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OECI CLINICAL Cancer Centre

Comparison between a convolution based and Monte Carlo based dosimetry software

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MRT DOSIMETRY
Metrology for clinical implementation of dosimetry in molecular radiotherapy

Aim

- In this work we compared two systems for dosimetry in MRT that use different techniques of calculation:

VoxelMed

AUSL-Reggio Emilia (Italy)

RAYDOSE

Cardiff University (UK)

$$\bar{D}_{(voxel_k)} = \Sigma_{h=0}^{N} \tilde{A}_{(voxel_h)} \times S_{(voxel_k \leftarrow voxel_k)}$$

$$S(voxel_k \leftarrow voxel_h) = \Sigma_i \Delta_i \cdot \frac{\phi_i(voxel_k \leftarrow voxel_h)}{m_{voxel_k}}$$

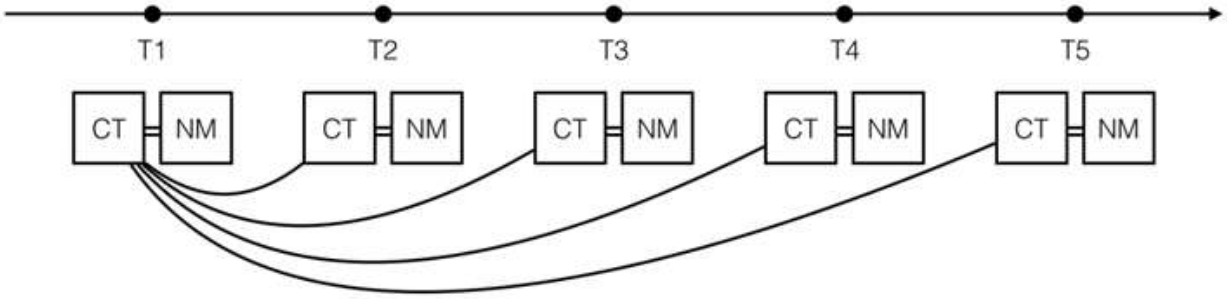
$$D = \left[\sum_{i=1}^{N-1} (\dot{D} \cdot \tilde{A}_{total}^{i \rightarrow i+1}\right] + [\dot{D}^N \cdot \tilde{A}_{total}^{tail}]$$

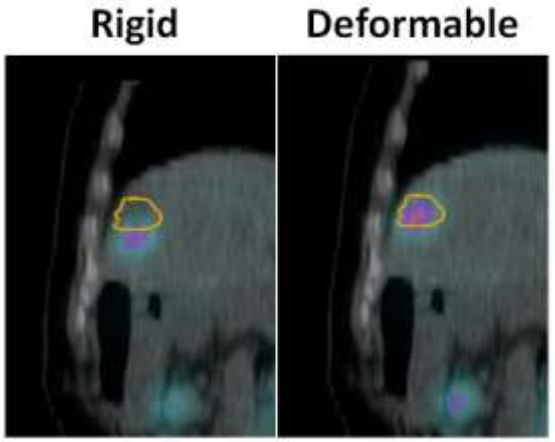
- The aim is to assess how calculation modality impacts on dosimetry results.

Material and methods

Study on **20 patients** enrolled in a PRRT clinical trial:

