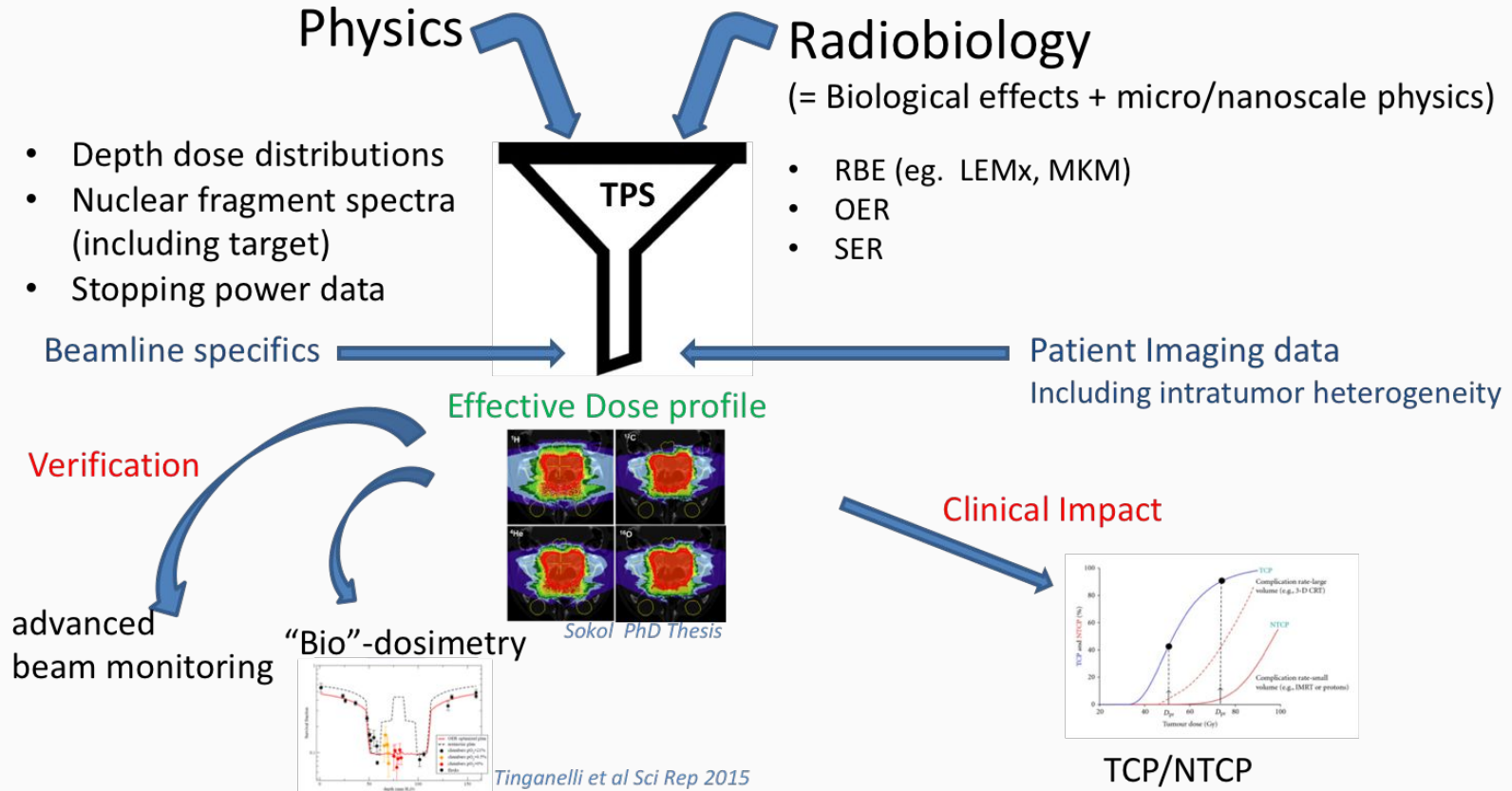


Update from MoVe IT: recent insights in the biological impact of target fragments

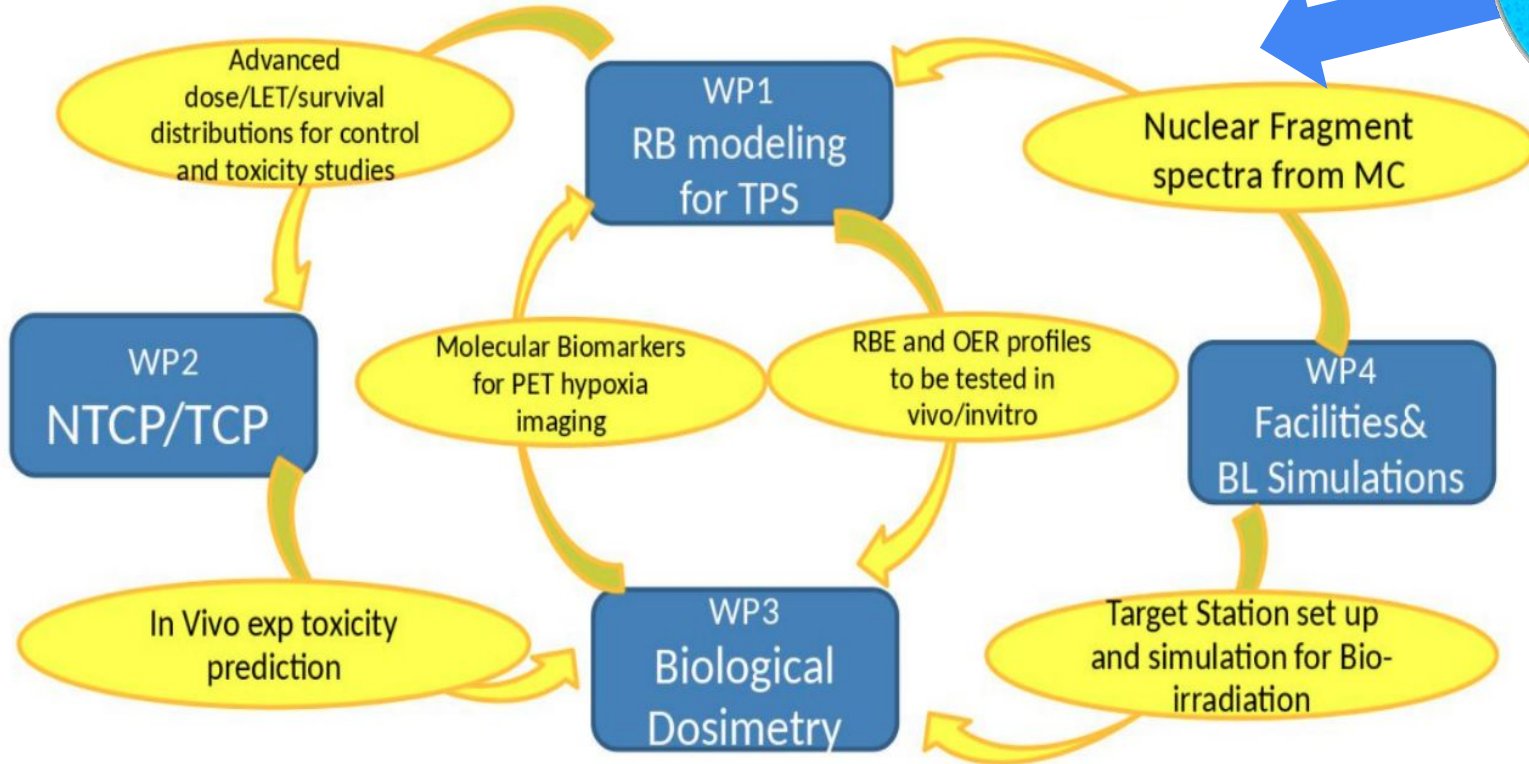
A. Attili, F. Tommasino, E. Bellinzona, E. Scifoni, E. D'Arسيè, A. Embriaco



The MoVeIT experiment

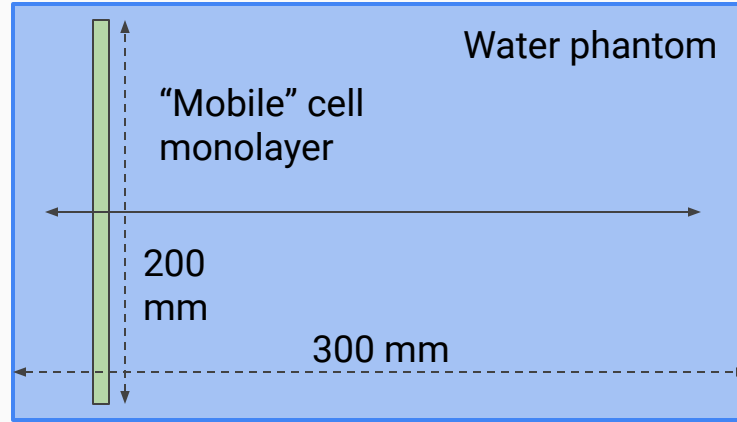


MoVe IT structure and links

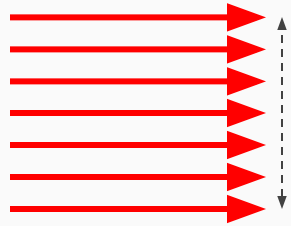


FragmentatiOn Of Target simulations - Geometry

pencil beam source
protons @ 160 MeV

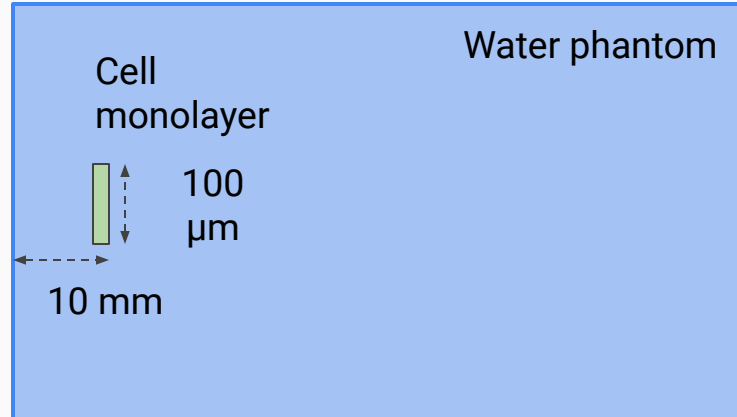


"plane" beam source

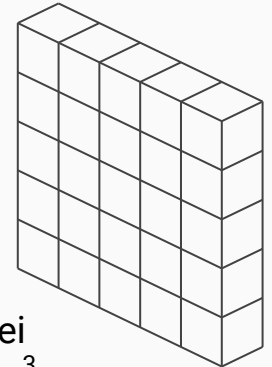


100 μm

protons @ 160 MeV

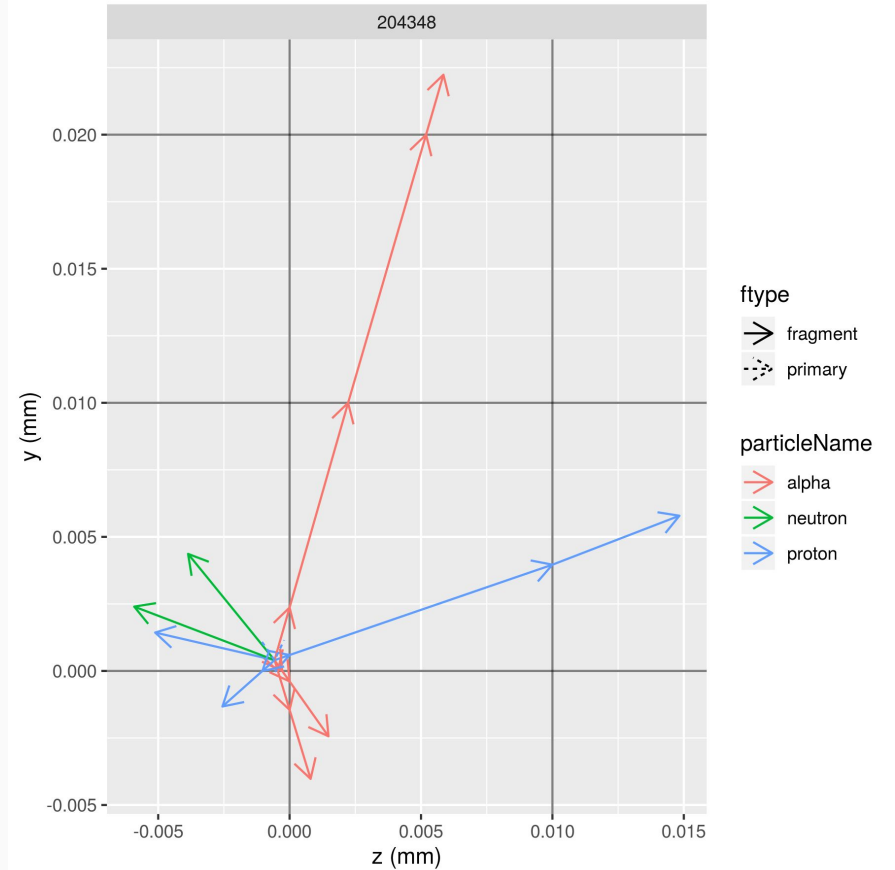
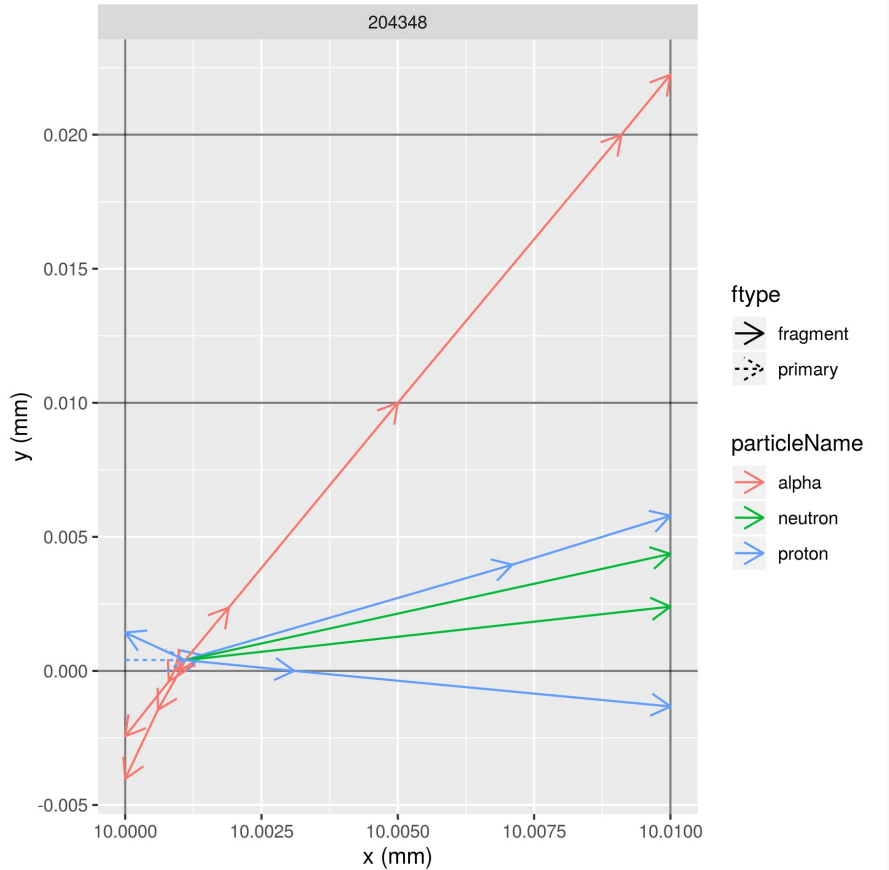


