Experimental evaluation of MCDTK, the Monte Carlo DICOM Tool-Kit

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Monte Carlo

- MC is considered the gold standard for radiation therapy dose calculations
- Simulates particle transport in linear accelerator and patient geometry using statistical sampling
- It offers an independent mechanism for checking TPS calculated dose distributions
- Excellent choice for checking dose at interfaces

Monte Carlo

- Accurate dose requires an accurate description of the accelerator and the patient

EGSnrc

- BEAMnrc:
  - modelling the linear accelerator geometry
  - obtain a description of the field (shape and fluence)
- DOSXYZnrc:
  - modelling the delivery of the field to the patient
  - obtain a description of dose deposition in patient

Treatment Specific

- Initial electron beam parameters are treatment independent – determined during model commissioning (selected for agreement with reference measurements)
- Collimator positions and rotations, machine and couch rotations, patient geometry and location all vary across treatments
- Automated simulation of treatments needs these variables set

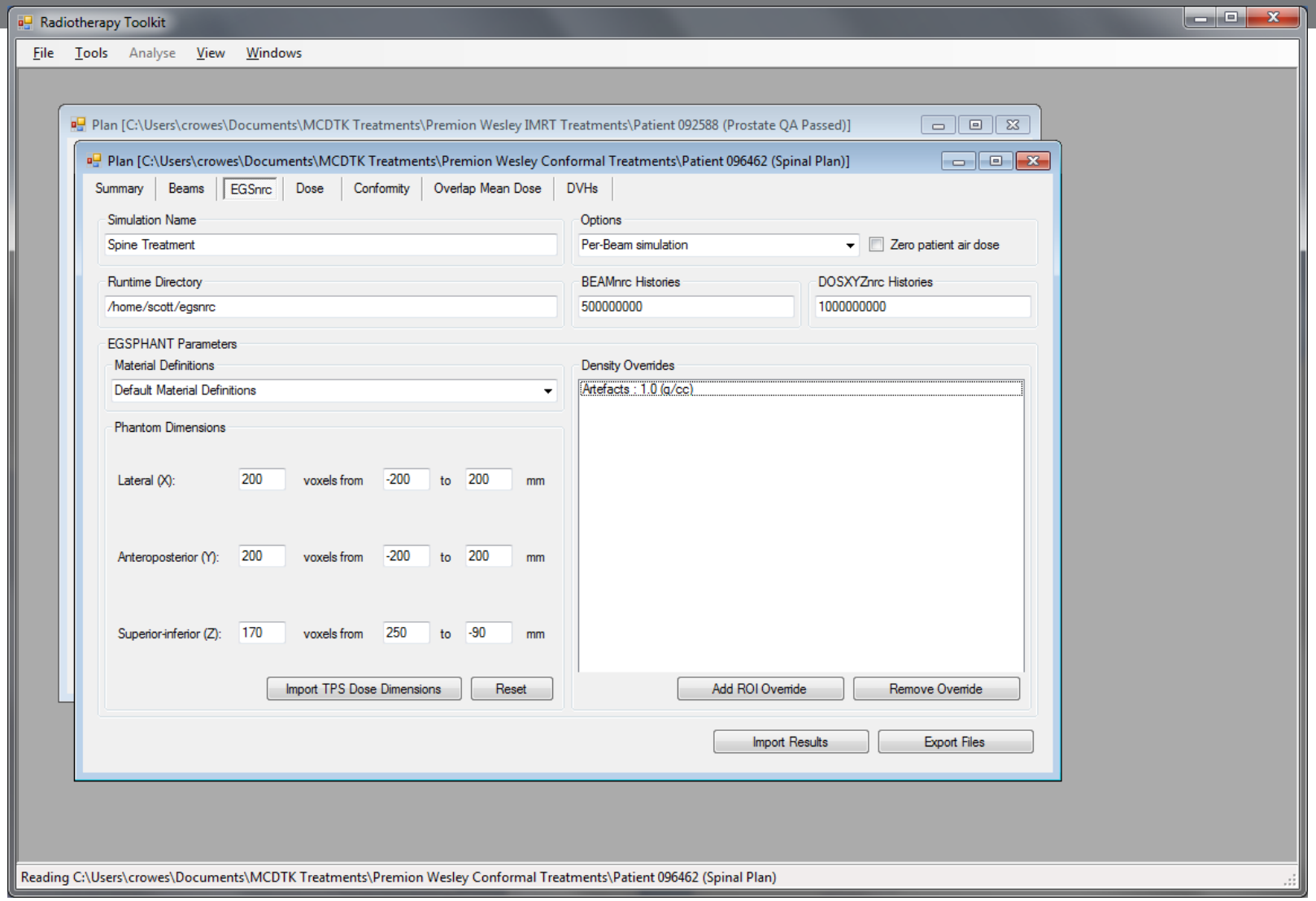
DICOM Framework

- Variables of planned radiotherapy treatments can be exported using DICOM framework
- Beam parameters (collimator positions and rotations, couch and gantry rotations, attachments, MU distribution) stored in RTPLAN file
- Patient structures stored in RTSTRUCT files
- Patient dose stored in RTDOSE files
- Patient geometry stored in CT files