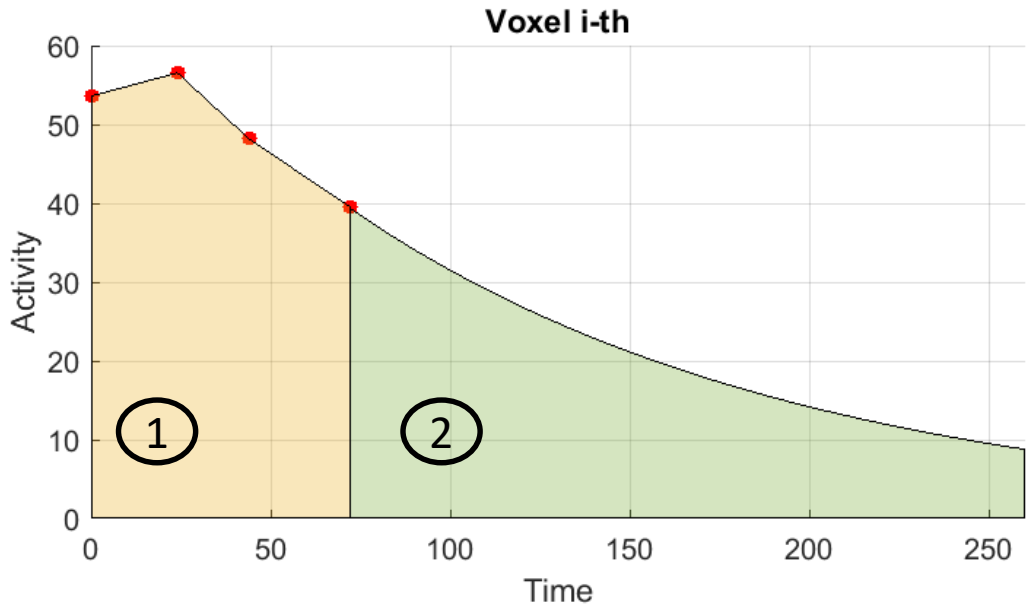
- Dosimetry at the first course of therapy after a therapeutic administration of **^{177}Lu-DOTATOC**.
- **5 SPECT/CT** scans with a Siemens Symbia T2 gamma camera at 1, 4, 24, 44, 72 h p.i.
- SPECT images were aligned to the first CT image using a **deformable registration** with the Velocity console (Varian Medical System, USA).





Grassi et al. Phys. Med. 45 (2018)

Both VoxelMed and RAYDOSE perform integration of Time-Activity curves using Trapezoidal and Analytical methods:



1. Integration by **Trapezoidal method of voxel activity**

2. Extrapolation by **whole organ activities**

VoxelMed → Bi-exponential: $Ae^{-a \cdot t} + Be^{-b \cdot t}$

RAYDOSE → Mono-exponential: $Ae^{-a \cdot t}$

- The **same set of images** and the **same VOI** were the starting point for dose calculation with both the software

- Absorbed doses were calculated for

Organs:
Left kidney
Right kidney
Liver
Spleen

Tumours:
Max 4 tumours per patient
Total 23 tumours were considered

21 out of 23 were hepatic lesions
(1 pancreatic and 1 lymph node)

- For the comparison RAYDOSE was considered as the reference and **Error (%)** of VoxelMed mean absorbed dose was calculated as follows:

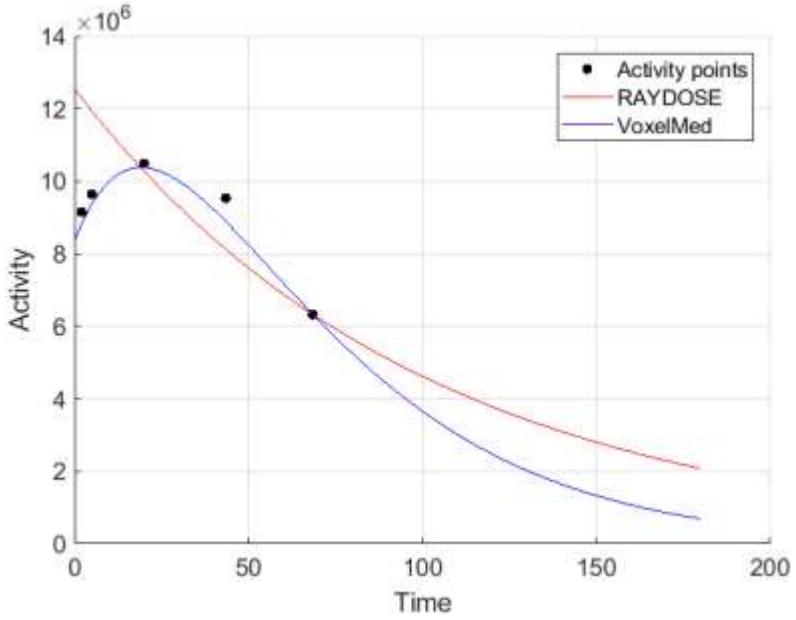
$$Error\ (\%) = \frac{VoxelMed - RAYDOSE}{RAYDOSE} \cdot 100$$

Furthermore **DVH** and **dose maps** were qualitatively compared, and the **Lin's concordance coefficient** was estimated

To strictly evaluate differences in calculation modality, comparison was also performed using the same **TIAC**:

Calculation with **VoxelMed** was repeated using **the same k** (the effective decay constant) used for RAYDOSE calculation.

