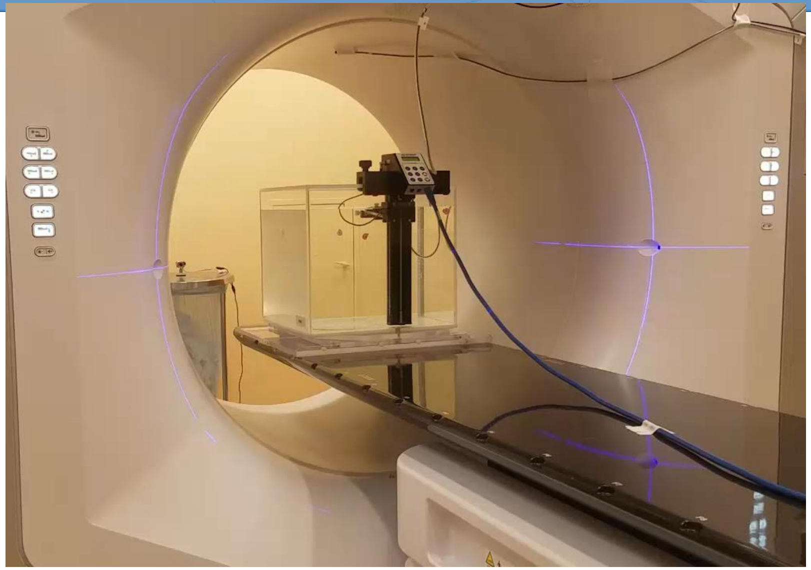


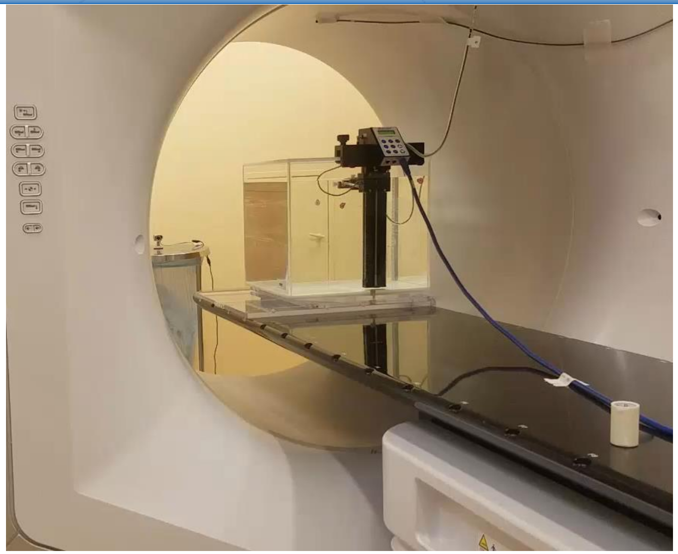
Section C – 1DS Best Practices

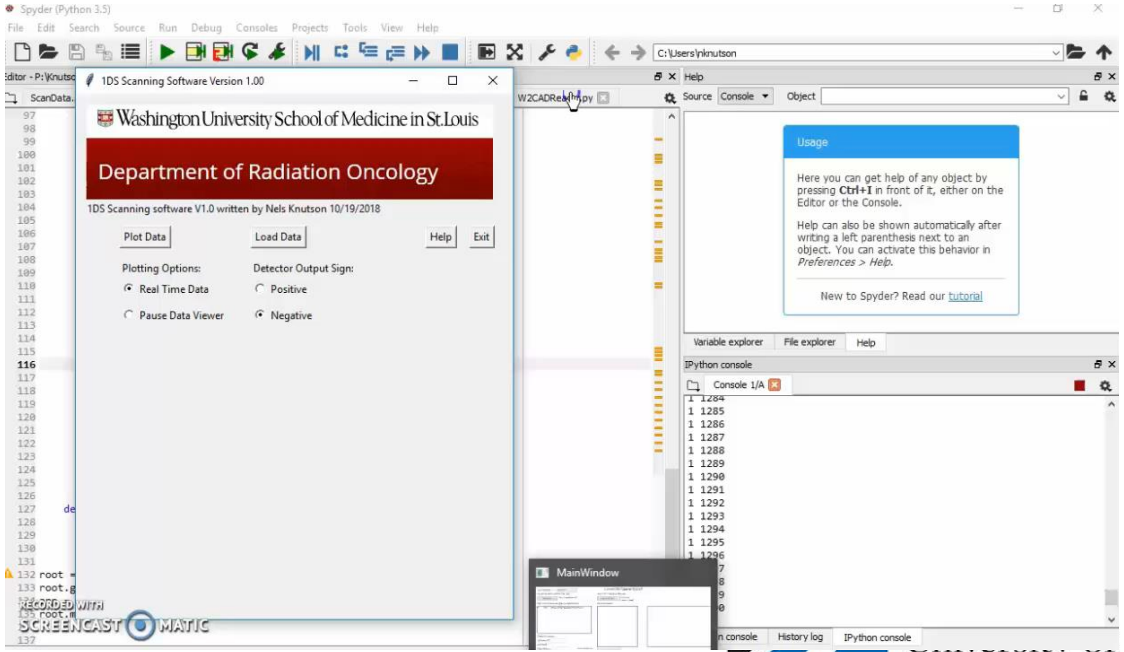
Accelerator beam data commissioning equipment and procedures: Report of the TG-106 of the Therapy Physics Committee of the AAPM

- Minimize cable in the beam and keep constant during scan
  - Check with Ppol at deepest depth largest Field Size
- Scan speed X electrometer rate ideally ~ 0.5 mm
- Electrometer noise can be high if collection rate < 200 ms
- Scan speed 5 mm/s is too fast due to water motion
- Accurate setup with MV imager is very helpful (Halcyon)
- Differences for large fields at deep depths can be predicted and corrected

