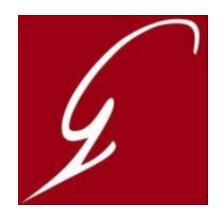


Università degli studi di Padova Master Degree in Physics

Introduction to Research



Geant4 Computational Dosimetry for the ISOLPHARM Project

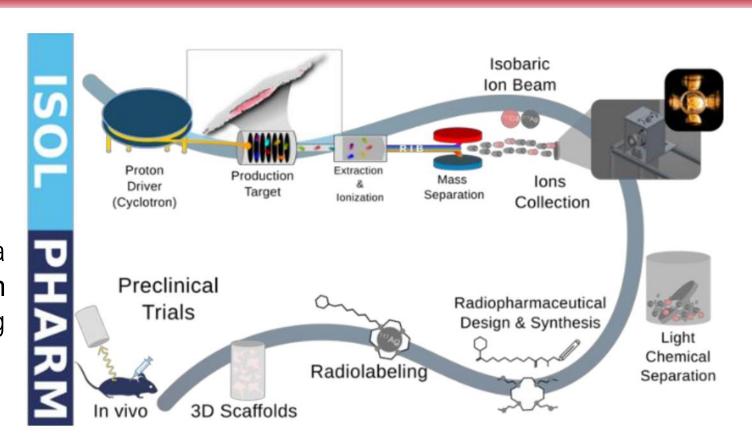


Emma Sonvico 21/10/2025

ISOLPHARM Project

Production of radionuclides for targeted radiopharmaceuticals.

A 30-70 MeV proton beam from a cyclotron hits a depleted Uranium Carbide target, generating neutron-rich radionuclides.

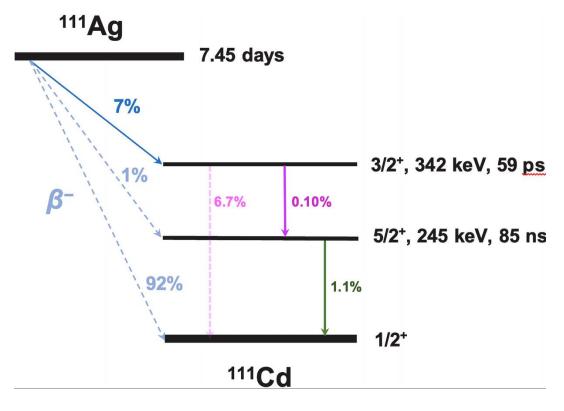


ISOL technique for radioPHARMaceuticals

Ag-111

The first chosen radionuclide for internal radiotherapy is **Ag-111**:

- β⁻ emitter (360 keV) -> induce cell death and deliver a cytotoxic radiation dose on the disease site;
- Medium half-life time (7.45 d);
- Medium tissue penetration (~1 mm);
- Low level of associated γ emission (\sim 6%).



Objectives of this intenship

The aim of this internship is to create a dataset of organ-to-organ S-values of Ag-111 radionuclide:

we will use specific biodistributions with a whole body heterogeneous source based on MOBY's voxel-based phantoms with Geant4 simulations.

The developed dataset can be used to improve the accuracy of absorbed dose calculations in small animals dosimetry and highlight the impact of the mouse and organs size on S-values calculation.



Dosimetric Formalism

Our study uses the internal dosimetry standard provided by the MIRD (Medical Internal Radiation Dose) Committee.

- Absorbed Dose [1Gy=1J/kg]:
- Cumulative Activity [Bq s]:
- S-values [Gy/Bq s]:
- Absorbed Dose Rate [Gy/s]:

$$D = -\frac{dE}{dm}$$

$$\tilde{A}(r_S, T_D) = \int_0^{T_D} A(r_S, t) dt$$

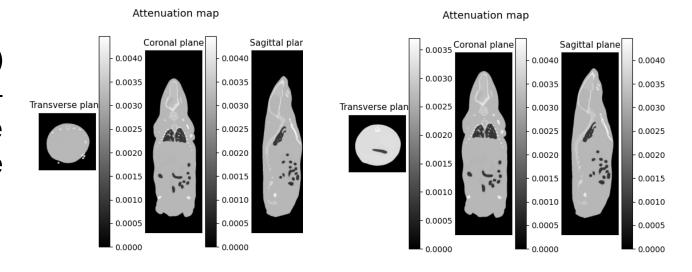
$$S(r_T \leftarrow r_S) = \sum_i \frac{n_i E_i \Phi(r_T \leftarrow r_S)}{m}$$