Cell monolayer

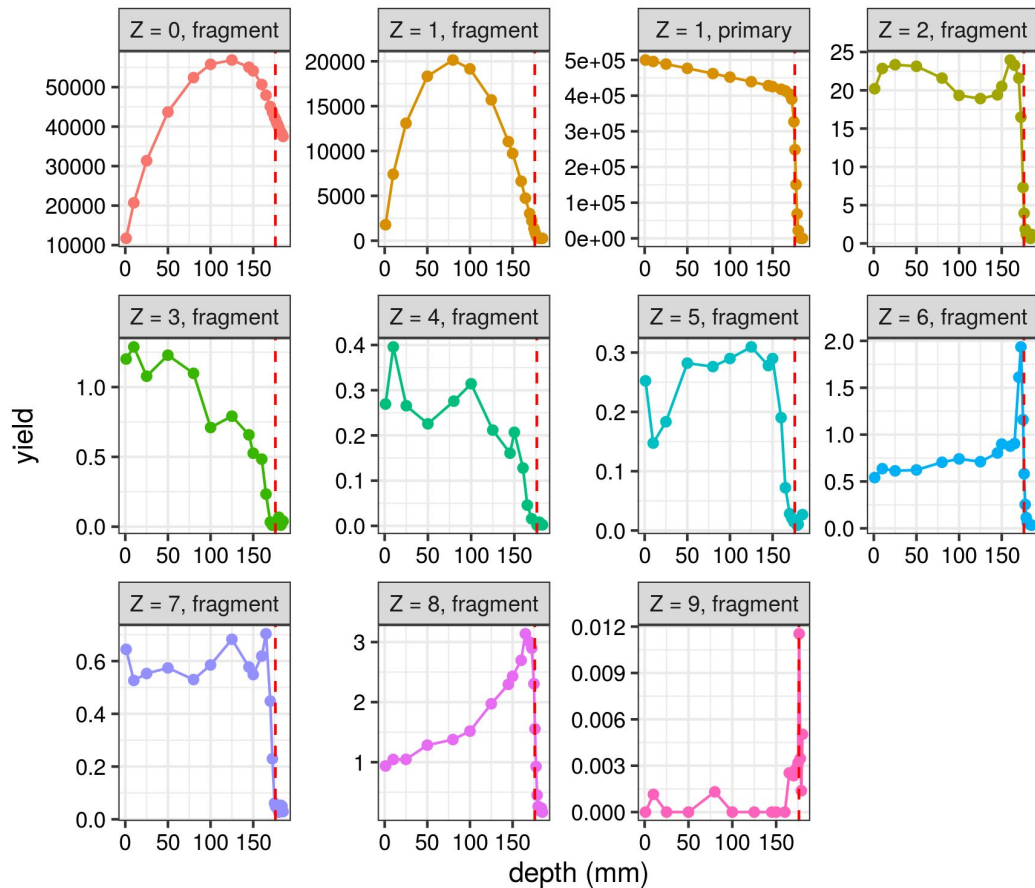
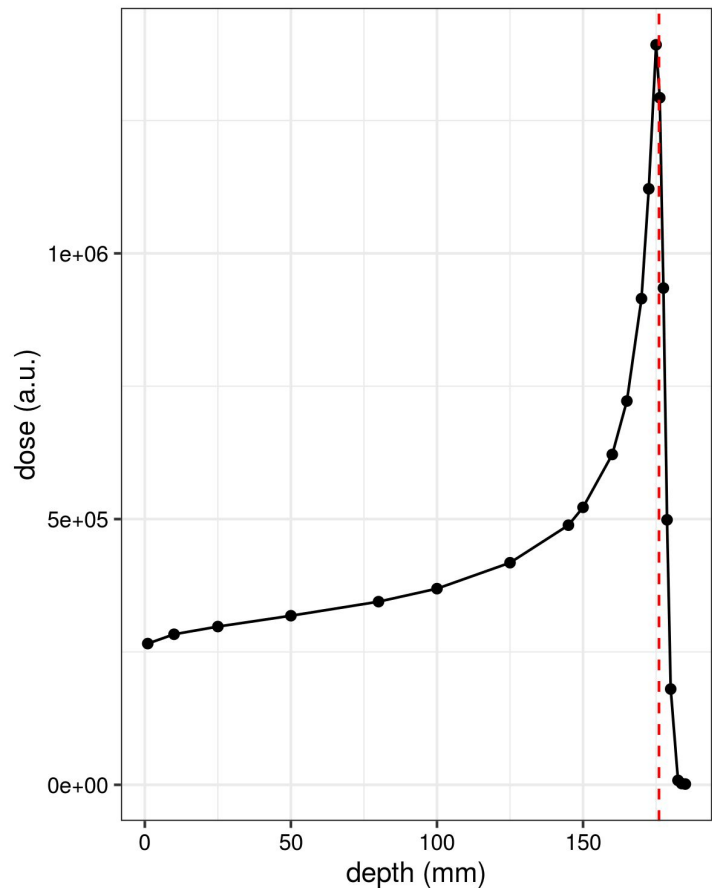


Voxel-cell nuclei
 $10 \times 10 \times 10 \mu\text{m}^3$

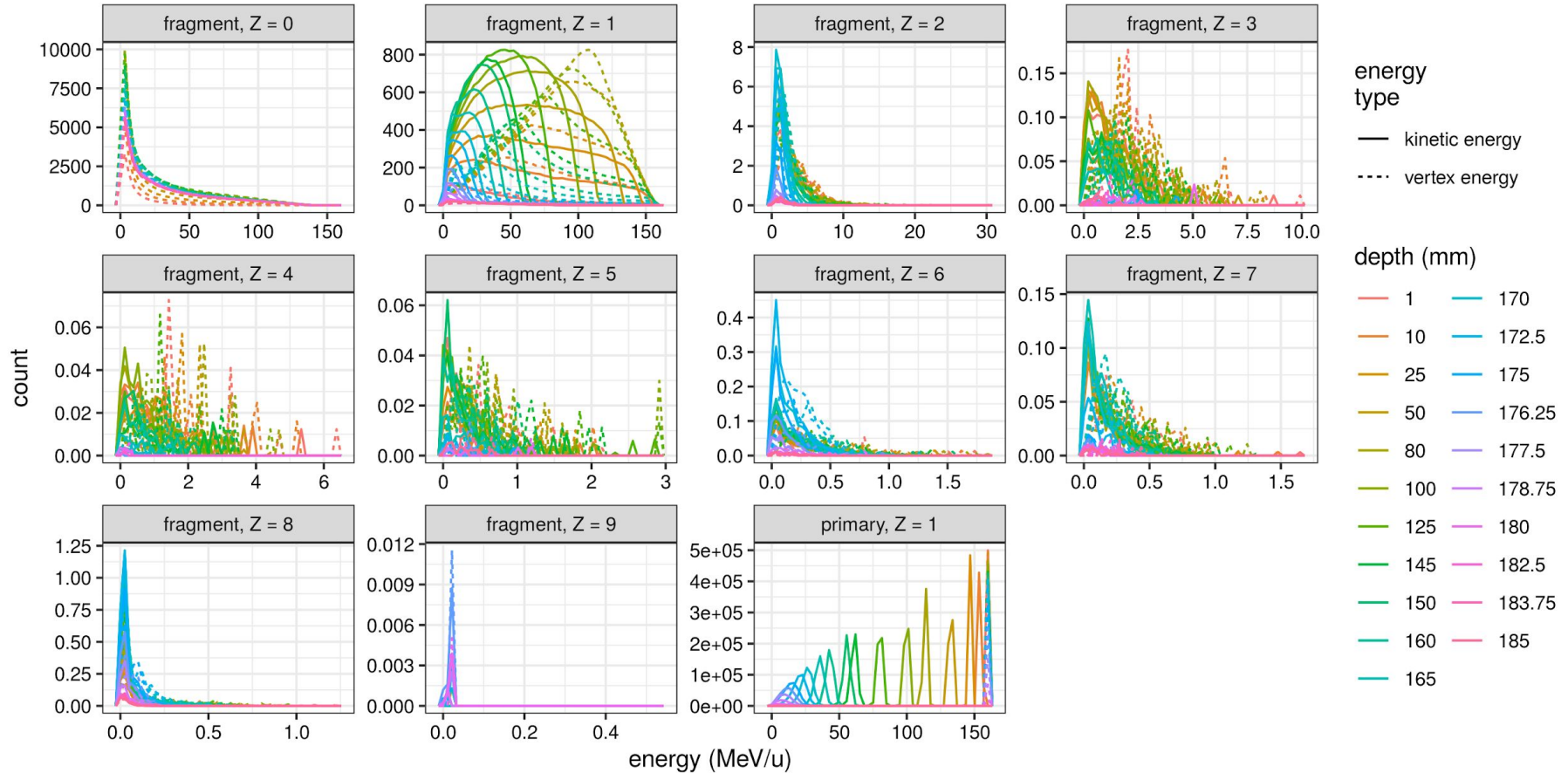
FragmentatiOn Of Target simulations - Geometry



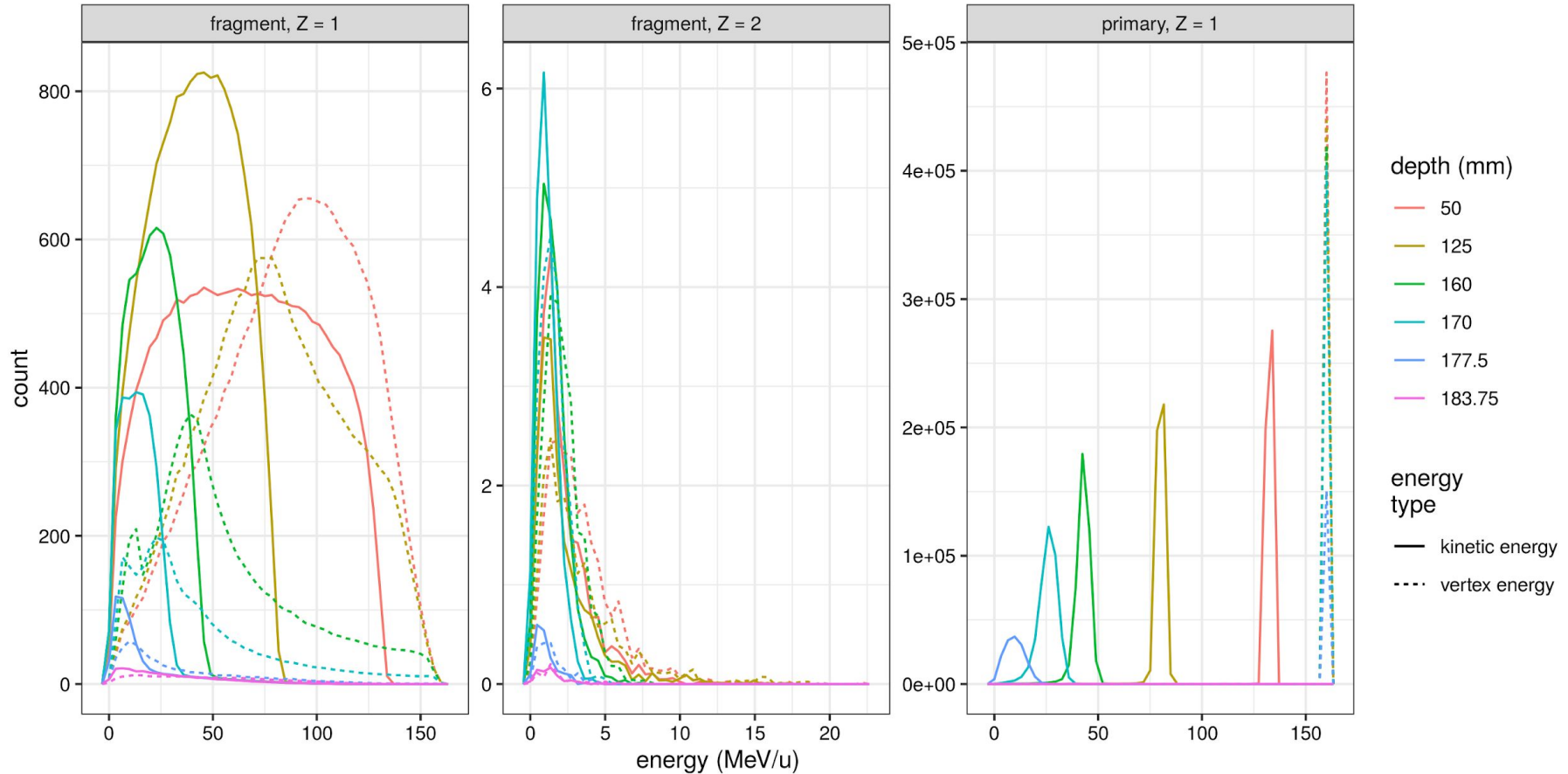
Dose & yield vs. depth (proton beam @ 160 MeV)