Improved1DS Scanning Workflow- Halcyon Example







System

- Halcyon
- Load XML

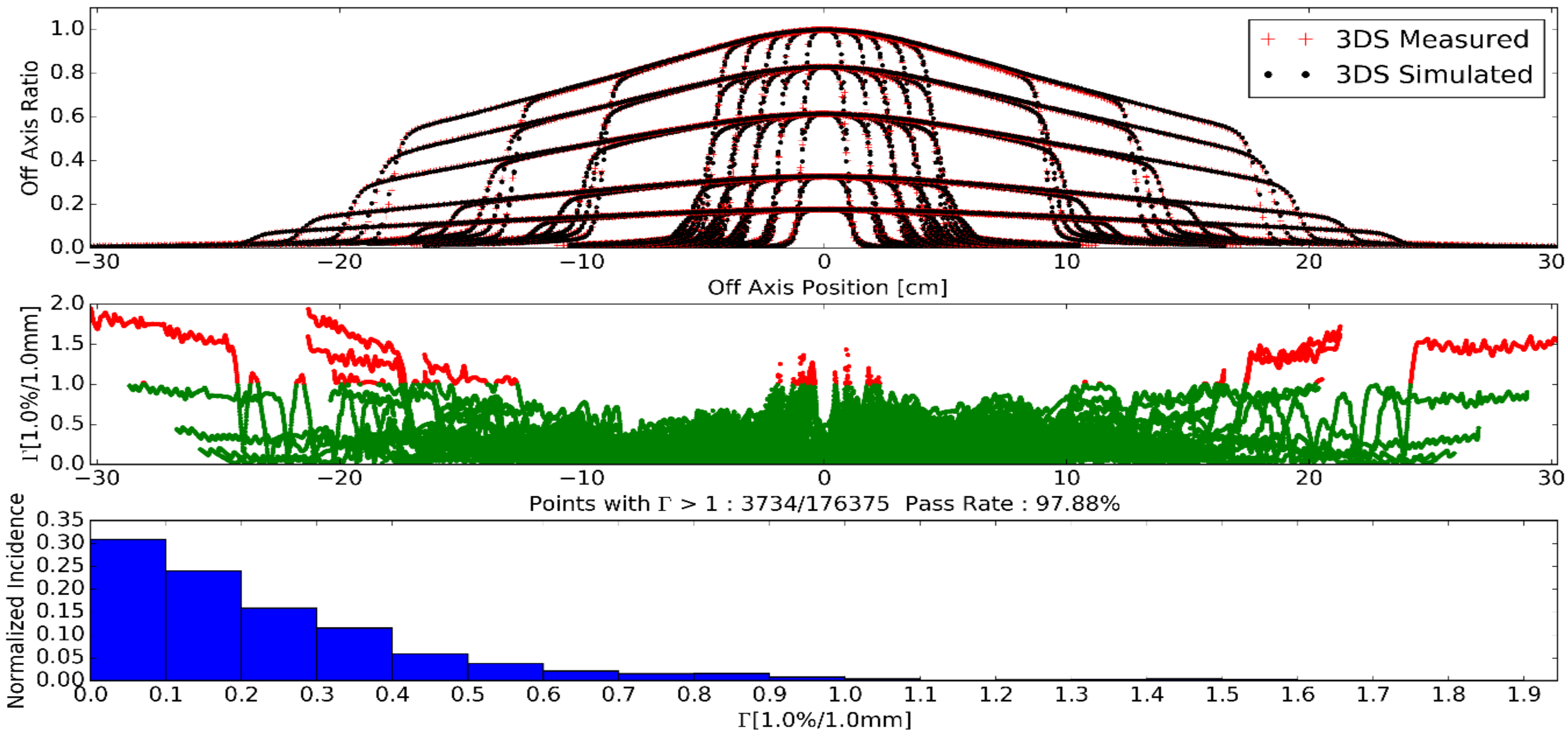
Events

- Beam On: XML runs with programmed pauses to change depth
- Beam Off

Water Tank/PCE Software Python EXE	Initiate Electrometer Measurement, Data Logging, and Python Data Viewer	Set initial Tank Depth	Change Depth At Each Pause In Beam Programmed in XML	Stop Measurement and Data Logging