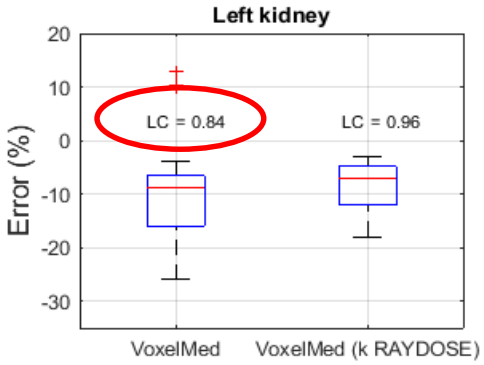
Different fitting curves:

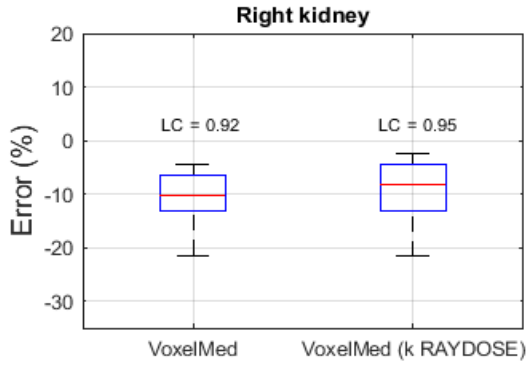


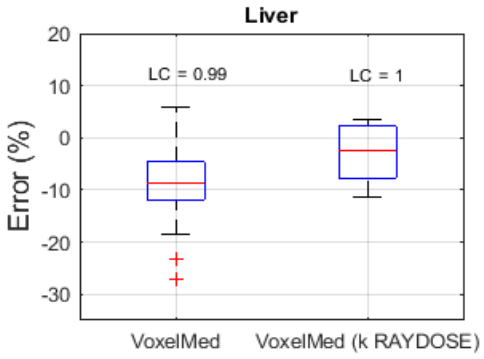
Comparisons were performed between:

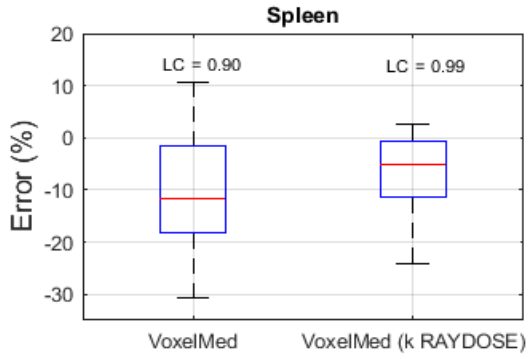
VoxelMed vs RAYDOSE & **VoxelMed (k RAYDOSE) vs RAYDOSE**