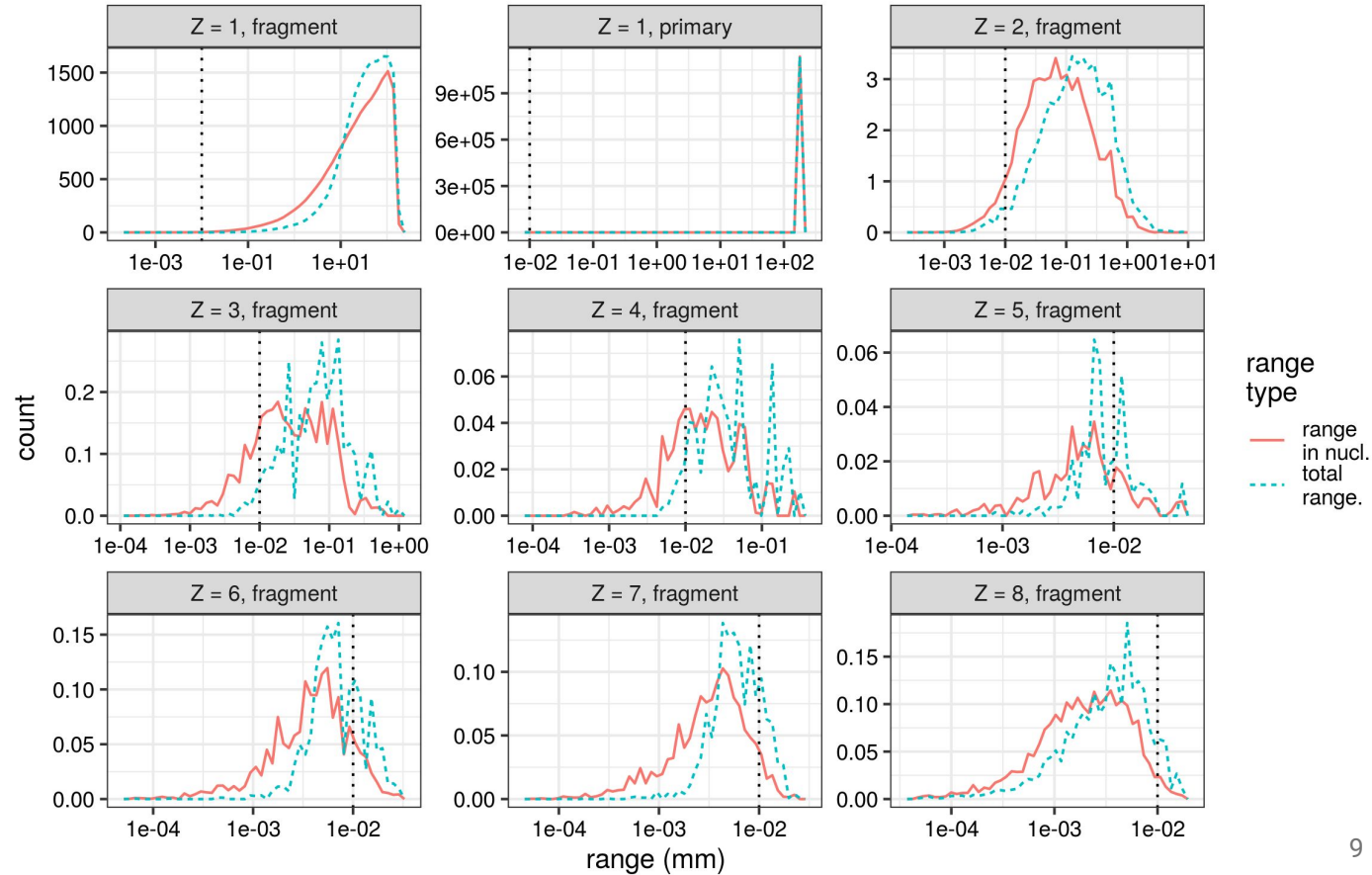
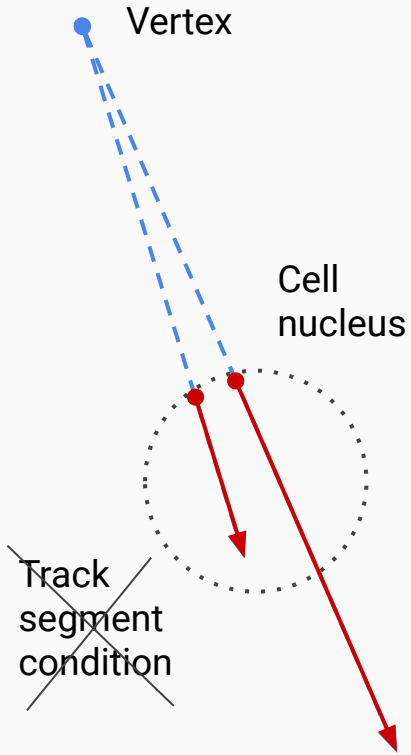
Kinetic and "vertex" energy (proton beam @ 160 MeV)



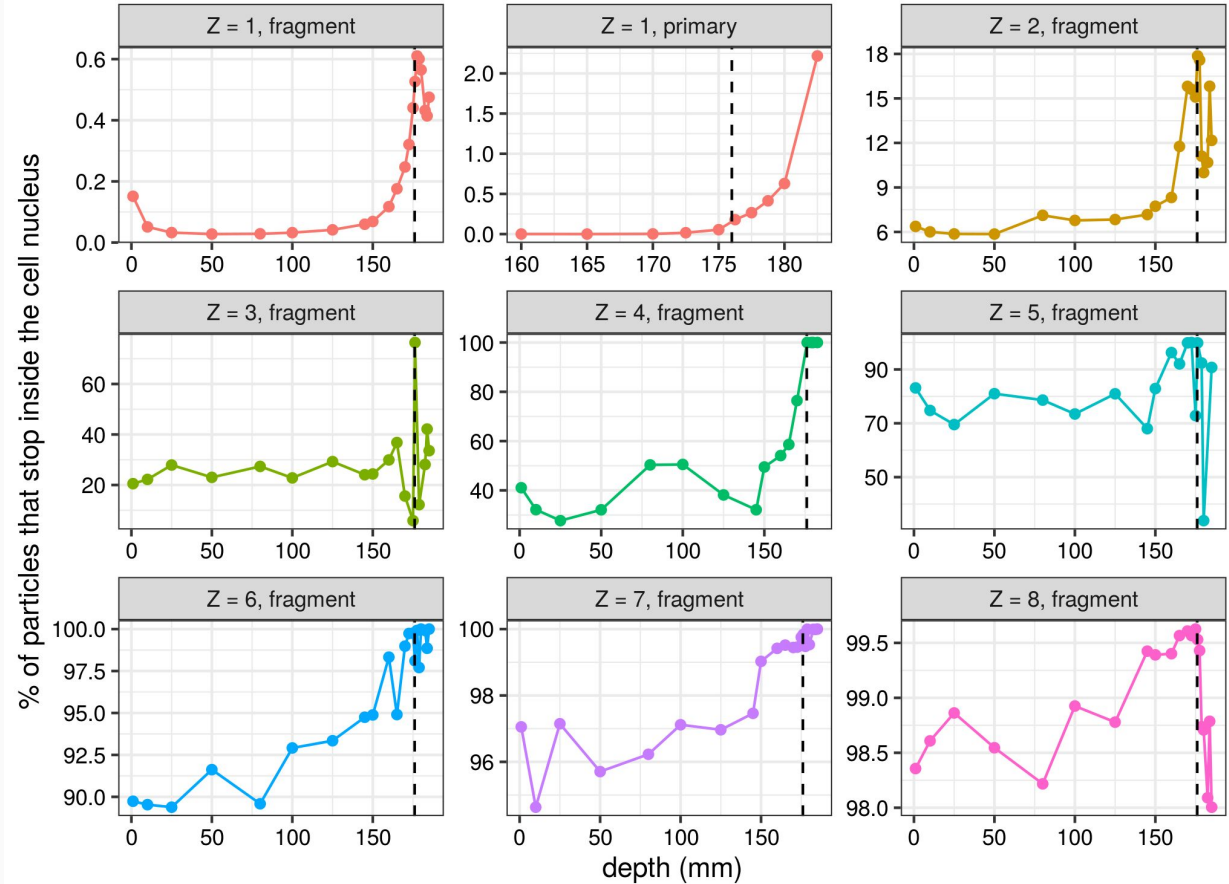
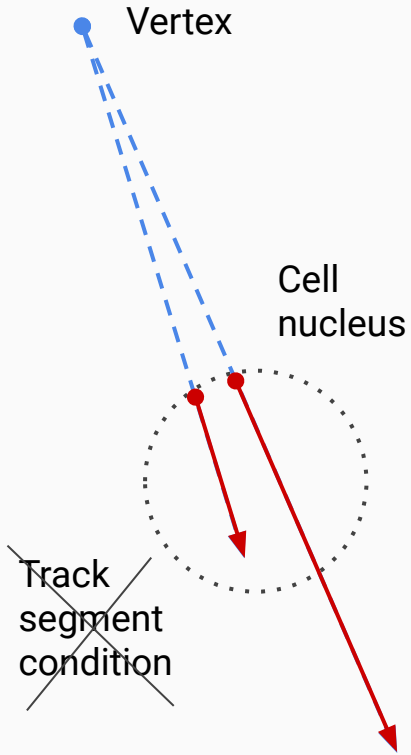
Kinetic and “vertex” energy (proton beam @ 160 MeV)



Residual range in cell nucleus considerations



Residual range in cell nucleus considerations



Biological impact - The relative Biological Effectiveness (RBE)

Relative Biological Effectiveness

RBE

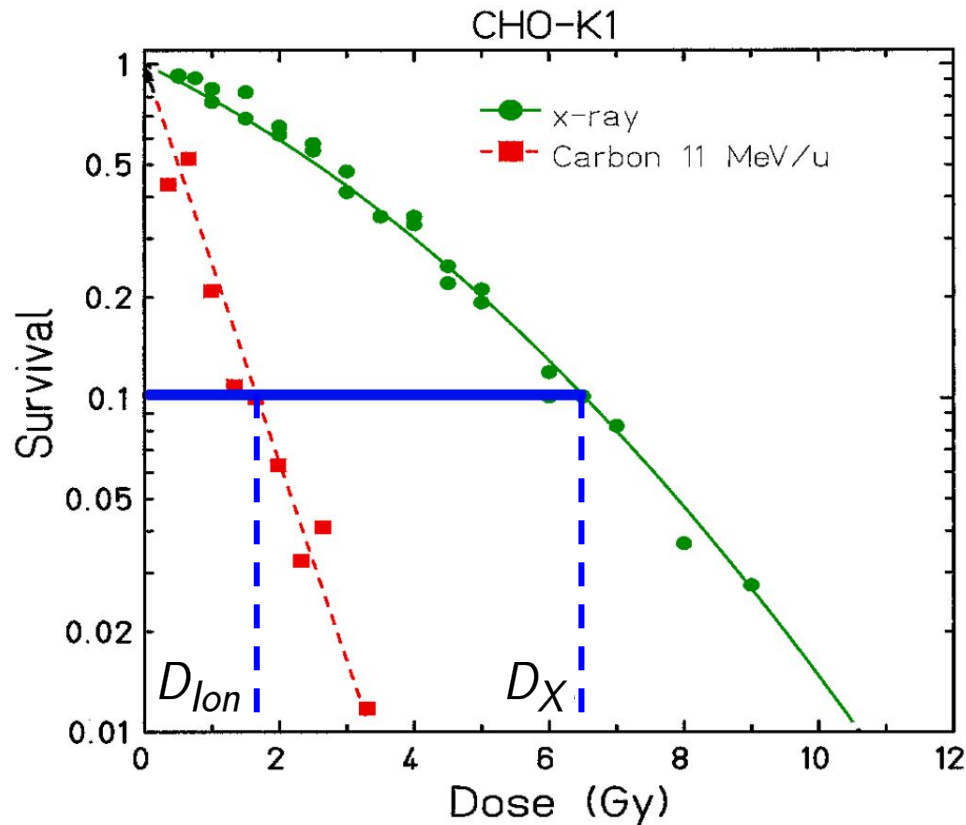
$$RBE_n = \frac{D_X}{D_{Ion}} \Big|_{S_X=S_{Ion}=n}$$

RBE ~ 1.1 for protons

RBE > 1 for ions

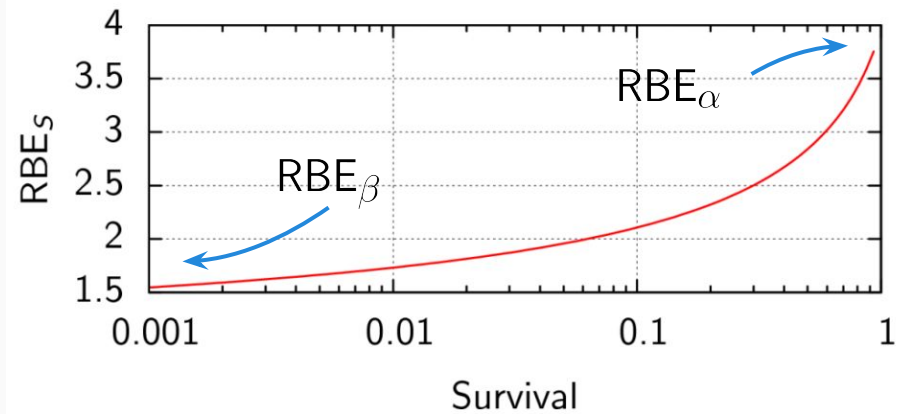
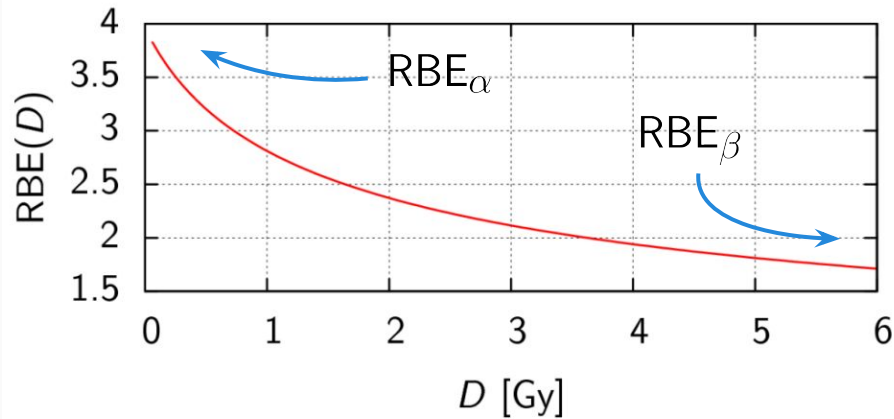
RBE-Weighted Dose (RWD):

$$RWD = D \times RBE$$



Biological impact - The relative Biological Effectiveness (RBE)

$$\left\{ \begin{array}{l} \text{RBE}_\alpha = \alpha/\alpha_X \\ \text{RBE}_\beta = \sqrt{\beta/\beta_X} \\ R = \alpha_X/\beta_X \end{array} \right. \longrightarrow \text{RBE} = R \left(-1 + \sqrt{1 + \frac{4}{R} \left(\text{RBE}_\alpha D + \frac{(\text{RBE}_\beta D)^2}{R} \right)} \right) / 2D$$