Time →

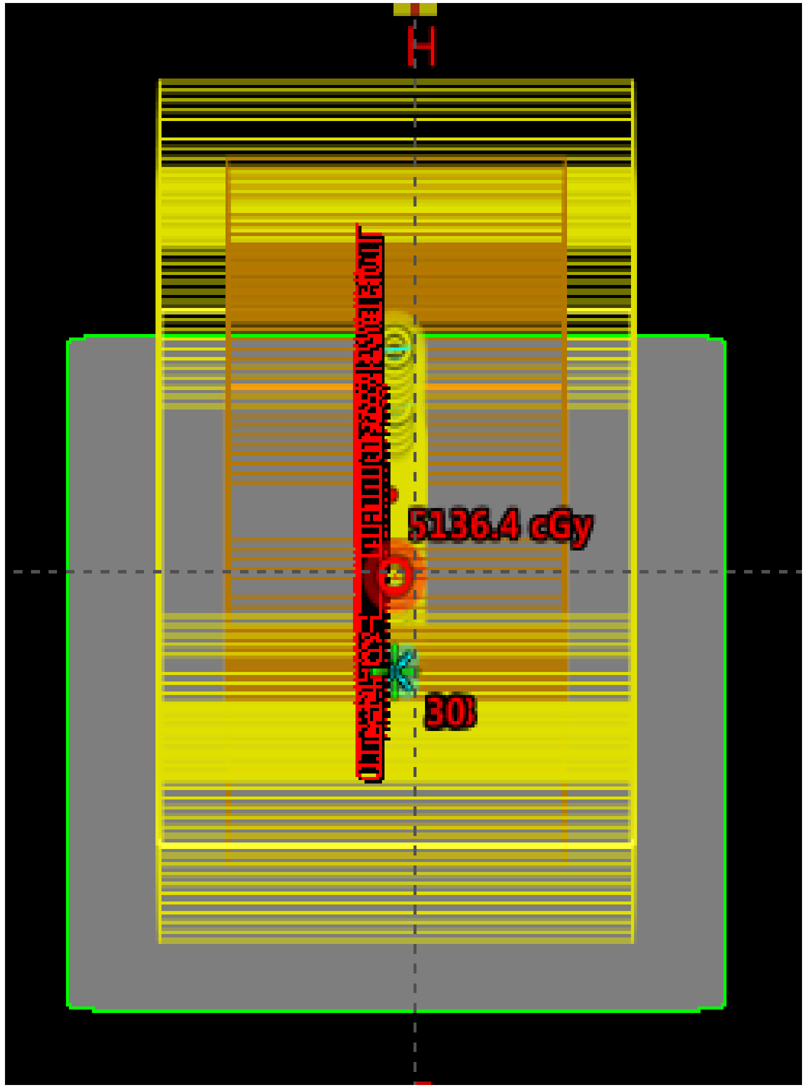
Section C – Results 3DS & TPS

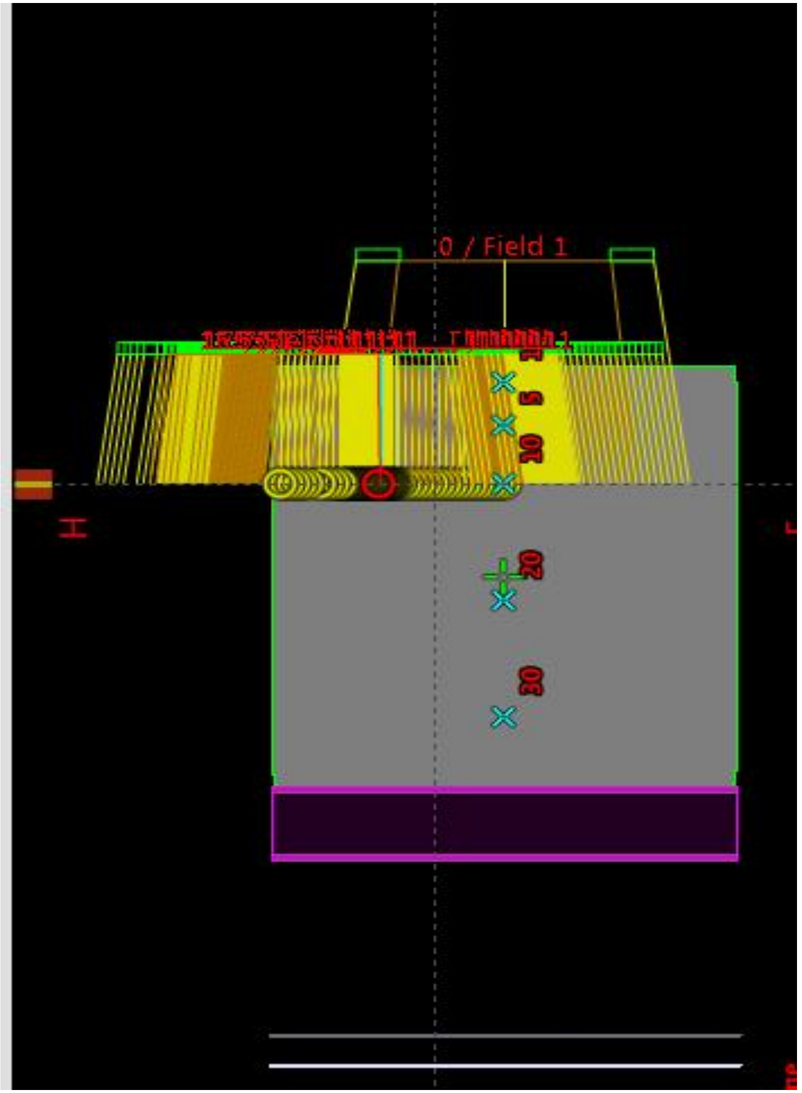


- 3DS_Measured vs 3DS_Simulated all within 2%/2mm

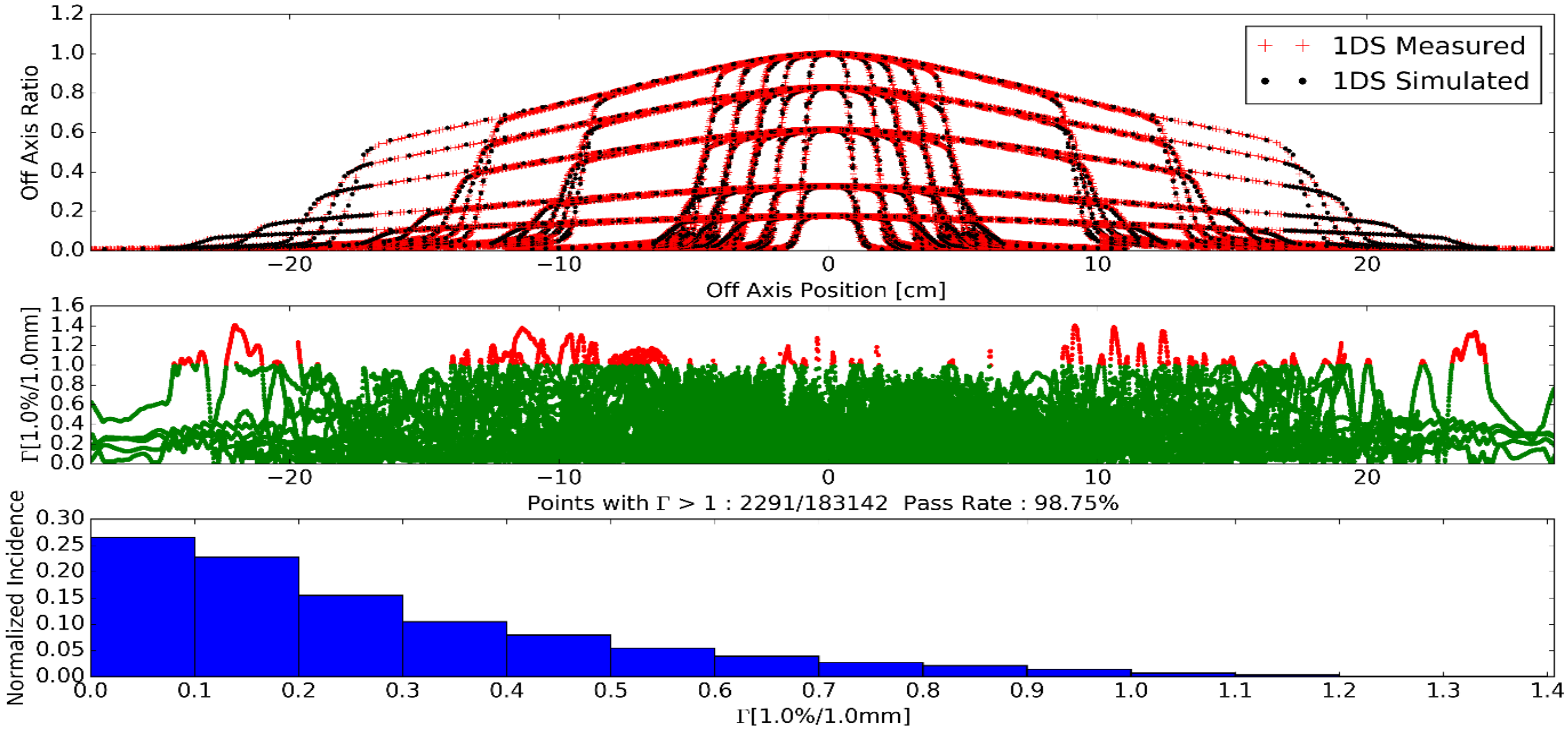
Section C – 1DS Simulation Methods

- 1D Tank (1DS_Simulated)
  - Profile created by calculating multiple plans to simulate the tank motion and recording dose to central voxels of phantom
  - 1mm spacing in penumbra
  - 5mm spacing in-field and in umbra