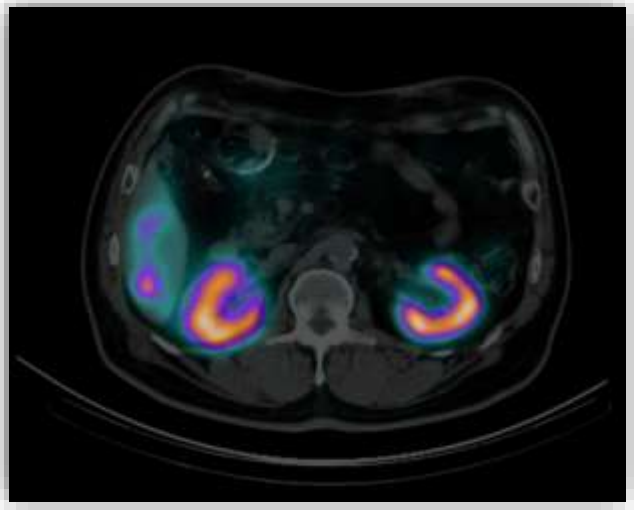
Results





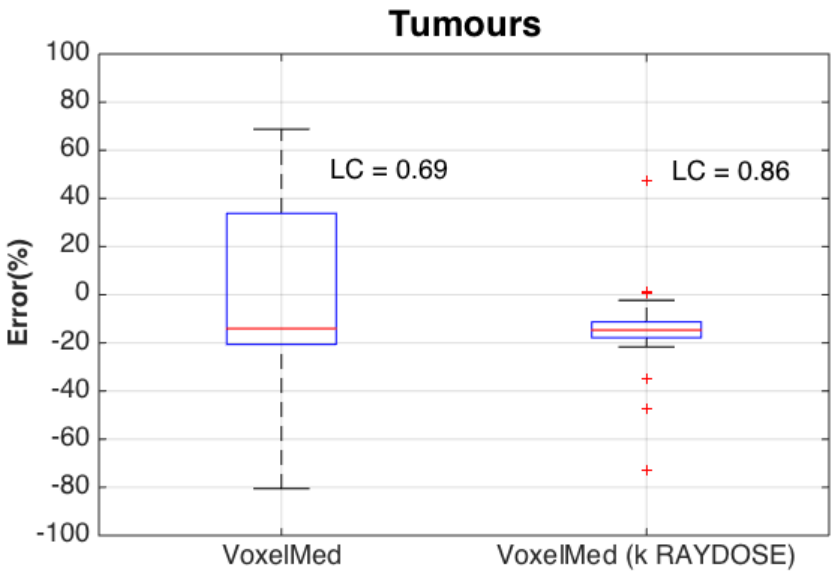






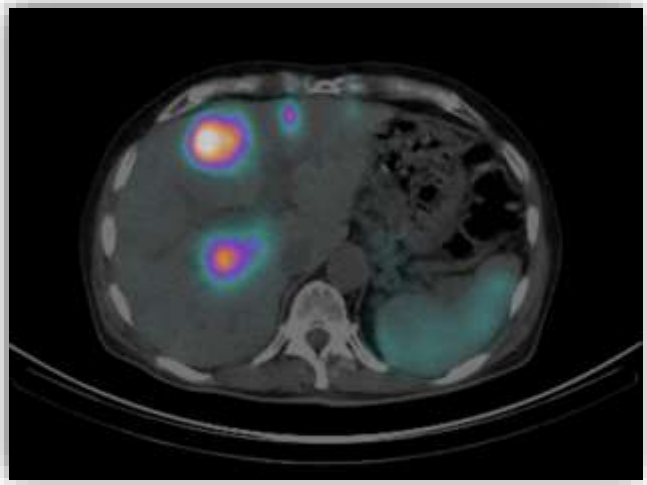
Mean Error (%)

Organ	VoxelMed	VoxelMed (k RAYDOSE)
Left kidney	-10,8	-8,3
Right kidney	-8,6	-9,2
Liver	-7,9	-0,9
Spleen	-6,1	-5,8



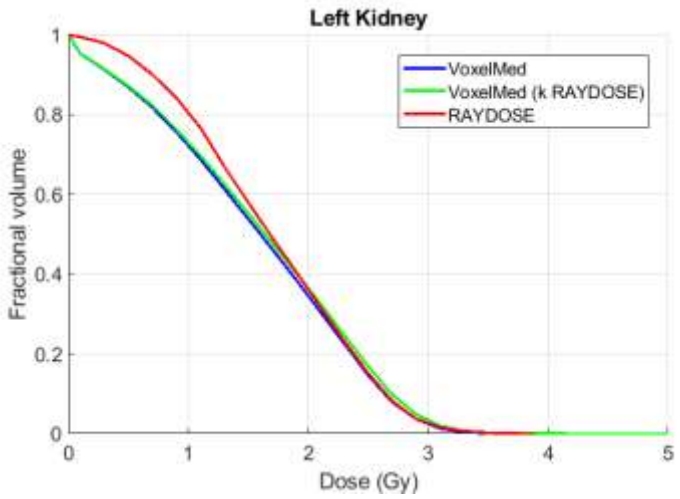
- For 3 tumours out of 23 Error (%) > 100%
- These differences were reduced when the same k was used
- Less variability and higher correlation was observed when the same k was used
- In case of VoxelMed (k RAYDOSE) Error(%)<0 for all the lesions (excluded outliers)