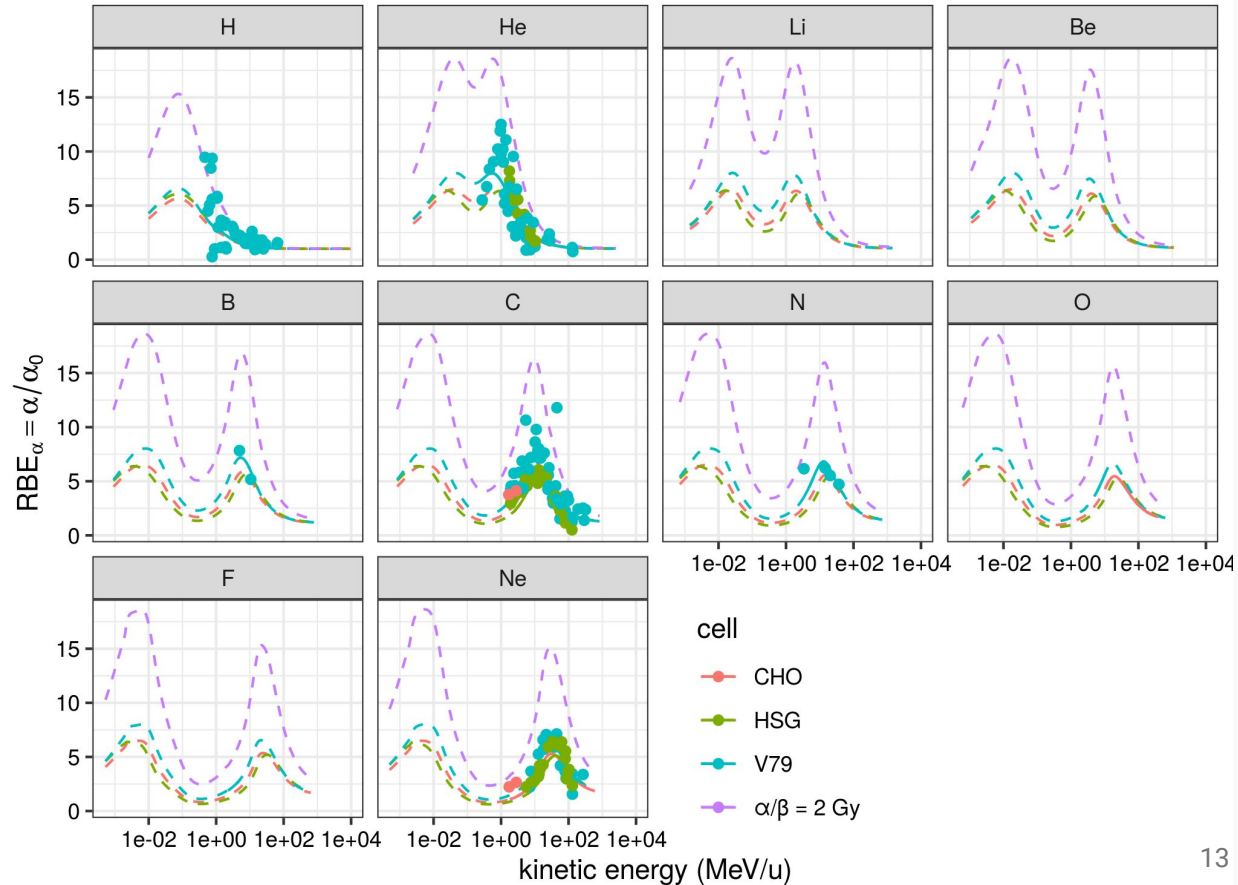


Choice of cell/model parameterization

cell	$\alpha_0 \sim \alpha x$ (Gy ⁻¹)	$\beta_0 \sim \beta x$ (Gy ⁻²)	rN (μm)	rd (μm)
$\alpha/\beta = 2$ Gy	0.1	0.05	4.5	0.35
HSG	0.313	0.0615	4.1	0.34
V79	0.184	0.02	4.1	0.26
CHO	0.3698	0.0706	5	0.3698

[Parameters from: Kase, Y., *et al.* (2008).
Biophysical calculation of cell survival
probabilities using amorphous track
structure models for heavy-ion irradiation.
Phys. Med. Biol., 53(1), 37–59.

Experimental data taken from PIDE v3.1
(Friedrich, T. *et al.*, 2019)]

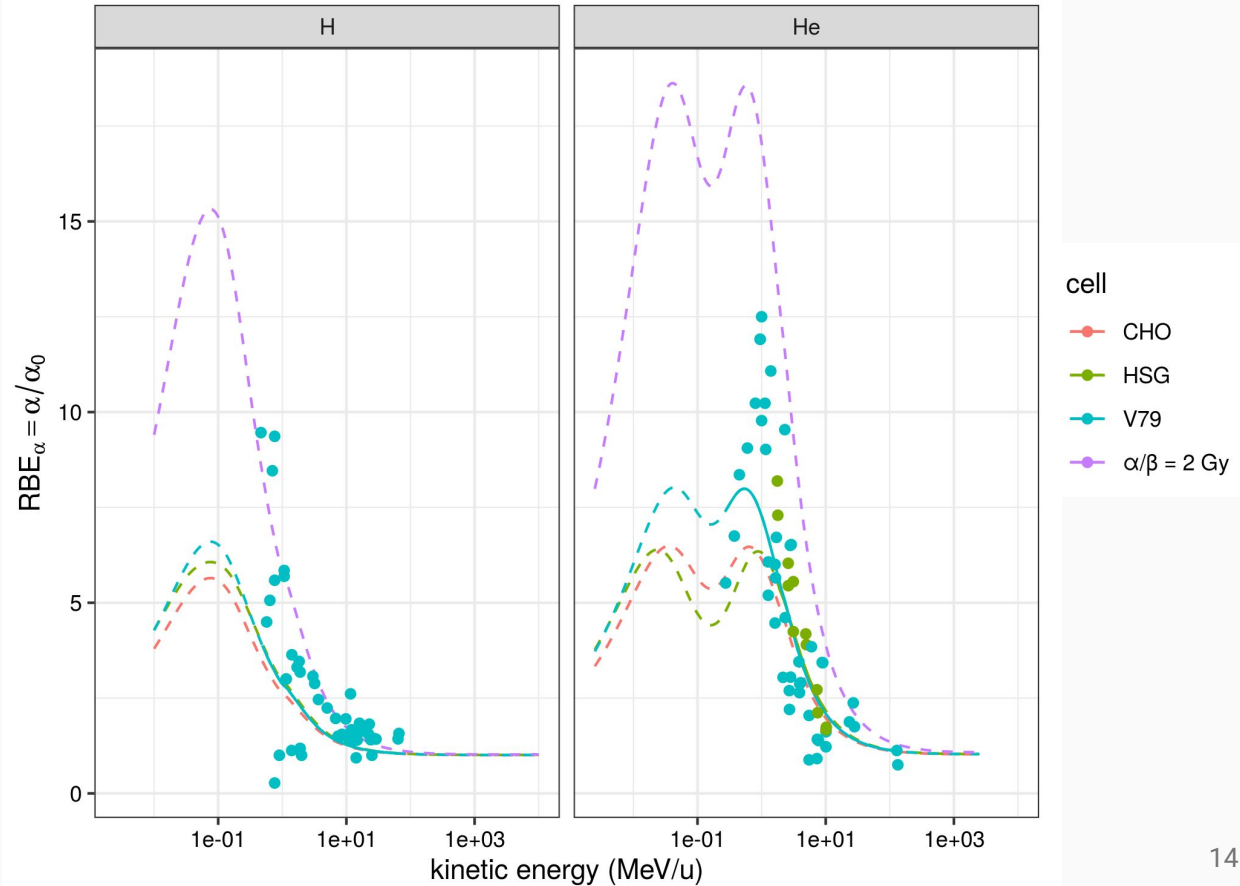


Choice of cell/model parameterization

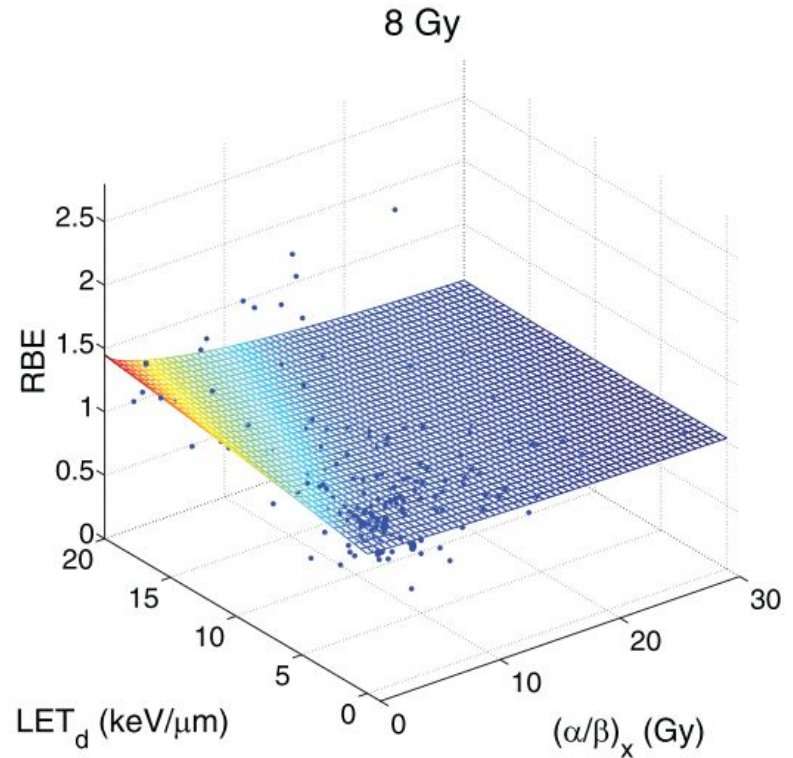
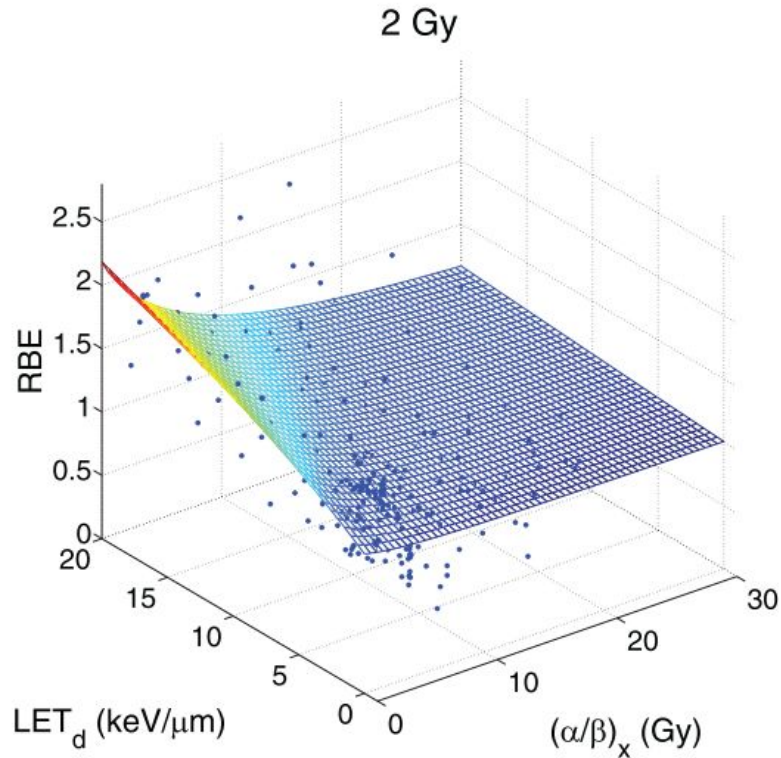
cell	$\alpha_0 \sim \alpha_x$ (Gy ⁻¹)	$\beta_0 \sim \beta_x$ (Gy ⁻²)	rN (μm)	rd (μm)
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Phys. Med. Biol., 53(1), 37–59.