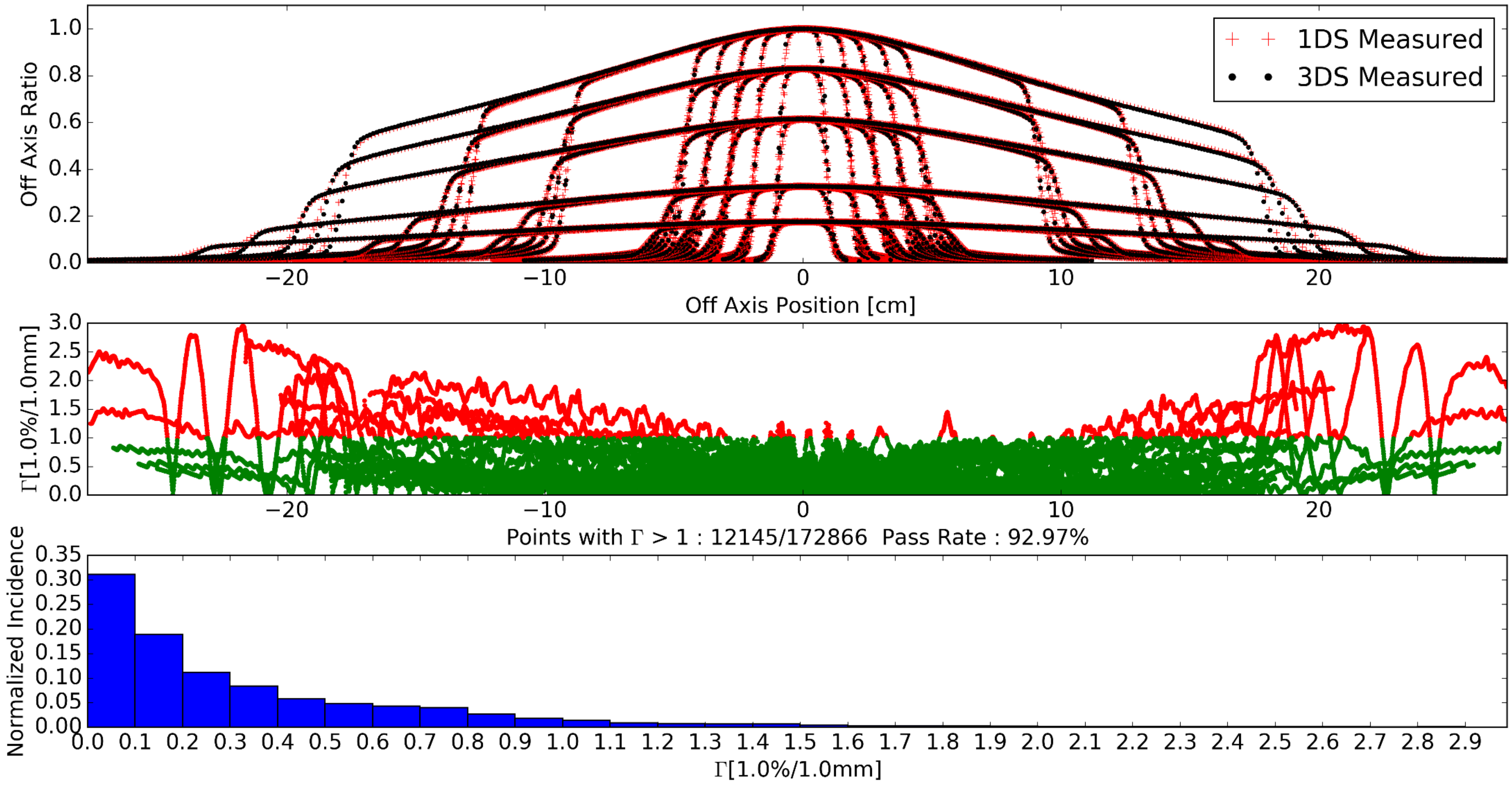


Section C – Results 1DS & TPS



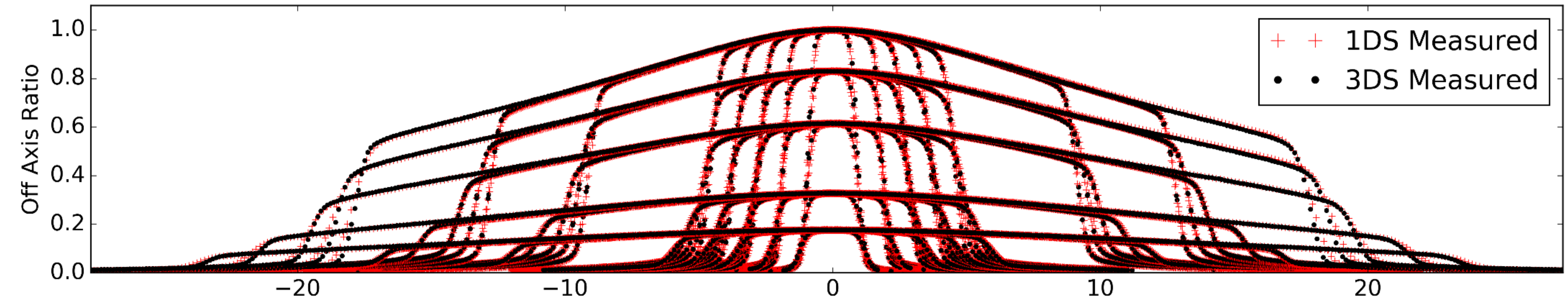
- 1DS_Measured vs 1DS_Simulated all within 1.5%/1.5mm

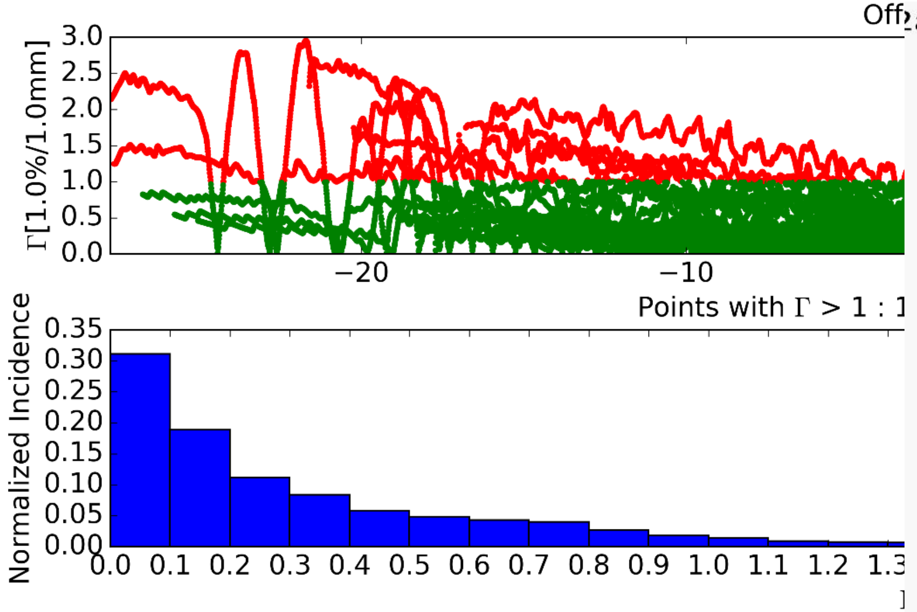
Section C – Results Cross-modality Measurements