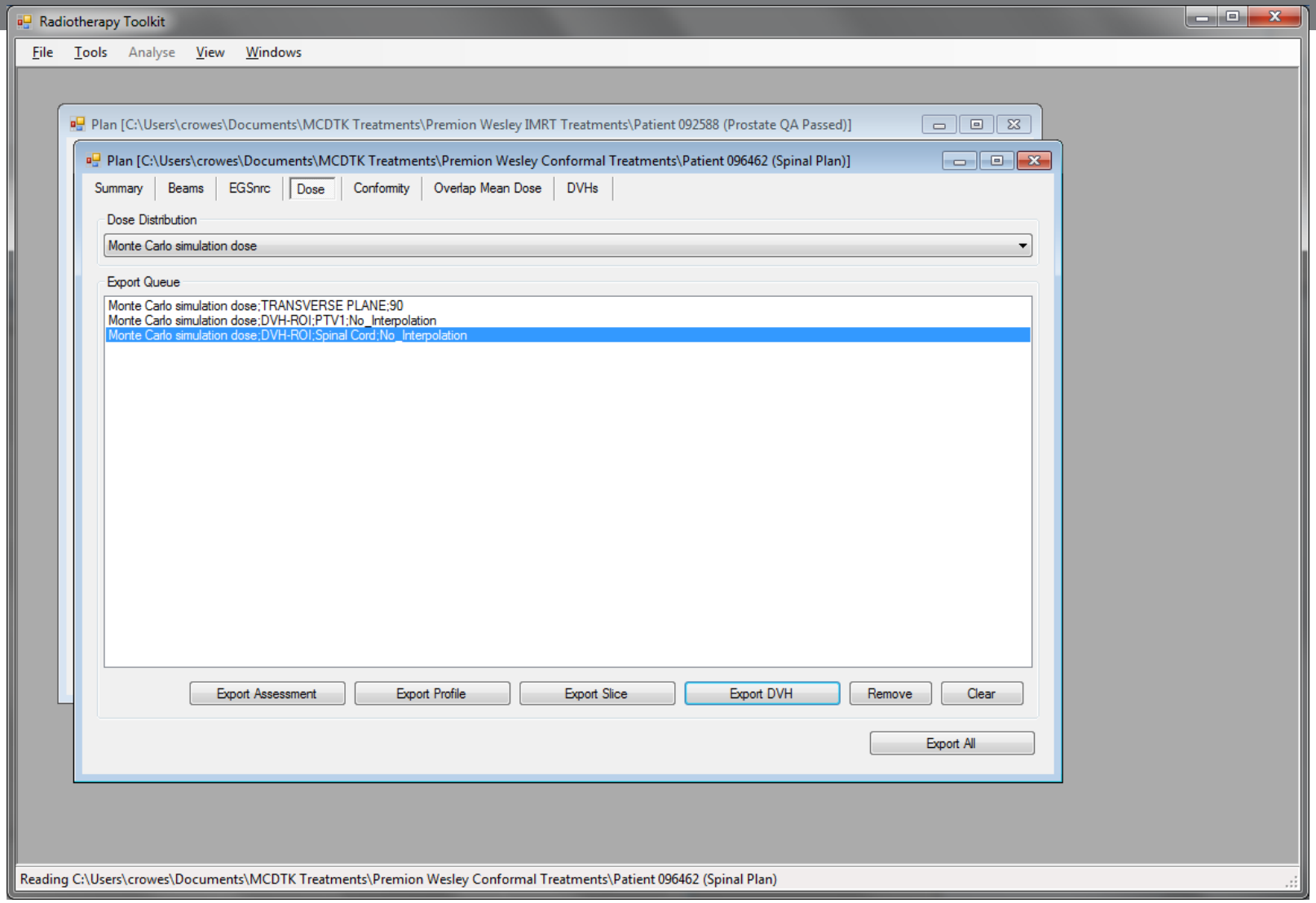
MCDTK Software

- Developed in C# (earlier version developed in Java)
- Produces MC input files for exported treatments
- Provides analysis tools for comparing MC and TPS calculated dose distributions
  - profile, plane and isodose exporting (csv for excel, GLE/PDF, MapCheck)
  - 3D gamma evaluations
  - dose metrics (DVHs, V(d) and D(v) coverages, dose homogeneity and conformity indices; compared against Emami/QUANTEC/etc. guidelines)