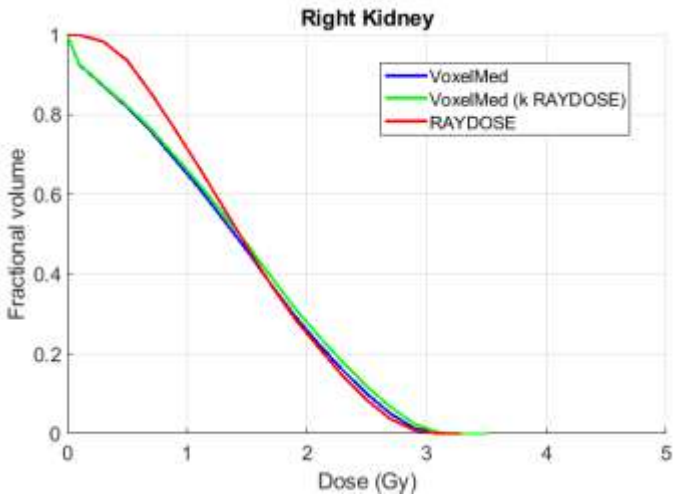
	VoxelMed	**VoxelMed (k RAYDOSE)**
Mean	-11,5	-16
Median	-17,6	-14,8
25th perc	-22,0	-19,0
75th perc	30,8	-11,8



Finally we qualitatively compared the **DVH** and **Dose maps**:

Example of a patient with typical Error (%)

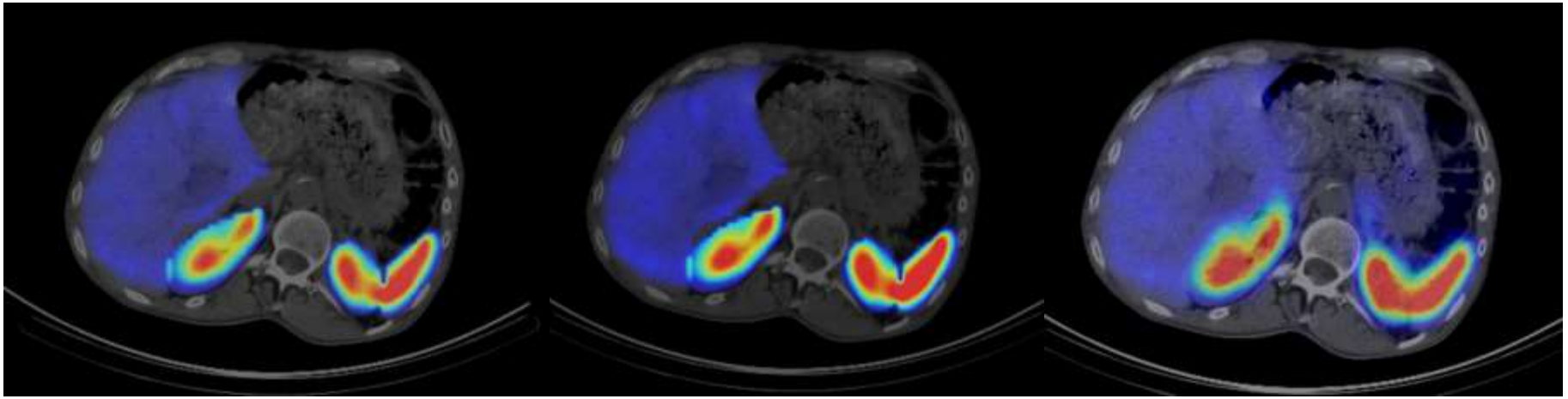




VoxelMed

VoxelMed (k RAYDOSE)

RAYDOSE



Conclusion

- A general underestimation of absorbed doses calculated with VoxelMed was observed, as compared to RAYDOSE: average -9% error was observed for organs, while -18% for lesions.

- Concordance between VoxelMed and RAYDOSE was good for organs (LC>0.84), while greater differences were observed for tumours (LC=0.62).

- Differences were reduced when the same k was used: -6% for organs and -15 for lesions. Also concordance was largely increased (LC>0,95 for organs and 0,86 for lesions).

- In conclusion convolution methods allows to perform high accuracy dosimetric calculations with reduced computational time.

- Particular attention must be paid to the activity fitting that could have a large impact on results.

Thank you for your attention