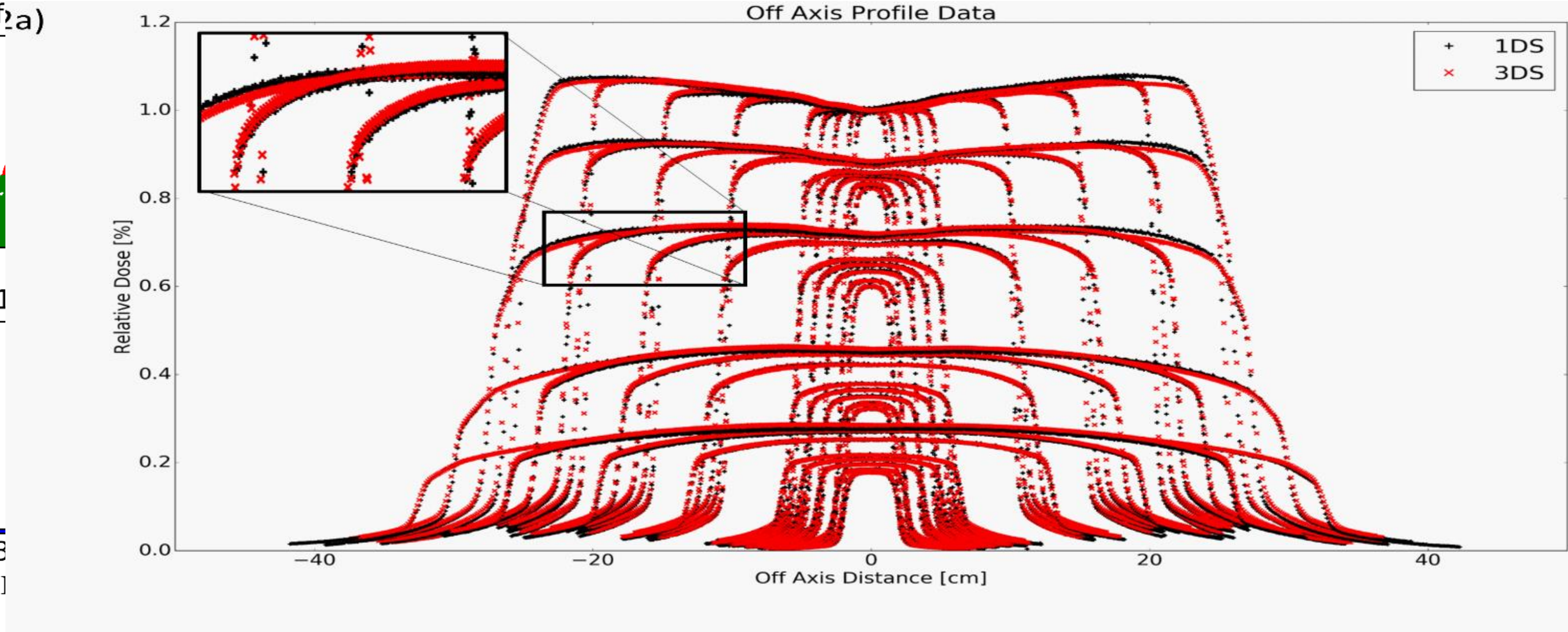


- 1DS_Measured vs 3DS_Measured all within 3%/3mm

Section C – Results Cross-modality Measurements

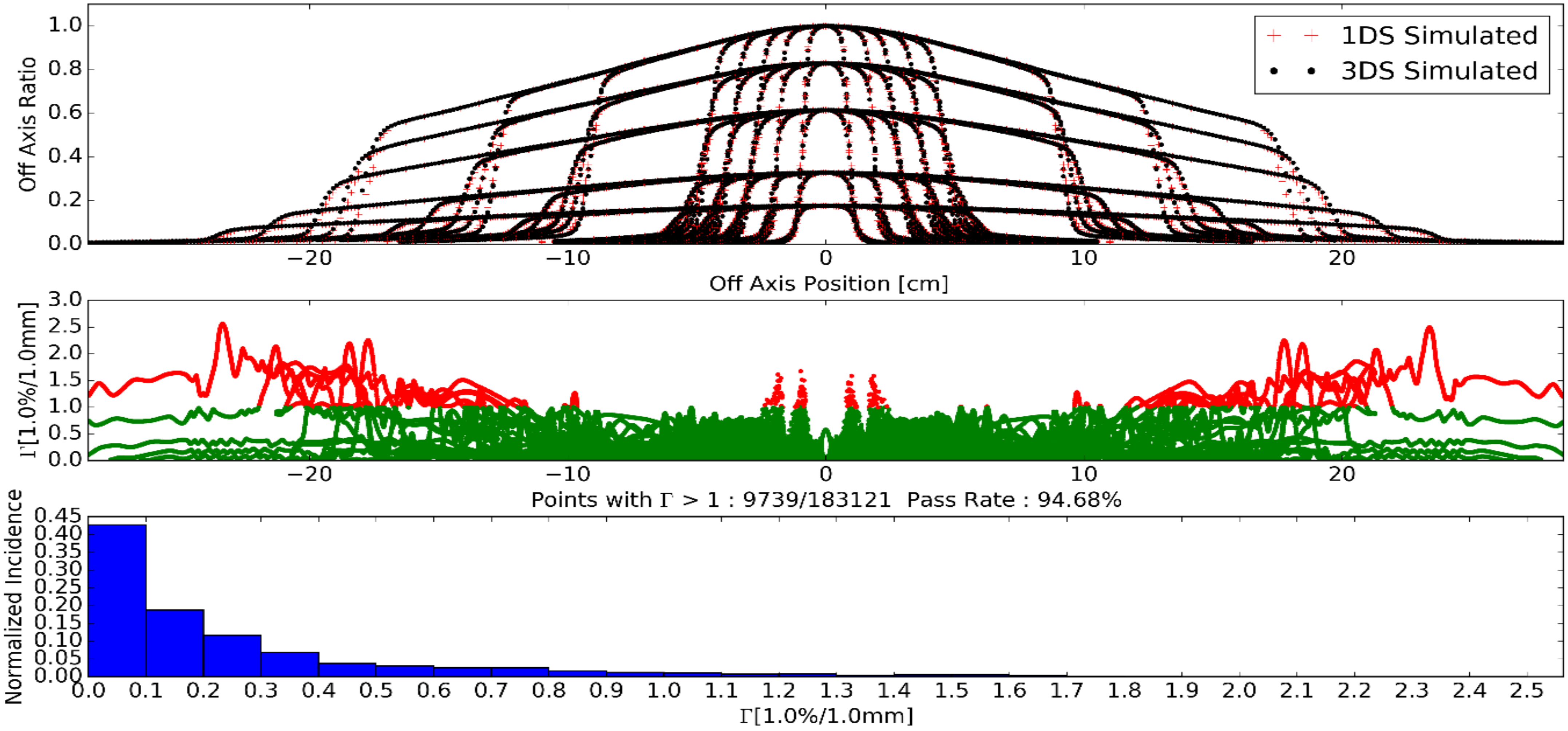






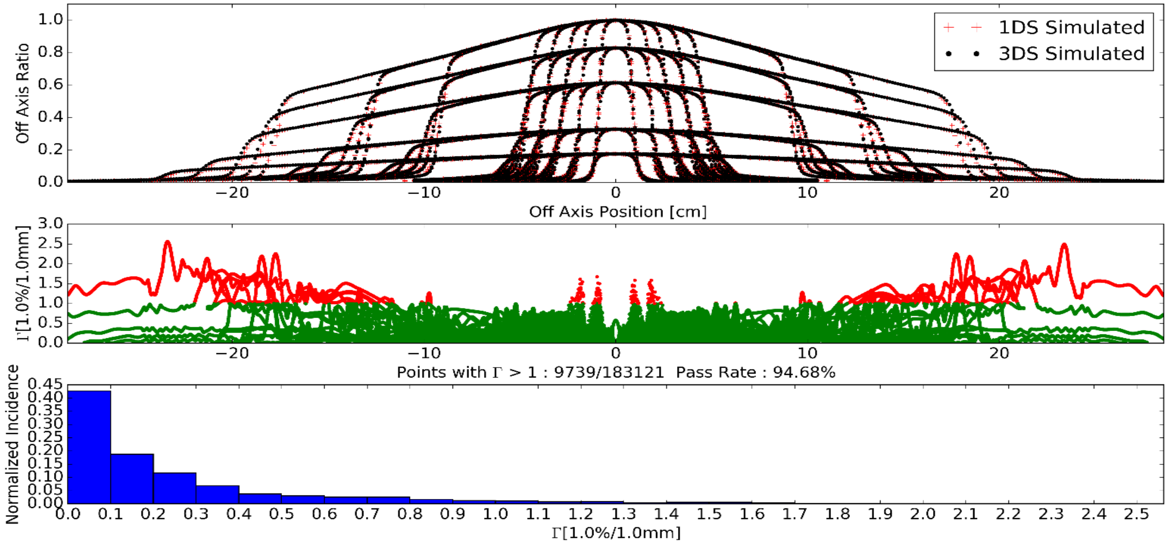
- Pretty similar to our previous result.