MCDTK Software



MCDTK Software



How it works

- Commissioned models are made into templates, with patient-specific variables replaced with break characters (i.e. !!X for X jaw position)
- Institute, planning system, particle type, nominal energy, linear accelerator name in plan file used to determine what template to use for simulation
- BEAMnrc and DOSXYZnrc input files generated using values extracted from DICOM input files (calculation of physical collimator positions, theta/phi/phi_col angles, etc)

How it works

- Phantom created using Hounsfield to mass density ramp (using scanner database and scanner name and energy as listed in CT file attributes) – similar to CTCREATE, but with materials and ramp separated
- Script to submit jobs to local queue system produced (QUT has cluster with 600+ cores)
- Files detailing how to add produced dose files created if necessary

Utilizing

- Dynamically generated bremsstrahlung splitting radii, calculated from jaw positions
- Analytical model of backscatter correction to machine output by H.H. Liu Et al
  - based on simulation results in treatment heads
  - applied to treatment MU distribution before simulation so that output variation in dynamic treatment is modelled correctly

Utilizing

- BEAMnrc-as-library sources (i.e. source 9 for conformal and IMRT fields, source 10 for static arc treatments, source 21 for dynamic arc treatments,) allowing “single simulation” dose distributions
- Leaf and jaw sequence files, for dynamic plans, where component modules support them
- C++ applications to add and weight segment results where leaf sequence files couldn’t be used (our BrainLab mMLC model atm ☹)

Supports

- Attachments
  - electron applicators (with cerrobend block cutouts described in treatment plan file)
  - stereotactic cones
  - jaw positions automatically set for flat profile (according to specs, i.e. 25x25 for 20x20 applicator)
- Dynamic wedges
  - STTs (corrected for backscatter) are used to calculate jaw position according to cimulative treatment MU

Supports

- MC phantom can be defined with arbitrary dimensions and resolutions
- CT mass density ramp independent of simulation materials (can specify database containing specific solid water ingredients, etc)
- CT overrides
  - replacing voxels in any defined rectangular volume or structure set (from TPS) with supplied mass density
  - used for couch correction or artefact overrides

Usage

- Commissioned templates for accelerators at 8 centres (across Melbourne, Sydney & Brisbane, Australia)
- Models of Elekta Precise/Synergy and Axesse and Varian 21iX and Novalis Tx (cones, BrainLab m3)
- Intending to make available at clinics (for research only) soon

Evaluating MCDTK

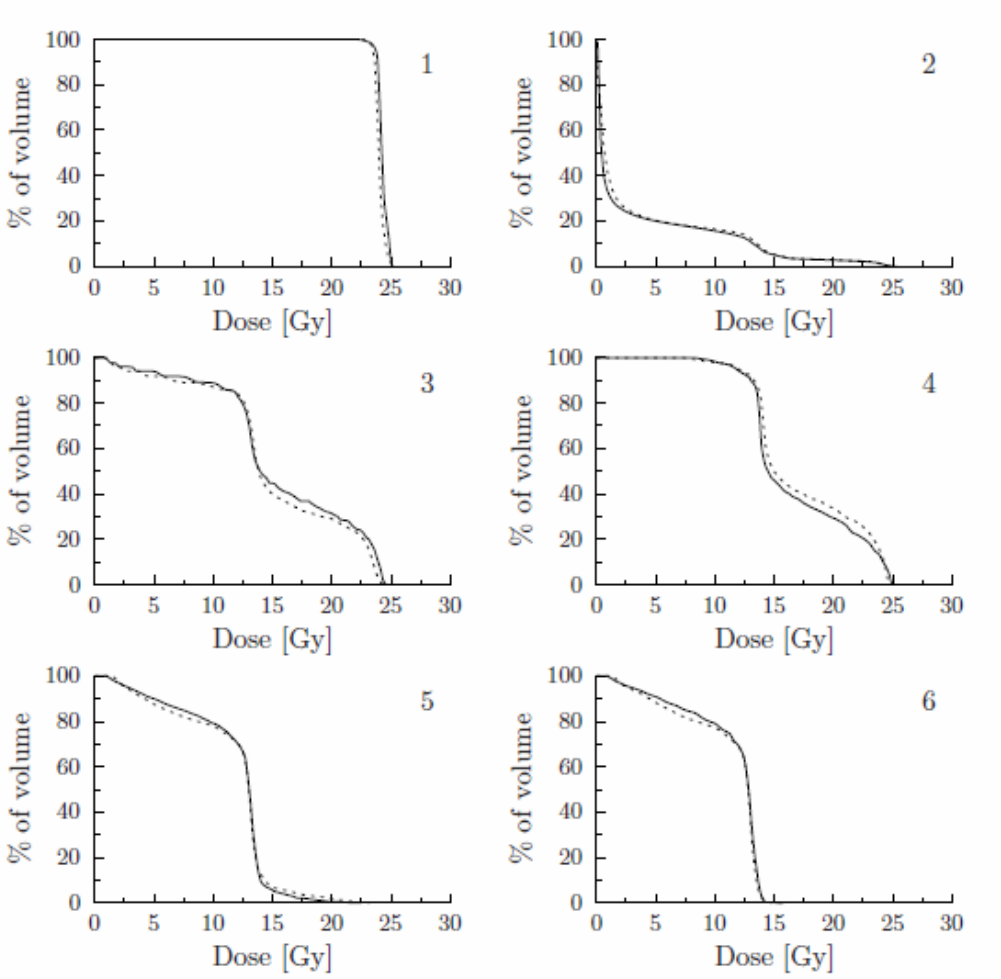
- Proceedings discussed comparison with TLD measurements in phantom done by Trans-Tasman Radiation Oncology Group (TROG)
- 4 field conformal prostate treatment done with Elekta Precise accelerator operating at 10 MV
- Synthetic replica of male pelvis
- Agreed with measurements at all 10 locations within confidence limits
- Predicted measured dose more accurately than planning system PB algorithm in 9 locations