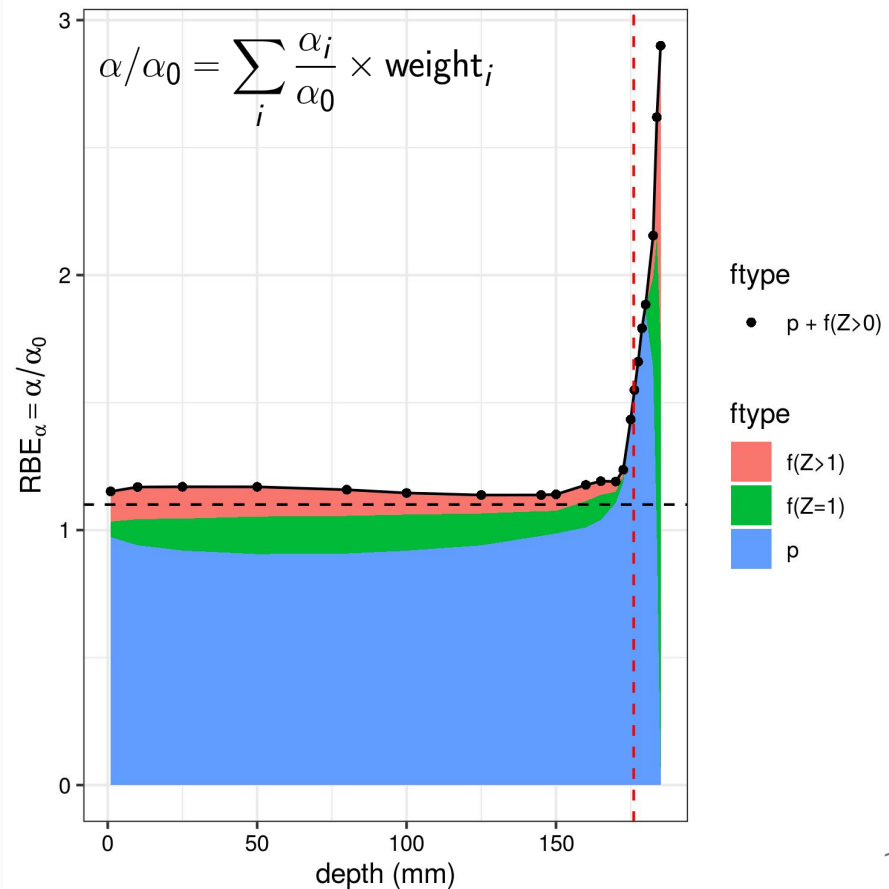
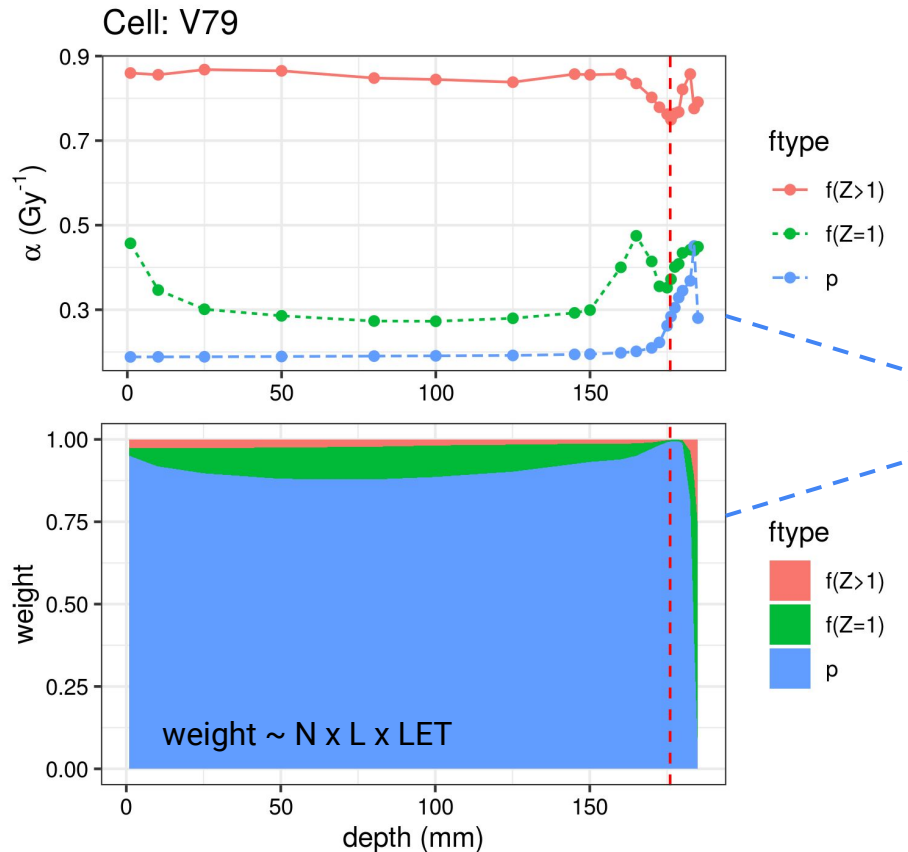
Experimental data taken from PIDE v3.1
(Friedrich, T. *et al.*, 2019)]



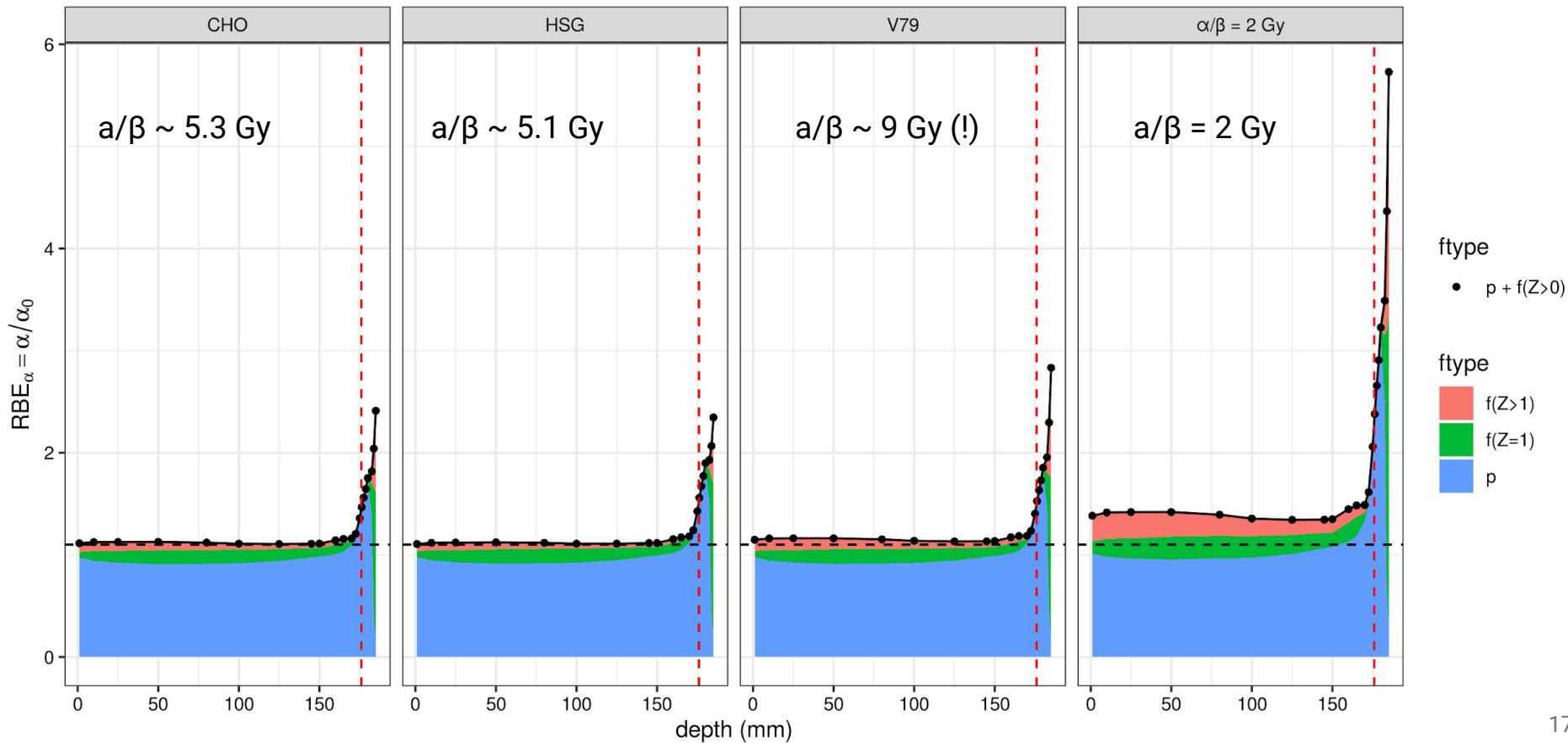
RBE vs. LET and α/β ratio



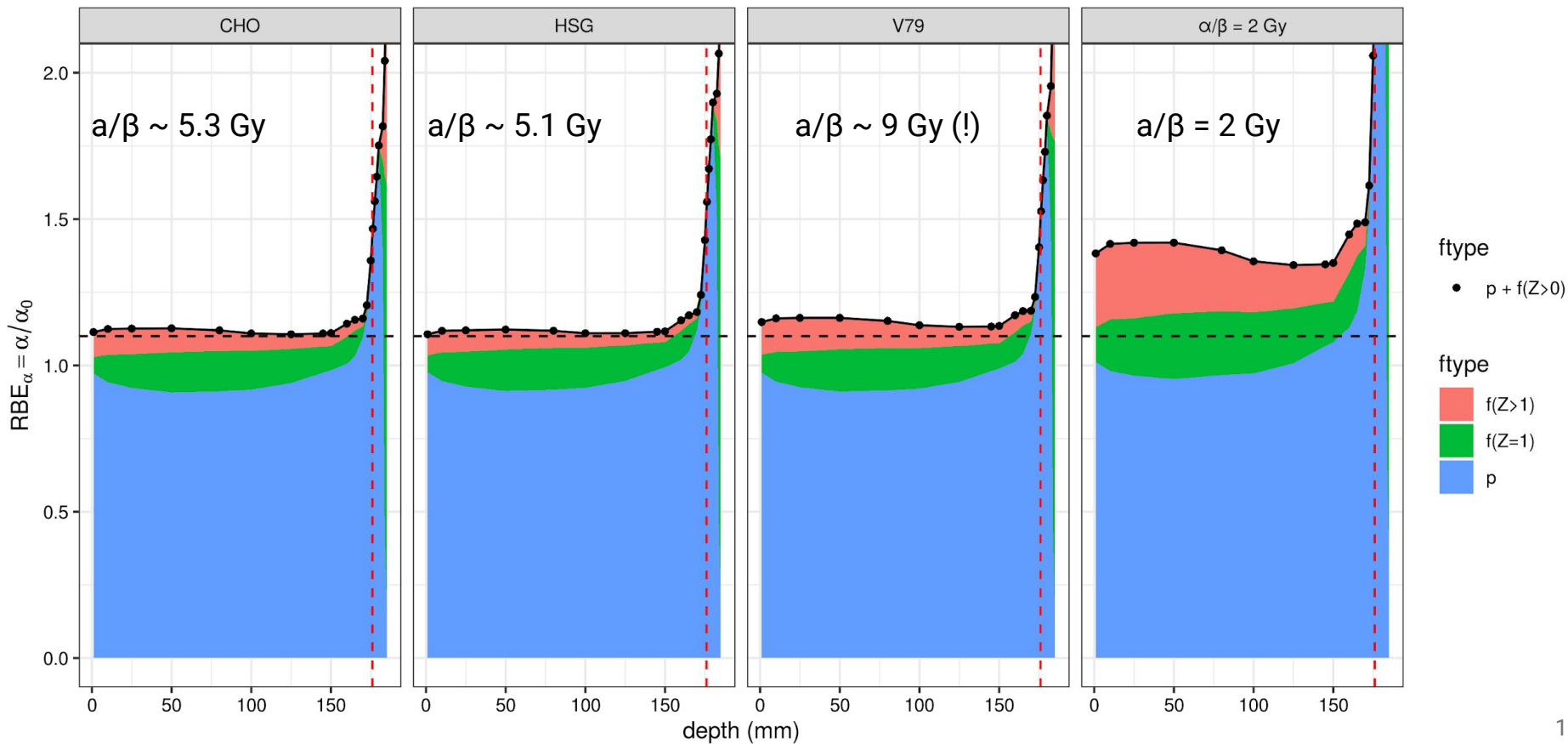
RBE contributions vs. depth (proton beam @ 160 MeV)



RBE contributions vs. depth, different cells



RBE contributions vs. depth, different cells (zoom in)



RBE, different cells (160 MeV proton beam, 10 mm)

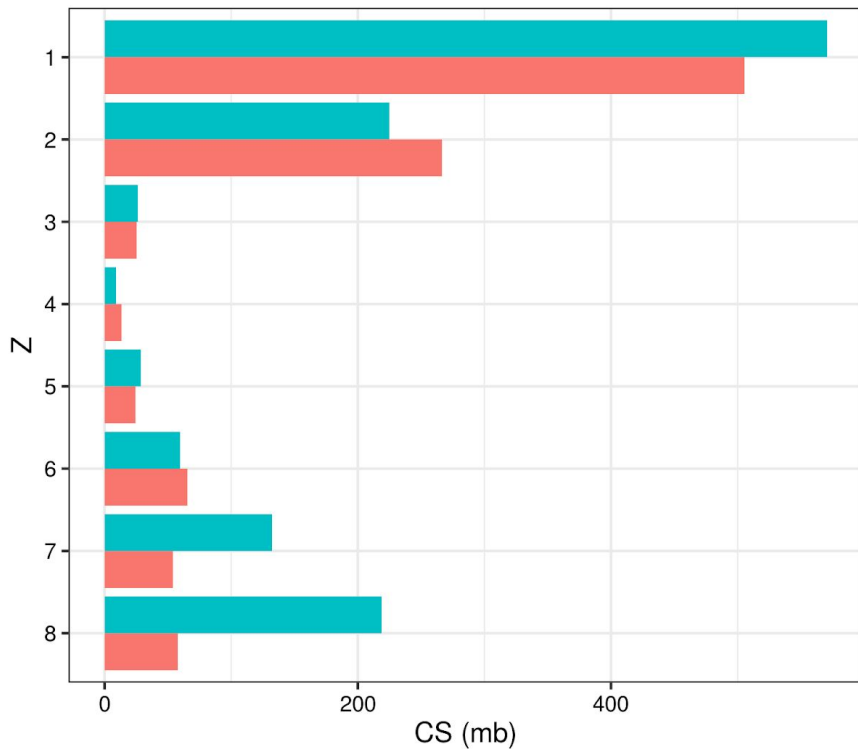
Cell	f _{type}	weight	RBE _α
HSG	f(Z>1)	0.03	2.97
	f(Z>0)	0.08	2.20
	f(Z=1)	0.05	1.81
	p + f(Z>0)	1.00	1.12
	p + f(Z=1)	0.97	1.07
	p	0.92	1.03

Cell	f _{type}	weight	RBE _α
CHO	f(Z>1)	0.03	3.55
	f(Z>0)	0.08	2.34
	f(Z=1)	0.05	1.74
	p + f(Z>0)	1.00	1.13
	p + f(Z=1)	0.97	1.06
	p	0.92	1.02