- Is this expected? Lets calculate and find out

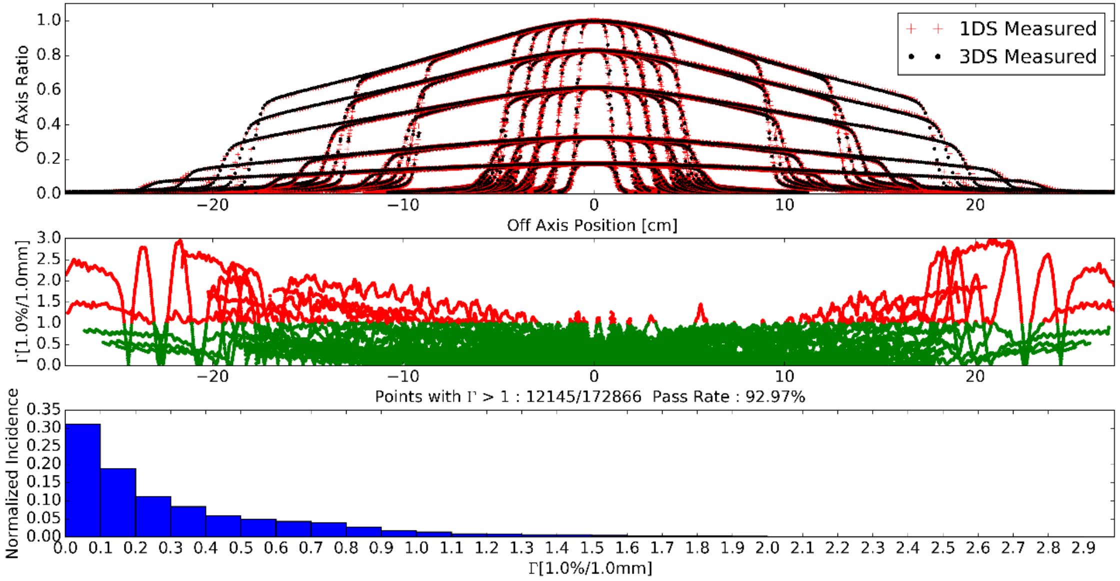
Section C – Results Cross-modality Simulation



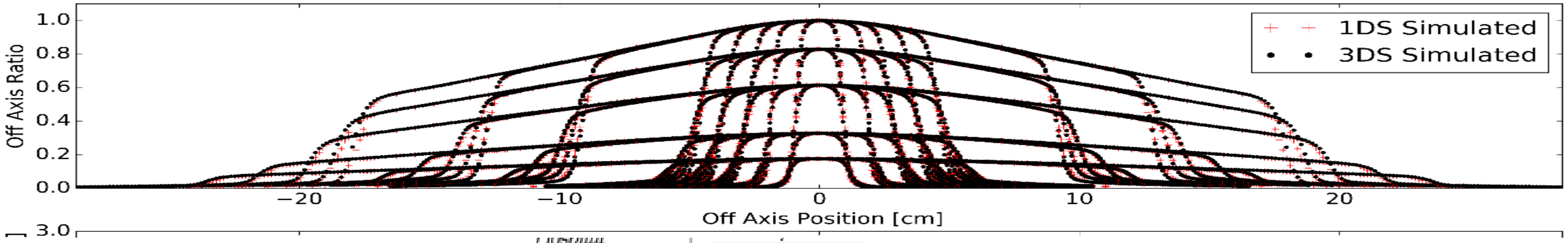
- 1DS_Simulated vs 3DS_Simulated all within 3%/3mm

