

# Optimization of the angular resolution of the VMAT dose calculation for the Delta<sup>4DVH</sup> Anatomy software

## H. Agostini, J.M. Nigoul, P. Farigoule

Department of Radiotherapy, La Timone University Hospital AP-HM, Marseille, France

## Introduction

The Delta<sup>4DVH</sup> Anatomy software option (Scandidos, Sweden) makes it possible from the measurements carried out on the Delta<sup>4</sup> phantom to calculate the doses delivered (according to two algorithms: PBc Anatomy or TMM Anatomy) in the patient geometry taking into account its heterogeneities. For Volumetric Modulated Arc Therapy (VMAT), it is possible to modify the angular resolution of the control points for the calculation in the Delta40VH Anatomy software thus making it possible to accelerate the computation by increasing the value of this angle, to the detriment of the precision. The aim of this work is to find a compromise between the rapidity of computation of the doses delivered in the patient anatomy and the precision of the results.

#### Materials et Methods

### Materials :

- Delta<sup>4</sup> phantom
  ScandiDos Delta
  Anatomy software .....
- Beam Modulator Synergy (Elekta AB, Sweden) Leaves of 4mm
- Work station with Windows XP 64-bit, Intel Xeon CPU E5640, 2.67 GHz, 17.9 GB RAM

#### Methods

- 5 prostate cases, 5 brain cases, 5 head and neck (H&N) cases
- 💠 Calculation of the dose delivered in the patient's anatomy (PBc and TMM Anatomy algorithms) with the reference angular resolution of 2 °, defined by the Treatment Planning System (TPS) Pinnacle V9.2 (Philips Medical System Inc, USA)
- Calculation of the dose delivered in the patient's anatomy with different angles (4°, 5°, 6°, 8°, 10° and 12°)
- Comparison of the results relative to the angular reference resolution (2°) using the dose-volume histograms (DVHs)
- 💠 Percentage dose differences between DVHs were calculated for target volumes (D95%, Dmean, D2%) and organs at risk (Dmean, D2%).
- Measurement and comparison of computation times

#### Results

ΟΡΤΙΝ	MAL ANGULA	R RESOLUTIONS	;
Localisation	Optimal angle	Computation time	Time saving
Prostate	6°	01:08:35 (27%)	03:06:29 (73%)
Brain	5°	00:34:03 (36%)	01:00:14 (64%)
H&N	5°	02:42:15 (44%)	03:29:46 (56%)

The computation time and the time saving are displayed in hours/minutes/seconds and as a percentage of the computation time performed with the angular reference resolution for the TMM Anatomy algorithm.

The optimal angle is that for which the dose differences are on the average close to one percent with a small standard deviation (SD).

Ptv prost

Prostate DVHs comparisor

- These differences are the highest for the H&N cases, probably due to the fact that the modulation is more important as well as the dose gradients.
- The comparison of the two algorithms did not show any significant differences in the choice of the optimal angle or computation time.

#### PATIENTS SUMMARY TABLES BY LOCATION FOR TMM ANATOMY ALGORITHM (DIFFERENCES IN %)

Prosta	ate (6°)	Dmean	D2%	D95%	Brair	Brain (5°)		D2%	D95%	H&N (5°)		Dmean	D2%	D9
PTV prost SD	Mean	-0.05	0.04	-0.29	DTV	Mean	-0.24	0.01	-0.54	ΡΤΥ Τ	Mean	-1.06	-0.74	-1
	SD	0.24	0.37	0.36	FIV	SD	0.39	0.71	0.64		SD	0.64	1.07	1
PTV p-sv SD	Mean	-0.32	-0.16	-0.94	Optic	Mean	0.47	-0.04		PTV Nodes	Mean	-1.10	-0.67	-1
	SD	0.27	0.24	0.44	chiasm	SD	1.21	1.42			SD	0.50	0.53	0.
Rectum SD	Mean	-0.44	-0.23		Brainstem	Mean	-0.58	-0.27			Mean	-0.93	-0.02	
	SD	0.84	0.34		Dramstern	SD	1.38	1.09		Spine cord				
Bladder SD	Mean	-0.12	0.06		Reve	Mean	-1.45	-0.2			SD	0.94	1.43	
	SD	0.64	0.32		in cyc	SD	4.66	2.84		D Devetid	Mean	-2.14	-1.90	
P fomoral	Mean	-0.92	-0.62		Leve	Mean	-1.30	-0.4		Rearound	SD	1.68	1.52	
head	sp.	2.62	1 77		Leye	SD	1.88	0.82		L Devetid	Mean	-0.60	-0.68	
incou	Maan	2.02	0.72							LParotiu	SD	3.48	2.23	
L femoral Mean head SD	IVIEdI	0.44	0.75								Mean	0	-0.97	
	0.94	0.86			Oral cavity SD			0.75	1.49					
Digestive	Mean	-0.09	-0.18											
system	SD	0.77	1.27											

In the tables are represented for each structure:

The average deviations from the reference resolusion of each analyzed dose on the 5 patients.

The standard deviation of deviations from the reference resolution of each analyzed dose on the 5 patients.

### Conclusion

It has been possible to determine an optimal angle (maximum angle for which the deviations from the reference resolution are on the average close to one percent with a small standard deviation) for each location studied. It would thus be possible in the future to save a considerable time (for example three hours out of a total of four hours for the prostate case) for the computation of the dose delivered in the anatomy of the patient. No significant differences were found between the two algorithms used. This study, however, focused on a small sample of patients and, if it allows to conjecture an optimal angle for each location, it can't constitute a reliable statistic. Further study will be needed to verify these results.