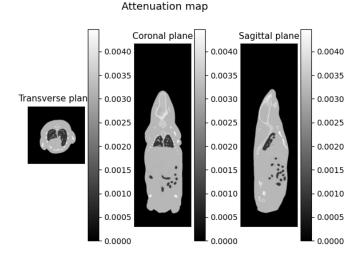
$$D'(r_T, T_D) = \sum_{r_T} \tilde{A}(r_S, T_D) S(r_T \leftarrow r_S)$$
 MIRD Equation

The MOBY Phantoms

MOBY (Mouse whole BodY)
 phantoms are based on a high resolution 3D Magnetic Resonance
 Microscopy (MRM) dataset for the
 organ/body surfaces;

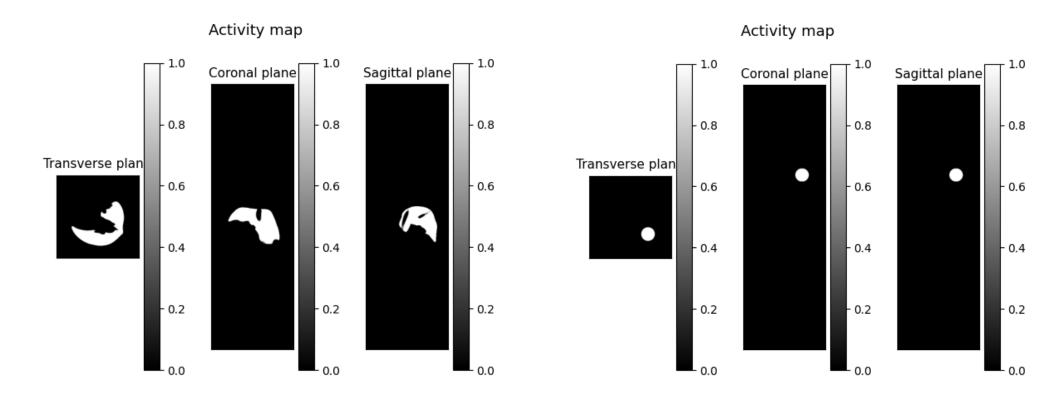
Voxel-based mouse models (15, 20, 25 g) -> Attenuation Maps: similar to a CT scan.





The MOBY Phantoms

- Activity Maps of single organs to recreate a PET- or SPECT- like matrix.
- A tumor can be generated as a sphere selecting its position and dimension.



Geant4 Simulation

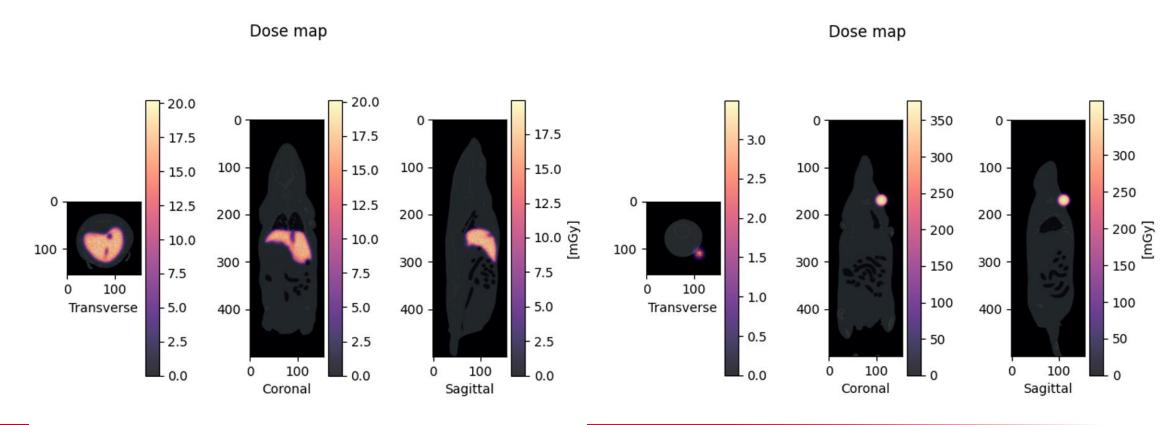
 Geant4 is a Montecarlo simulation code in C++ developed by CERN to model interactions of radiation with matter.