Section C – Results Cross-modality Simulation



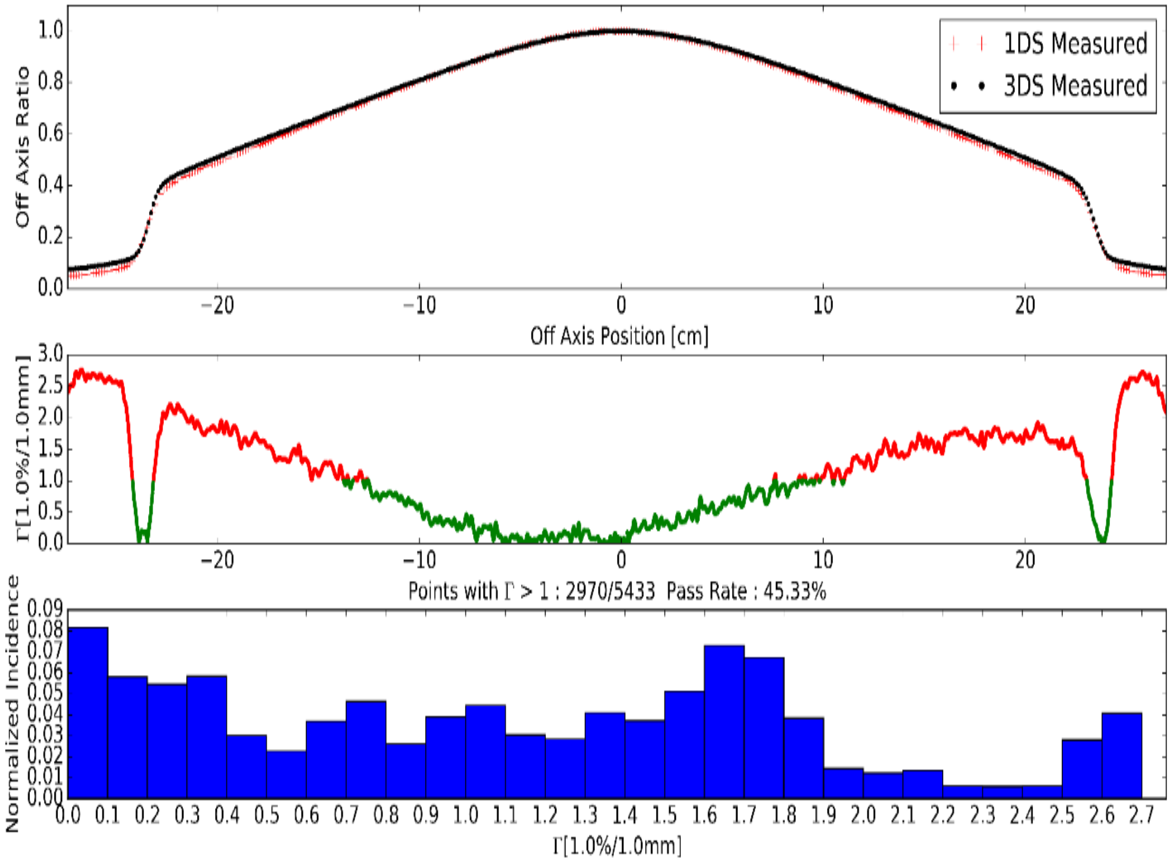


- The measured differences between 1DS and 3DS look very similar to the calculated differences!
- Can we use this ratio as a phantom size correction?