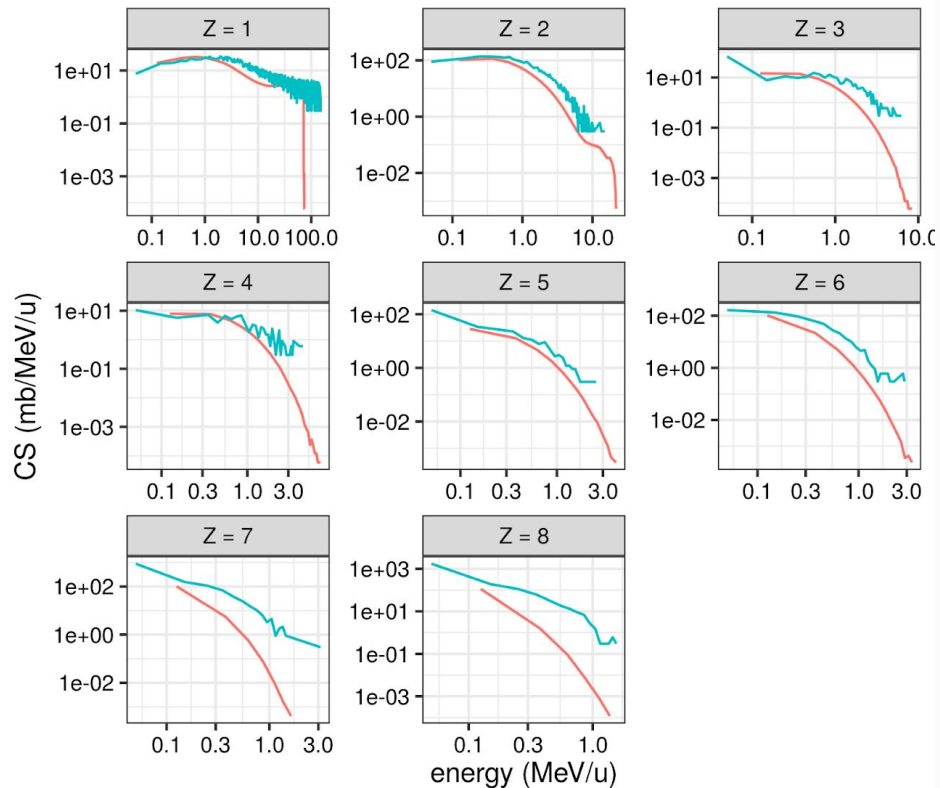
Cell	f _{type}	weight	RBE _α
V79	f(Z>1)	0.03	4.65
	f(Z>0)	0.08	2.80
	f(Z=1)	0.05	1.88
	p + f(Z>0)	1.00	1.17
	p + f(Z=1)	0.97	1.07
	p	0.92	1.02

Cell	f _{type}	weight	RBE _α
α/β = 2 Gy	f(Z>1)	0.03	10.49
	f(Z>0)	0.08	5.68
	f(Z=1)	0.05	3.28
	p + f(Z>0)	1.00	1.44
	p + f(Z=1)	0.97	1.19
	p	0.92	1.06

Cross Section (CS) estimates

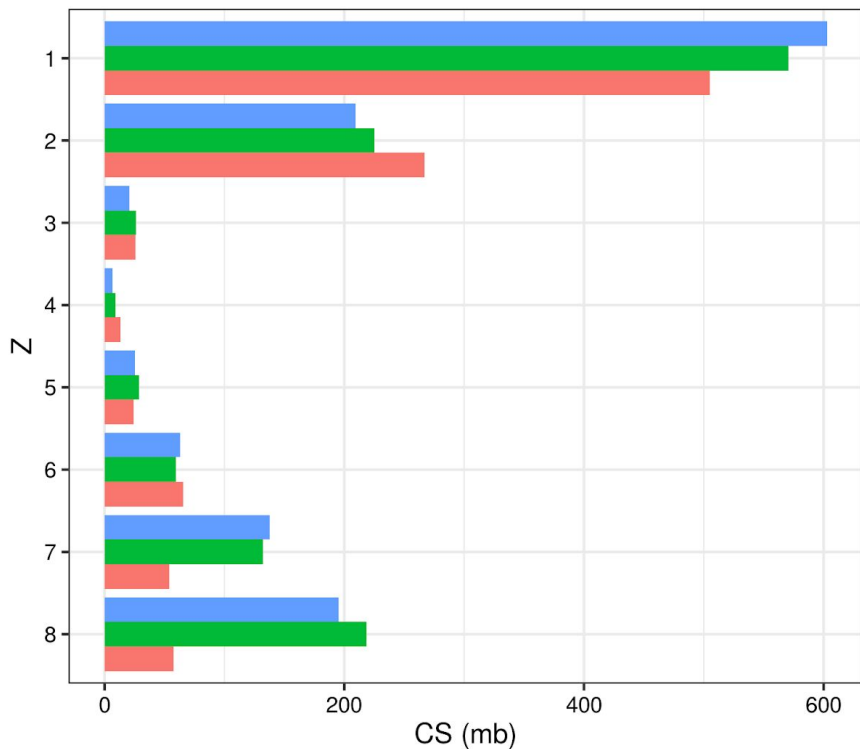


tool ■ fluka (150 MeV) ■ geant4 (150 MeV)

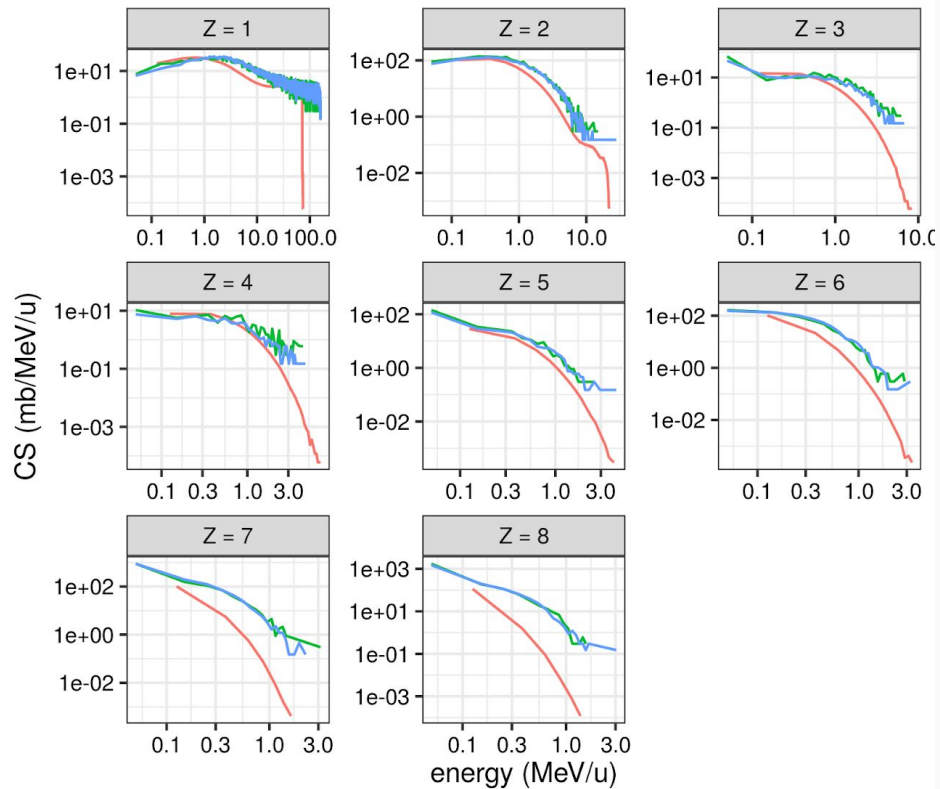


tool — fluka (150 MeV) — geant4 (150 MeV)

Cross Section (CS) estimates

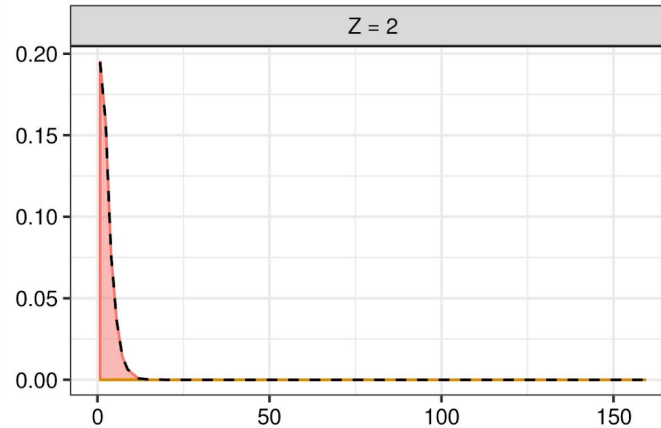
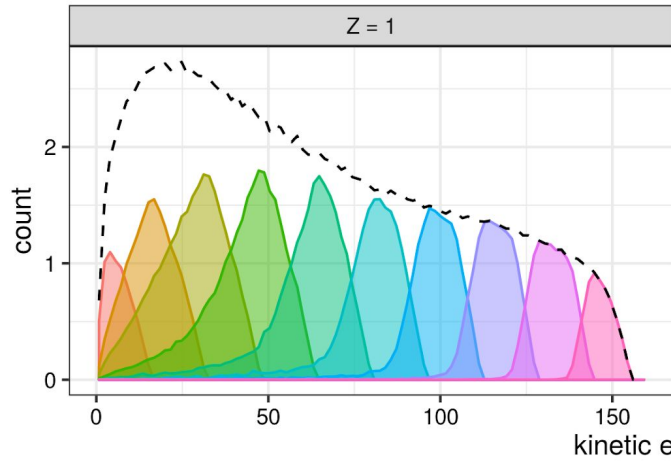
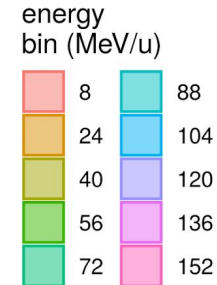
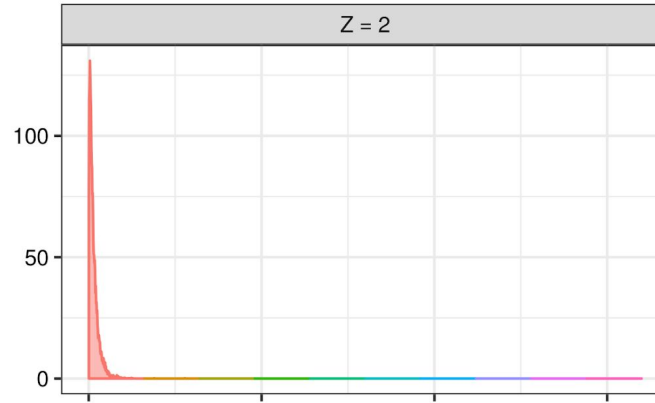
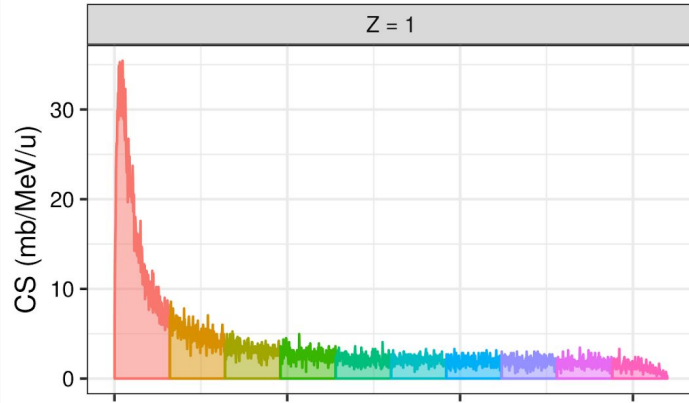


tool ■ fluka (150 MeV) ■ geant4 (150 MeV) ■ geant4 (160 MeV)