- The Attenuation and Activity maps are imported and 10⁷ events of an Ag-111 decaying in the source organ are generated. The MOBY phantom is made a sensitive detector.
- The output files:
 - o dose histograms of a 3d matrix of voxels containing the deposited energy;
 - TTree of a list of individual dose hits for each event and its voxel coordinates.

Geant4 Simulation

- The dose histograms' values are converted from MeV/g in Gy and normalized.
- -> Absorbed Dose Maps



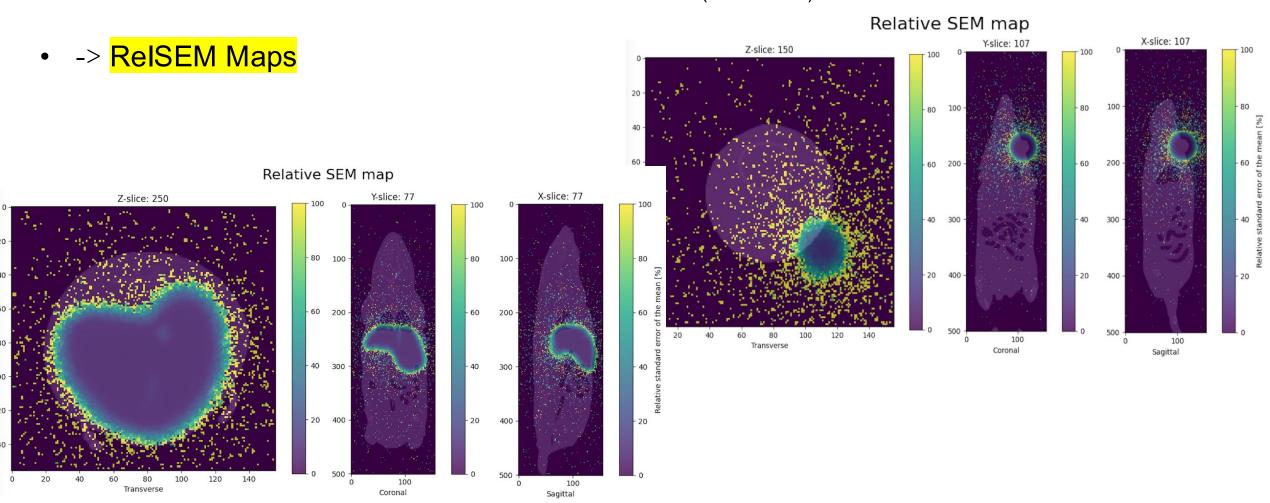
S-values

The S-values are calculated as the dose rate per unit of activity [Gy/(Bq*s)].