Evaluating MCDTK

Table 1: Point dose values obtained from TLD measurements, pencil-beam calculations made by the treatment planning system (PB) and Monte Carlo calculations made using MCDTK (MC). All doses are in Gy.

Location	TLD dose	PB dose	MC dose
Prostate centre	1.93±0.01	2.02	1.93±0.07
Left femoral head	1.10±0.01	1.12	1.10±0.04
Right femoral head	1.06±0.01	1.12	1.09±0.03
Left seminal vesicle	1.97±0.02	2.09	1.98±0.04
Right seminal vesicle	1.99±0.02	2.09	1.97±0.04
Base of seminal vesicles	1.99±0.02	2.09	1.97±0.02
Anterior rectal wall	1.95±0.02	2.06	1.97±0.05
Prostate apex	1.91±0.02	2.01	1.93±0.06
Anorectal sphincter	1.19±0.02	1.21	1.21±0.03
Out-of-field	0.08±0.01	0.06	0.07±0.05

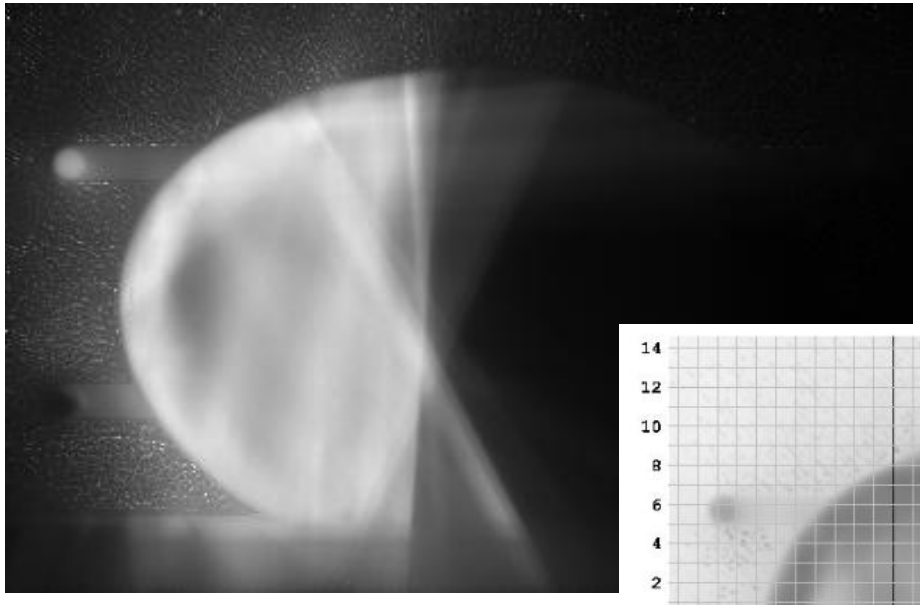
Evaluating MCDTK



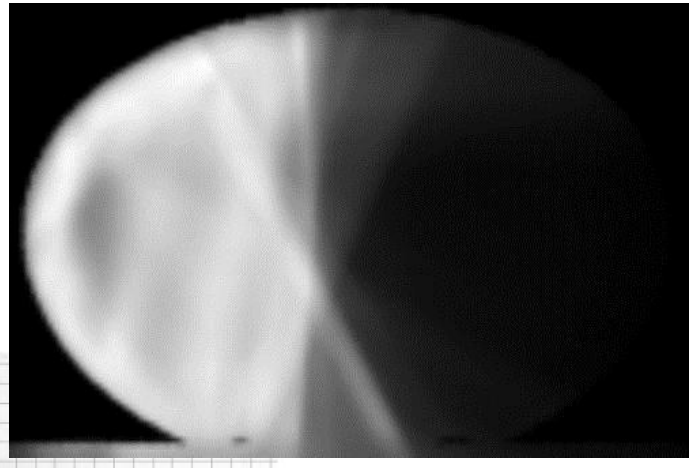
- Small differences in DVHs in
  1. PTV
  2. entire phantom
  3. bladder
  4. rectum
  5. left femoral head
  6. right femoral head

Other evaluations: Film

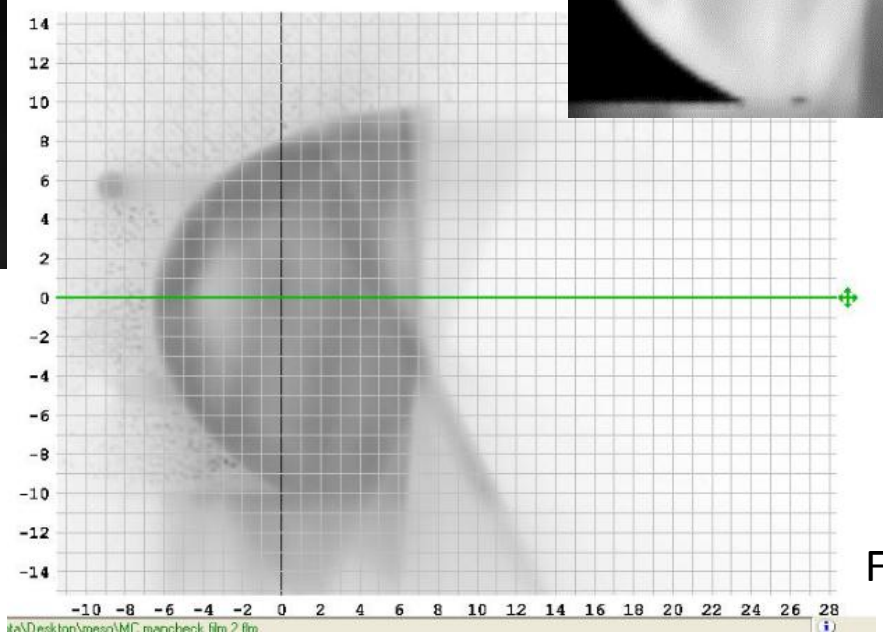
- QA for mesothelioma treatment



MC

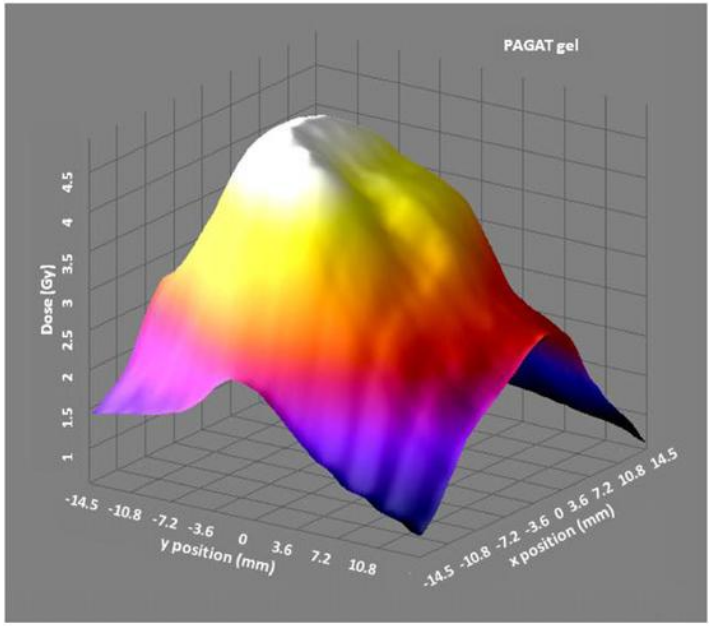


TPS



Film

Other evaluations: Gel



PAGAT Gel

MC