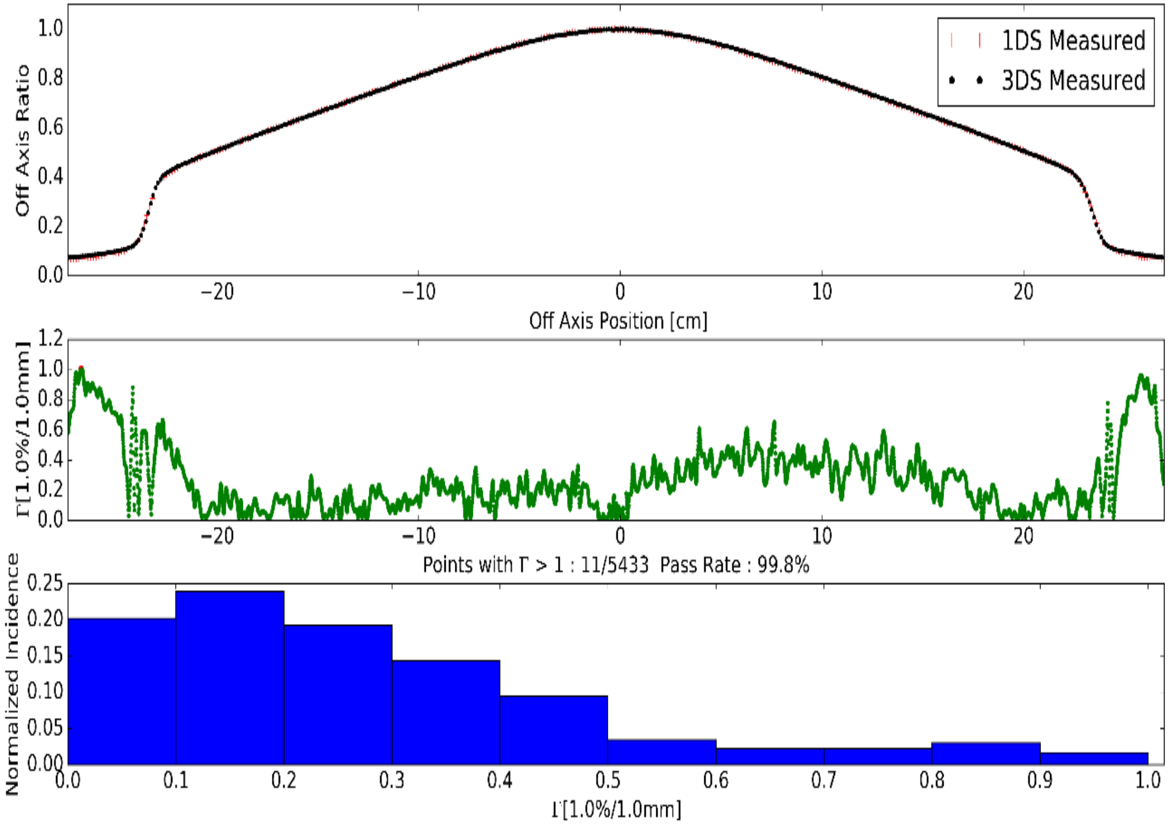


Section C – 1DS to 3DS

Uncorrected

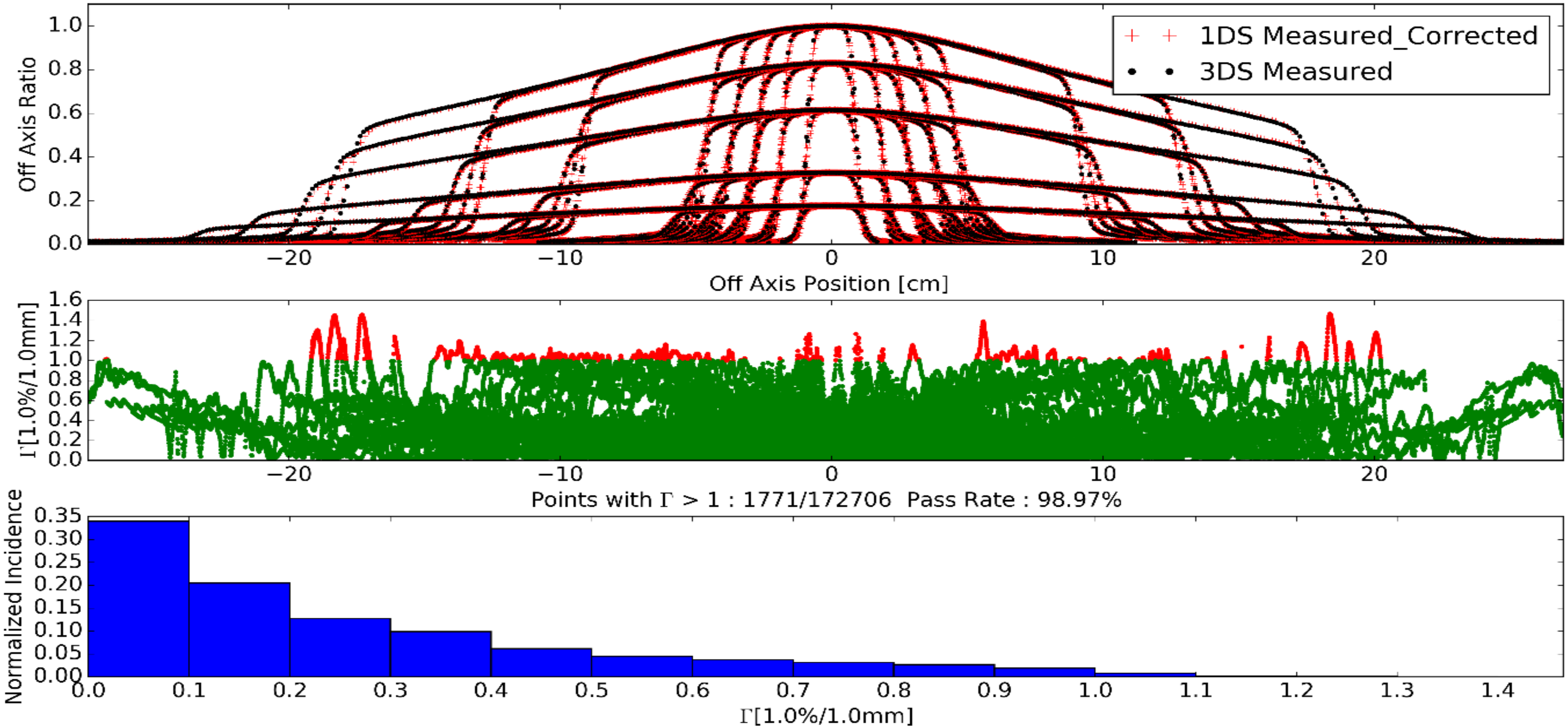


Corrected In-field & Out-of-field



- In-field $CF_{fit}(r) = \frac{D_{1DS}}{D_{3DS}} = 1 + Ar^2$ Out-of-field $CF_{fit}(r) = \frac{D_{1DS}}{D_{3DS}} = Ar + B$

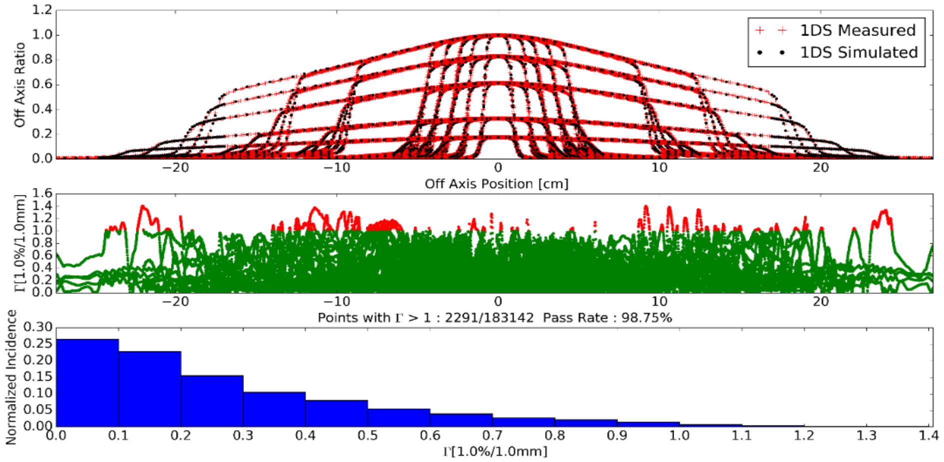
Section C – Results Post Correction

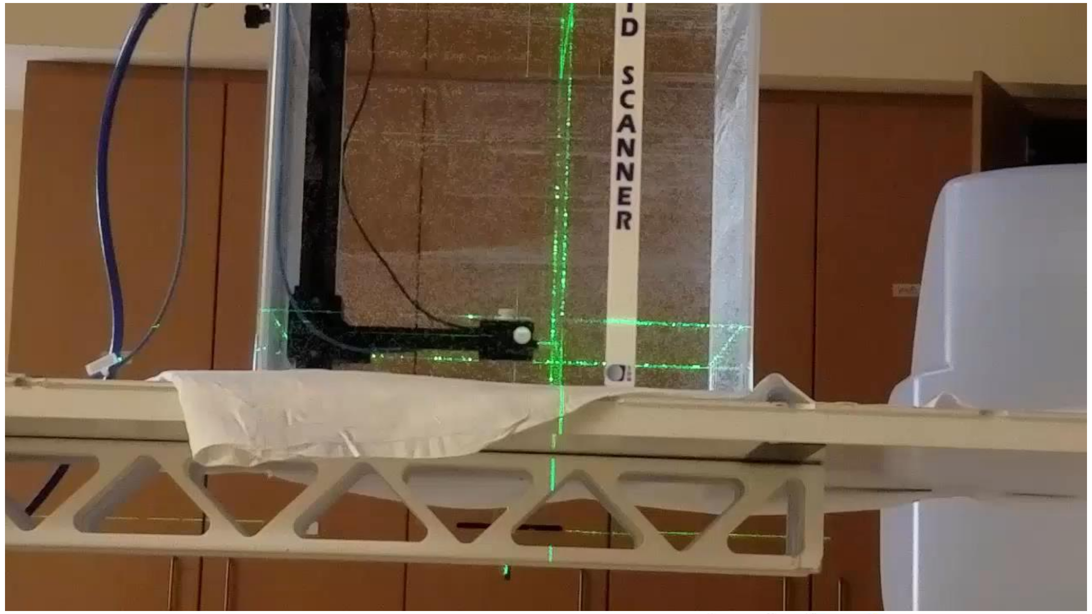


- 1DS_Measured_Corrected vs 3DS_Measured all within 1.5%/1.5mm

Conclusions

- 1DS Method shows promise
- Very portable
- Potentially less than 10% of 3D tank cost
- A great validation tool for annual QA or incidental QA.
- With TPS changes could be used for commissioning
- Potential for automation!
  - Hope you saw Dr. Y Hao's talk Monday



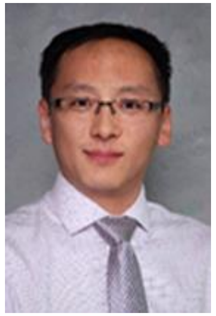


Acknowledgements

- Thanks to all Co Authors, Co Workers, Teachers, Mentors, & Friends





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Thank You All For Your Time and Attention- Questions?

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