	SOURCE ORGAN								
TARGET ORGAN	kidney	liver	lungs	muscle	pancreas	spleen	testes	${ m thyroid}$	tumor
brain	1.1278e-15	1.6161e-15	3.3433e-13	4.6852e-13	1.2973e-15	1.2734e-15	3.1745e-16	2.4354e-14	3.7624e-15
\mathbf{heart}	4.8130e-15	2.4131e-12	1.2275e-11	1.2370e-12	6.7414e-15	6.9400 e-15	1.0559e-15	1.0184e-14	$1.4654e ext{-}14$
$_{ m kidney}$	2.3500e-10	1.9736e-12	5.2169 e-15	1.0642e-12	1.2714e-11	8.2023e-12	2.6072e-15	1.5094e-15	2.3546e-15
liver	2.6493e-12	4.8887e-11	2.7147e-12	6.1927e-13	2.8457e-12	9.6948e-15	1.5378e-15	3.6507e-15	6.5364e-15
$_{ m lungs}$	5.1095e-15	1.6072e-12	1.1372e-10	9.9518e-13	5.7789e-15	5.5772e-15	9.6573 e-16	1.3965e-11	1.7974e-13
pancreas	1.2591e-11	3.1726e-12	6.7776e-15	7.1334e-13	1.9232e-10	2.9298e-11	2.3188e-15	2.0859e-15	3.1176e-15
$_{ m spleen}$	4.0254 e-12	1.0393e-14	6.4750 e-15	1.4001e-12	1.6294e-11	6.6383 e-10	2.0883e-15	1.6729e-15	2.4329e-15
testes	2.9306e-15	1.6369e-15	8.6304 e-16	1.5803e-12	2.6585e-15	2.6036e-15	2.4019e-10	5.4219e-16	7.8362e-16
$_{ m thyroid}$	1.8985e-15	3.9618e-15	1.5979e-11	2.5257e-12	3.6616e-15	1.3269 e-15	5.4956e-16	3.7387e-09	1.2033e-14
tumor	2.5870e-15	7.1295e-15	2.4498e-13	1.4862e-12	2.9159e-15	2.5076e-15	6.0918e-16	1.2713e-14	5.6413e-10
		SOURCE	ORGAN						
TARGET ORGAN	kidney	liver	lungs	muscle	pancreas	spleen	testes	thyroid	tumor
brain	6.8390 e-16	1.1320e-15	1.4653 e-13	2.1790e-13	7.7108e-16	7.6143e-16	2.2695 e-16	1.1296e-14	4.3413e-15
\mathbf{heart}	2.9806e-15	1.0417e-12	6.4297e-12	6.7167e-13	5.1832e-15	3.7506e-15	5.8384e-16	7.1653e-15	7.0510e-15
$_{ m kidney}$	1.4589e-10	9.7280e-13	3.5204e-15	5.4430e-13	6.5206 e-12	3.5353e-12	1.8196e-15	1.2734e-15	1.3149e-15
liver	1.3031e-12	2.9414e-11	1.3959e-12	3.1798e-13	1.4002e-12	6.6591e-15	9.9380e-16	2.6401e-15	8.7533e-15
$_{ m lungs}$	3.5823e-15	8.4400e-13	7.2072e-11	5.0976e-13	4.3034e-15	4.0213e-15	5.9635e-16	7.8285e-12	8.7533e-15
pancreas	6.4599e-12	1.5824e-12	4.2837e-15	3.8462e-13	1.2087e-10	1.5314e-11	1.8276e-15	1.5145e-15	1.4426e-15
$_{ m spleen}$	1.7206e-12	6.2893e-15	3.4725e-15	7.4382e-13	8.6725e-12	4.2531e-10	1.6503e-15	1.4252e-15	1.3227e-15
testes	1.9985e-15	1.1854e-15	6.5327e-16	8.0651e-13	1.7414e-15	1.4539e-15	1.4952e-10	3.3368e-16	3.6061e-16
$_{ m thyroid}$	2.0339e-15	2.6737e-15	9.7902e-12	1.3441e-12	1.2425e-15	9.2486e-16	3.0875e-16	2.5094e-09	1.9894e-14
tumor	9.8807e-16	1.5824e-15	9.5314e-15	1.3736e-12	1.5665e-15	1.3966e-15	2.9190e-16	2.1380e-14	5.6459e-10

ReISEM

 The information on the total dose deposited in each voxel for each event is used to calculate the Relative Standard Error of the Mean (ReISEM).



S-values' Uncertainties

- For each source target couple, the activity map of the target is used as a mask to calculate the reISEM on the Svalue.
- *Expectation*: the uncertainty of a specific source organ S-values is bigger for a smaller and more distant target organ.
- However, the increased *stochastic variance* of the energy deposited in closer organs has to be considered.
- → Increase the statistics and decrese the number of voxels.
- → For now, associate the relSEM calculated for a **source**-**source** organs couple to all the S-values with that source.