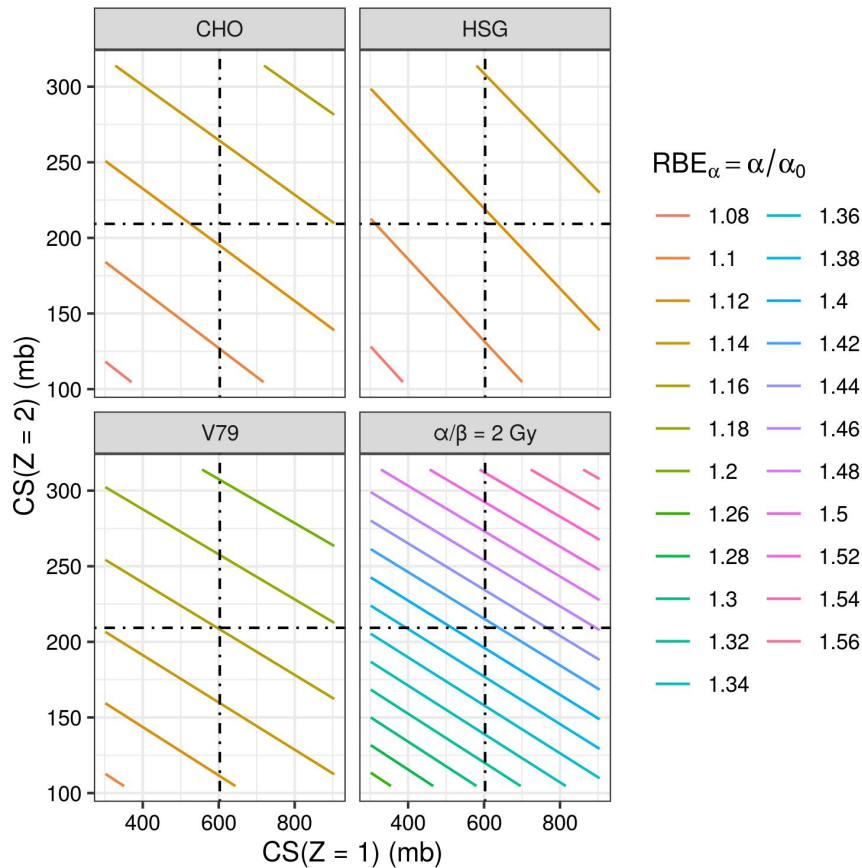
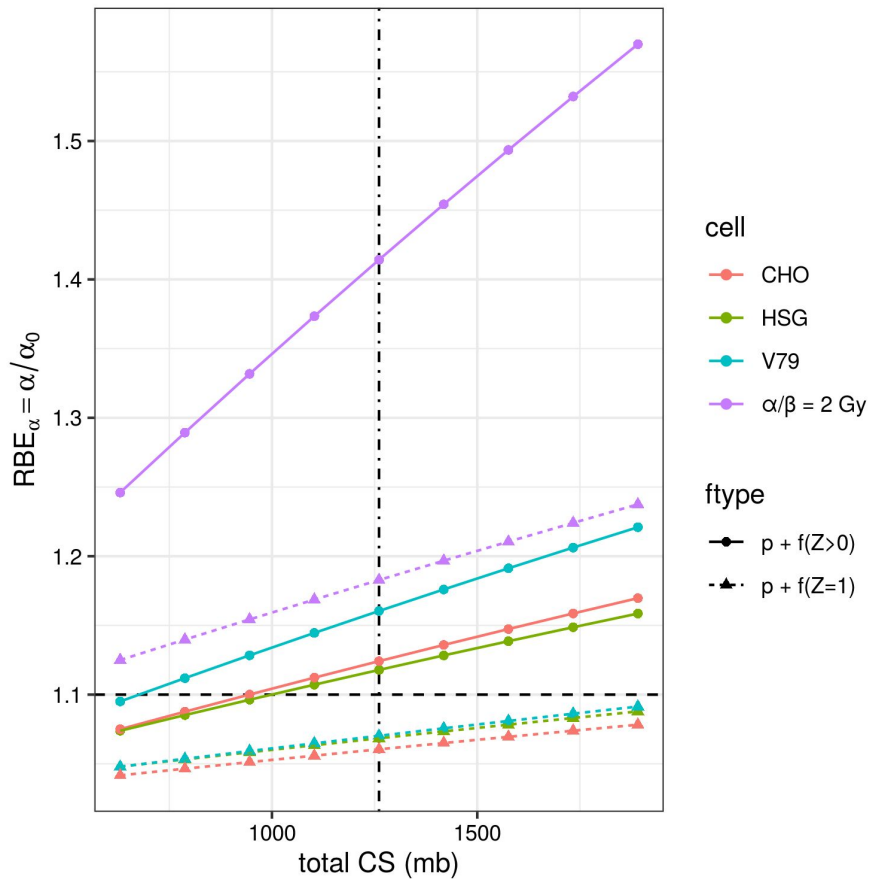
tool — fluka (150 MeV) — geant4 (150 MeV) — geant4 (160 MeV)

RBE vs. CS - energy components (evaluated at 10 mm)

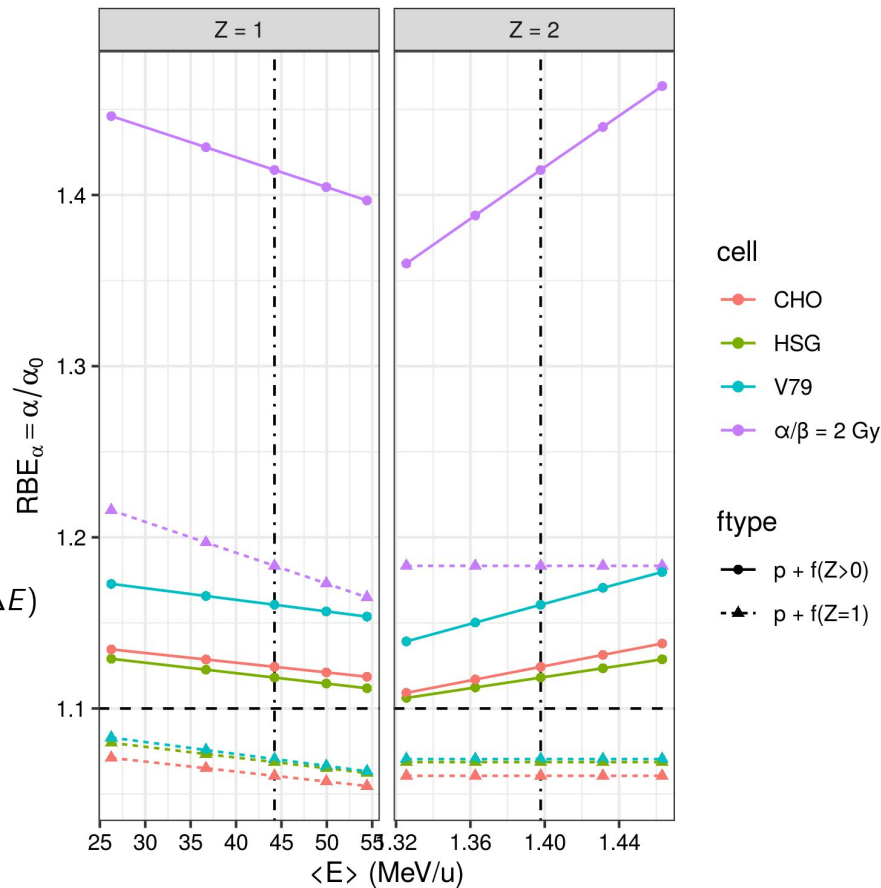
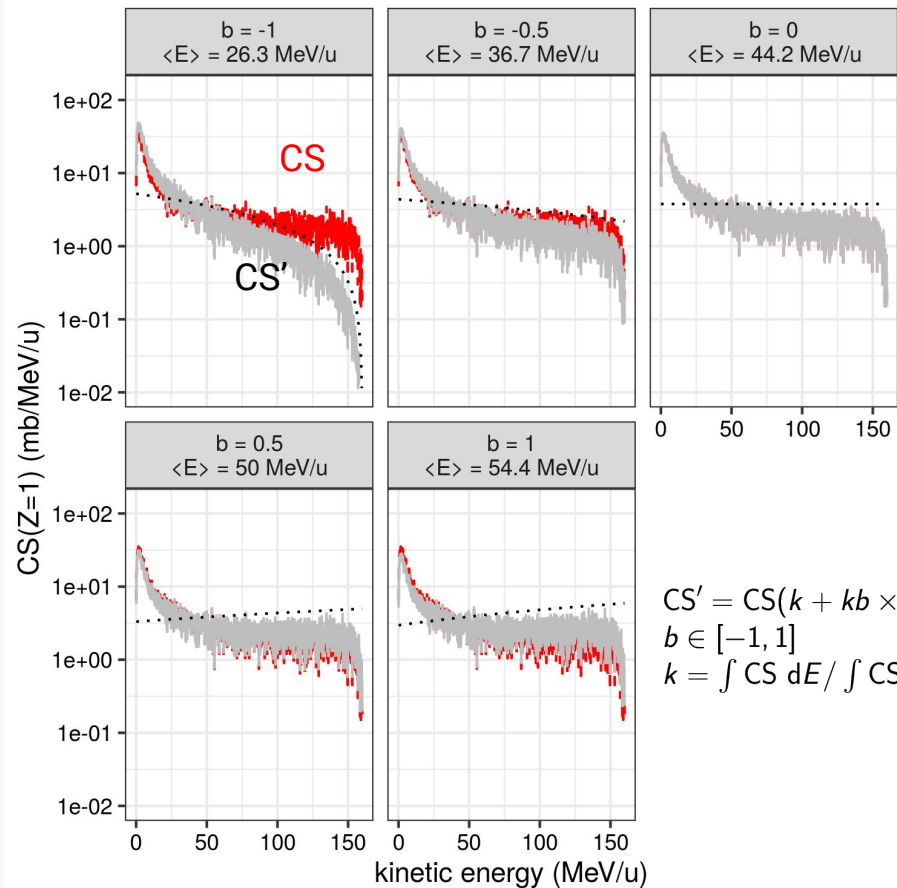


Z = 1,2 energy components of CS tracked in cell nucleus

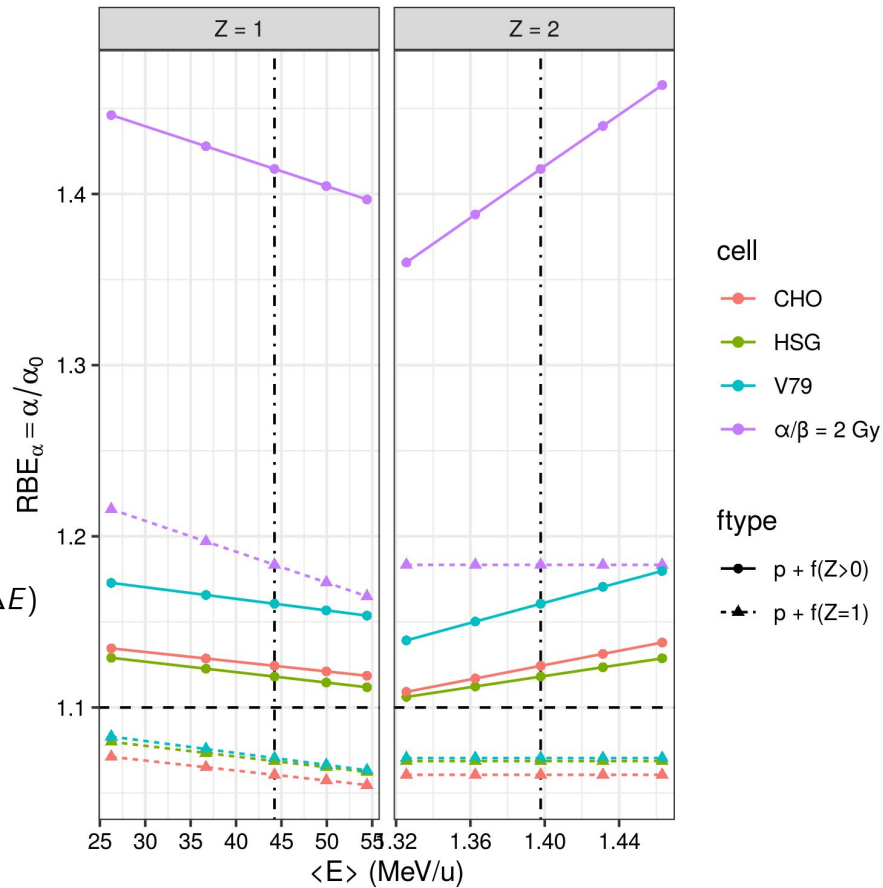
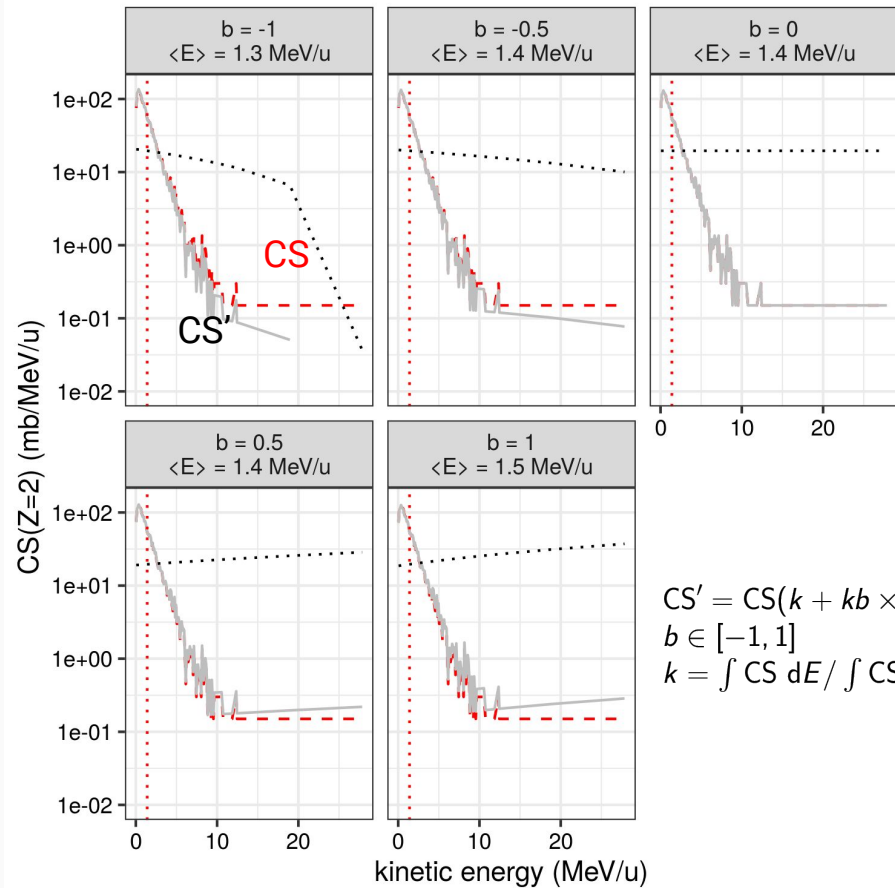
RBE vs. total and partial CS (evaluated at 10 mm)



RBE vs. differential CS (evaluated at 10 mm)



RBE vs. differential CS (evaluated at 10 mm)