	$15~\mathrm{g}$	20 g	$25~\mathrm{g}$
Blood	2.32~%	2.67~%	2.85~%
Bone	10.95~%	8.16~%	8.68~%
Brain	2.27~%	2.62~%	2.83~%
Heart	1.81~%	2.09~%	2.24~%
Kidney	2.42~%	2.84~%	3.06~%
Liver	5.27~%	6.26~%	6.77~%
Lungs	3.50~%	4.09~%	4.39~%
Muscle	17.86~%	21.21~%	22.94~%
Pancreas	2.69~%	3.15~%	3.38~%
Spleen	1.44~%	1.68~%	1.80~%
Testes	2.40~%	2.82~%	3.03~%
Thyroid	0.61~%	0.69~%	0.74~%
Tumor	1.56 %	1.56 %	1.56 %

Dose Rate Calculation

• The mean absorbed dose rates $D'(r_T, T_D)$ are estimated through the MIRD equation, where we use:

- this study's S-values dataset;
- Injected activity per mass data from an Ag-111 biodistribution experiment carried out by the ISOLPHARM group in March 2024 at the CAPiR laboratory in Catania.

 $D'(r_T, T_D) = \sum_{r_T} A(r_S, T_D) S(r_T \leftarrow r_S)$

TARGET ORGAN	Average Injected Activity per Grams $(\%/g)$	Rel. Err.
Blood	0.034	0.294
Bone	0.040	0.152
Brain	0.435	0.287
Heart	0.090	0.318
Kidney	0.385	0.300
Liver	0.770	0.285
Lungs	1.200	0.293
Pancreas	0.040	0.161
Spleen	0.320	0.340

Dose Rate Calculation

	TARGET ORGAN	m DOSE~(Gy/s)	Relative Error
	Brain	3.37×10^{-7}	0.283
	Heart	1.20×10^{-7}	0.184
	Kidney	1.63×10^{-7}	0.271
15 g Mouse	Liver	3.76×10^{-7}	0.278
6	Lungs	4.37×10^{-7}	0.281
	Pancreas	4.94×10^{-8}	0.154
	Spleen	1.07×10^{-7}	0.328
	Testes	2.09×10^{-11}	0.174
	Thyroid	5.95×10^{-8}	0.288
		-	

	TARGET ORGAN	$\mathbf{DOSE} \; (\mathbf{Gy/s})$	Relative Error
e	Brain	3.59×10^{-7}	0.196
	Heart	1.18×10^{-7}	0.132
	Kidney	1.68×10^{-7}	0.191
	Liver	3.79×10^{-7}	0.197
	Lungs	4.52×10^{-7}	0.200
	Pancreas	3.22×10^{-8}	0.141
	Spleen	1.13×10^{-7}	0.230
	Testes	2.12×10^{-11}	0.120
	Thyroid	6.18×10^{-8}	0.204

TARGET ORGAN	$\mathbf{DOSE}\; (\mathbf{Gy/s})$	Relative Error
Brain	3.69×10^{-7}	0.166
Heart	1.19×10^{-7}	0.113
Kidney	1.70×10^{-7}	0.162
Liver	3.80×10^{-7}	0.168
Lungs	4.55×10^{-7}	0.170
Pancreas	4.36×10^{-8}	0.0864
Spleen	1.16×10^{-7}	0.195
Testes	2.20×10^{-11}	0.109
Thyroid	6.04×10^{-8}	0.174

25 g Mouse

Conclusions and Future Prospectives

- We developed a comprehensive S-value dataset for Ag-111 in 3 mice (15, 20, 25 g) using voxel-based MOBY phantoms and Geant4 simulations.
- The S-values dataset was employed to calculate the mean absorbed dose rates for key organs.
- Mouse size and organ dimensions significantly impact S-values.
- The developed S-values dataset will improve the accuracy of absorbed dose calculations in preclinical studies.
- The observed dependency of uncertainties on distance was likely due to stochastic variance inherent in Montecarlo simulations.
- Future work:
 - Improve the number of events/simulations to achieve a more physically accurate dataset;
 - o **Decrease the number of voxels** in the MOBY phantoms to agevolate the computing.