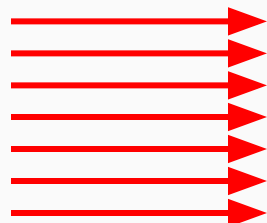
Field size effects on the RBE (evaluated at 10 mm)

pencil beam source

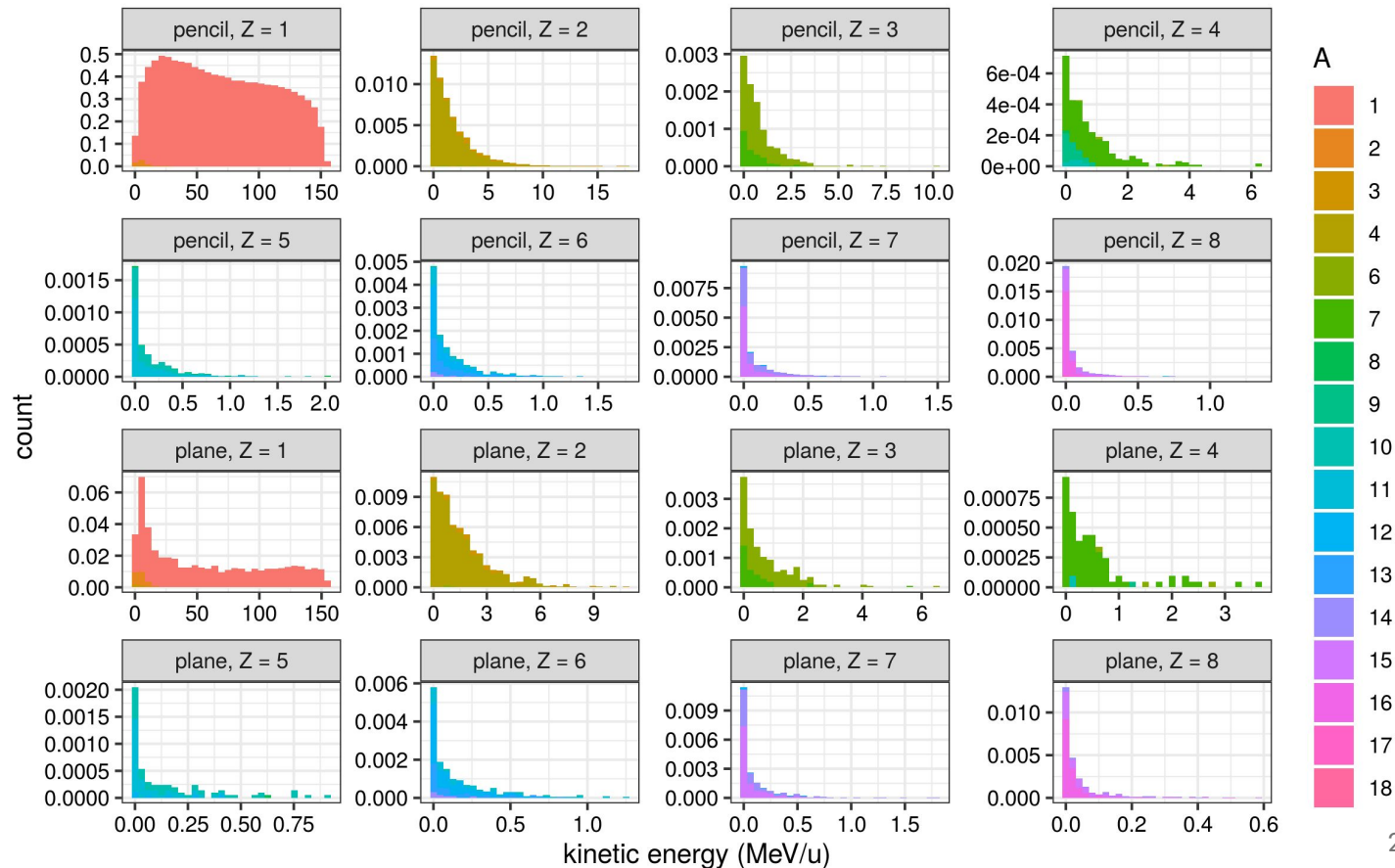


protons @ 160 MeV

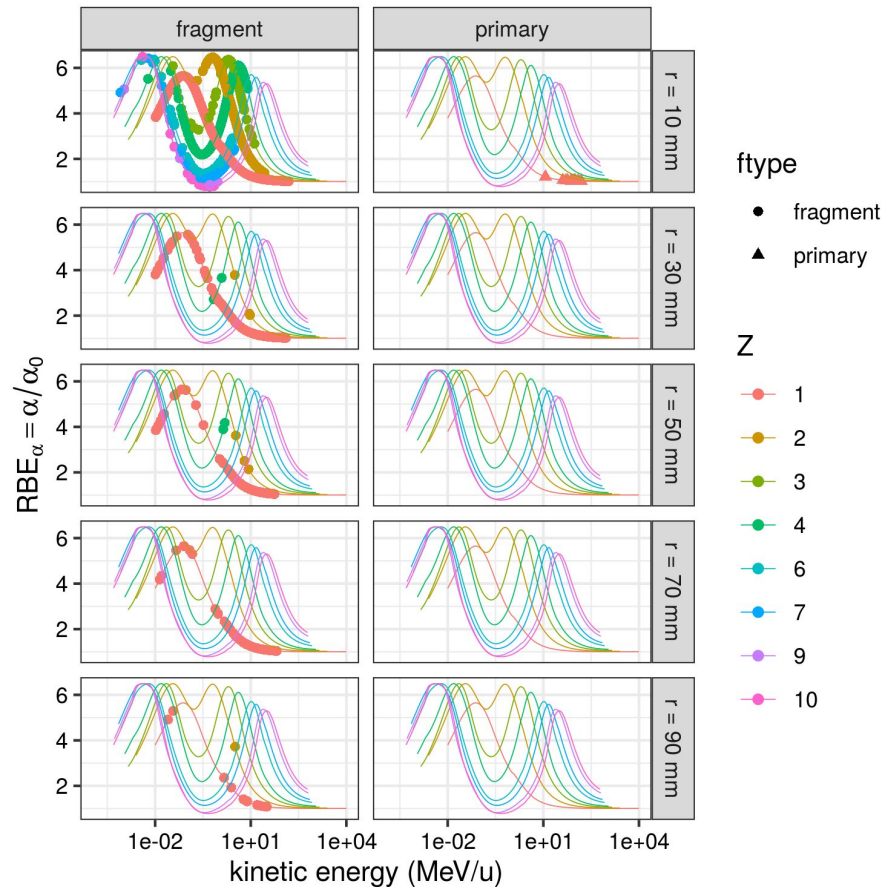
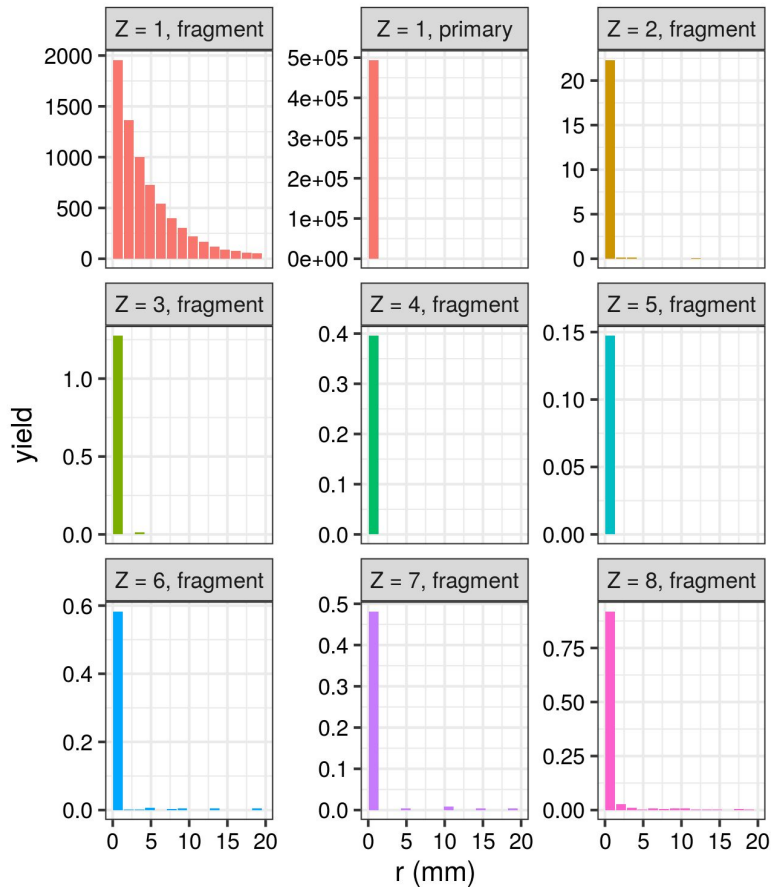
“plane” beam source



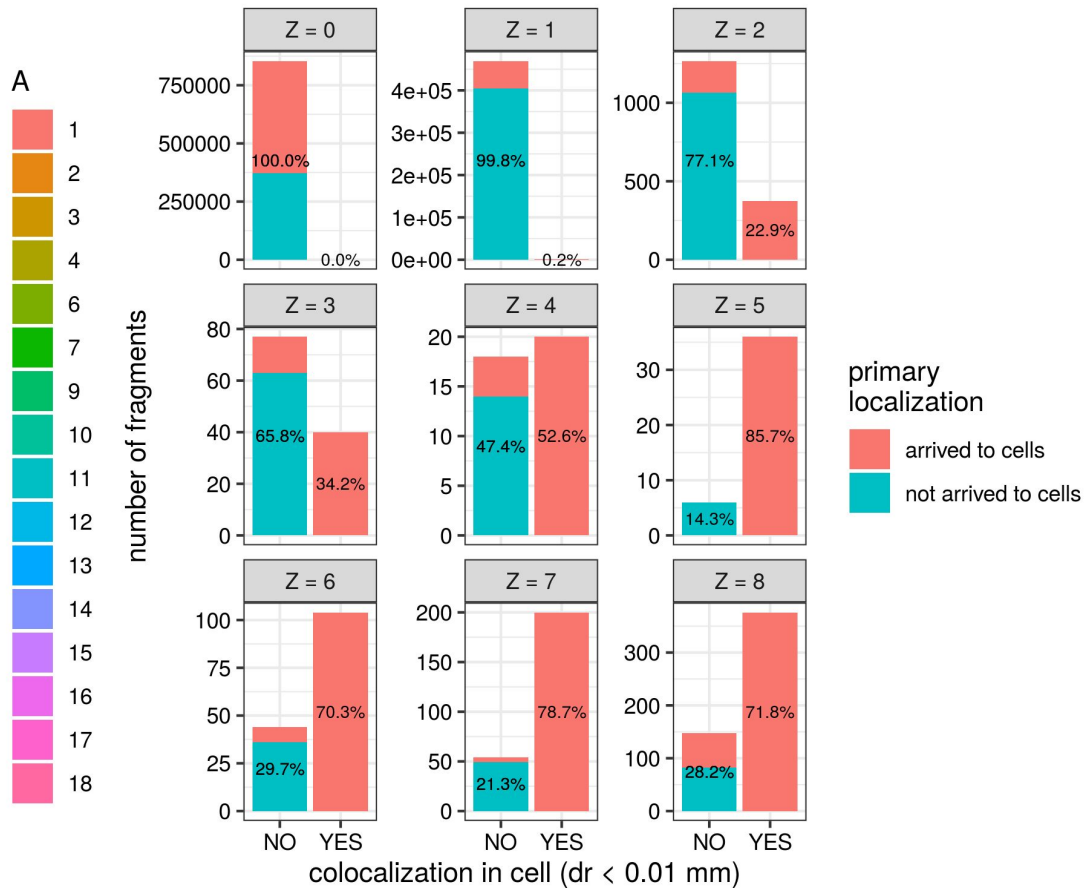
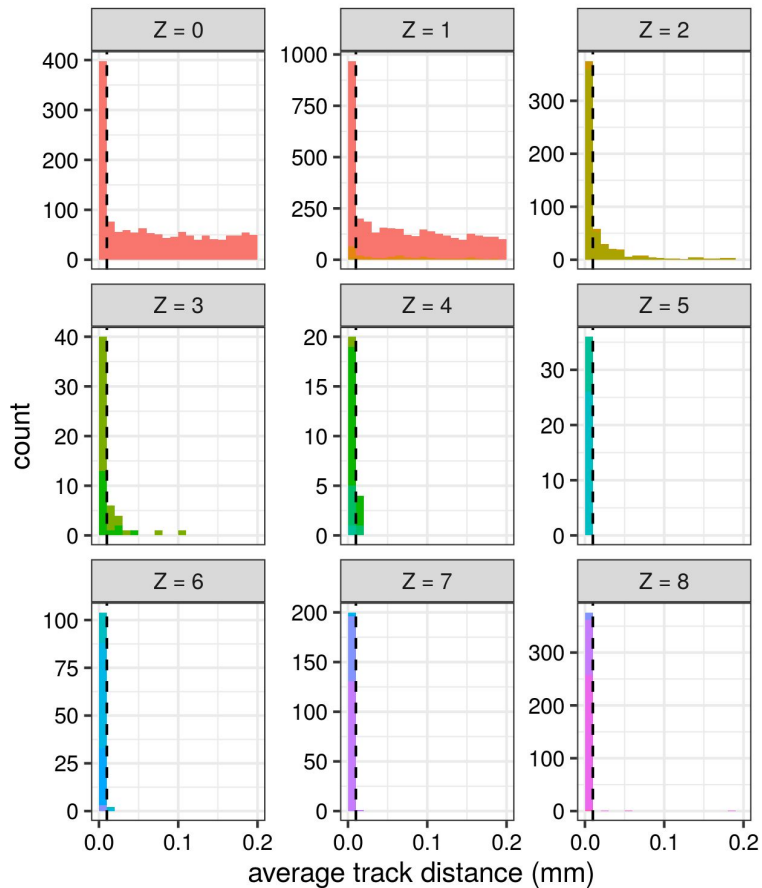
protons @ 160 MeV



RBE radial dependence (evaluated at 10 mm)



Pair distribution for tracks (evaluated at 10 mm)



Conclusions

- We implemented a “MICRO” MC simulation using a thin mobile monolayer of voxels ($10 \times 10 \times 10 \mu\text{m}^3$) to sample the microscopic energy deposition in cell nuclei volumes.
- We have observed a sensible RBE contribution (RBE=1.12-1.44) from target fragmentation ($Z=1$ and $Z>1$, from water molecules) using 160 MeV protons and the “nominal” CSs implemented in MC codes (geant4 & fluka) combined with a MKM-based radiobiological evaluation.
- A RBE sensitivity analysis on the production CS (total and differential) shows:
 - interplay between LET and range of fragments.
 - dependence on the specific cell line.
 - higher sensitivity for cells with low α_x/β_x ratio.
- Geometrical conditions of the irradiation and the field size effects might play a role.

Next steps

- Extension of existing radiobiological models to better account for:
 - inapplicable track segment conditions (inclusion of track length in LEM and MKM).
 - tracks colocalization in cell (MC approach for both LEM and MKM).
- Study of Oxygen fragmentation.
- RBE vs. total and differential CS for complete irradiated 3D volume (monoenergetic beams, SOBP → patient, using Trip98/RPlanit).



- Later on...substitution of “nominal” CSs implemented in MC codes with the experimental CSs from FOOT experiment.