

# Incorporating biological factors in radiation therapy treatment planning

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- ► Main therapeutic advantage: *Bragg peak* in energy deposition
- Most of the energy is deposited toward the end of its trajectory in a sharp peak
- Advantageous in IMPT as the energy and intensity of individual pencil beams can be manipulated to deposit a highly conformable dose to the tumour volume, with a low dose on entry and no exit dose





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- May be quantified through various biological endpoints
- Quantification of radiobiological effects can be incorporated into treatment plan optimization algorithms
- Seek a dose distribution that is both physically and biologically favourable





# Definition

Relative Biological Effectiveness (RBE): the dose delivered using a specific modality and energy that yields the same biological effect as a reference dose in a reference modality;

$$RBE_{} = \frac{Dose \text{ of reference radiation}}{Dose \text{ of test radiation}}.$$
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- In-vivo prediction of the RBE, however, is required for radiation therapy
- In-vitro cell data on its own is unsatisfactory





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### Definition

Restricted RBE for complex damage: ratio of the number of DSBs in the modality of interest to the number generated in a reference modality depositing the same dose;

$$RBE_{cd} = \left(\frac{\#DSB \text{ induced by test radiation}}{\#DSB \text{ induced by test radiation}}\right)_{same \text{ dose}}.$$



(2)



Modeling DNA damage Linear energy transfer (LET)

 Differential loss of kinetic energy over distance given by stopping power (dE/dl)



Figure: Image cropped from Fig 1 in [Lomax et al., 2013].

Modeling DNA damage Linear energy transfer (LET)

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Modeling DNA damage Linear energy transfer (LET)

- Differential loss of kinetic energy over distance given by stopping power (dE/dl)
- Microdosimetry: linear energy transfer (LET) is used instead – which is stopping power but with energy delivered to highly energetic knock-on electrons subtracted
- Density of ionisations along track can therefore be measured using LET and is closely related to the kinetic energy of the particle



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Figure: Image cropped from Fig 1 in [Lomax et al., 2013].

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Modeling DNA damage Single particle interaction model

Approximate a section of the DNA as a cylinder





Modeling DNA damage Single particle interaction model

- Approximate a section of the DNA as a cylinder
- ► Use the energy dependent mean free path λ(E) between successive ionisations to determine the distribution of clustered lesions [Van den Heuvel, 2014]



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Modeling DNA damage Single particle interaction model

- Approximate a section of the DNA as a cylinder
- ► Use the energy dependent mean free path λ(E) between successive ionisations to determine the distribution of clustered lesions [Van den Heuvel, 2014]
- ► Angular dependence: larger θ ⇒ longer path through DNA ⇒ higher LET and greater likelihood of inducing clustered damage









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Problem is equivalent to setting an isotropic point source at the boundary of the cylinder







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- Reduces mathematically to that of the distribution of projections of a point source on a line-piece







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- Reduces mathematically to that of the distribution of projections of a point source on a line-piece
- Solution: Cauchy distribution







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Modeling DNA damage Single particle interaction model

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- Damage response function: expected yield of DSBs given by [Van den Heuvel, 2014]

$$F_{\rm cd}(E) = (a-b)\frac{2}{\pi} \left[ \tan^{-1} \left( \frac{E-E_0}{\Gamma/2} \right) \right] + b \quad (3)$$







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► Units: Gbp<sup>-1</sup>Gy<sup>-1</sup>







Modeling DNA damage Single particle interaction model

▶ Parameters *a*, *b*,  $\Gamma$ , and *E*<sub>0</sub> fitted through a two-stage  $\chi^2$  minimisation



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Modeling DNA damage Single particle interaction model

- ▶ Parameters *a*, *b*,  $\Gamma$ , and *E*<sub>0</sub> fitted through a two-stage  $\chi^2$  minimisation
- ▶ 1. Differential Lorentz distribution  $dF_{cd}/dE$







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Modeling DNA damage Single particle interaction model

- $\blacktriangleright$  Parameters  $a,~b,~\Gamma,~{\rm and}~E_0$  fitted through a two-stage  $\chi^2$  minimisation
- ▶ 1. Differential Lorentz distribution  $dF_{cd}/dE$
- > 2. Cumulative Cauchy distribution  $F_{cd}$
- Good agreement with microscopic Monte Carlo software MCDS [Semenenko and Stewart, 2004]

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Monte Carlo





Dose deposited in each voxel D[i, j.k] of the patient CT



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Figure: Image from Figure 6(b) in [Van den Heuvel, 2014].

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- Yield of complex damage M<sub>cd</sub>[i, j, k] can be calculated using the response function

$$\mathsf{M}_{\mathsf{cd}}[i,j,k] = \mathsf{D}[i,j,k] \times \frac{\int_{\mathbf{0}}^{E_{\max}[i,j,k]} \Psi_{ijk}(\mathcal{E}) \mathcal{F}_{cd}(\mathcal{E}) d\mathcal{E}}{\int_{\mathbf{0}}^{E_{\max}[i,j,k]} \Psi_{ijk}(\mathcal{E}) d\mathcal{E}}$$
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 $RBE_{cd} = M_{cd,p}/M_{cd,\gamma}$ (5)

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Further considerations Oxygen level modeling

 Amount of oxygen binding that can occur has a saturation behaviour





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Further considerations Oxygen level modeling

- Amount of oxygen binding that can occur has a saturation behaviour
- Can be modeled using second order D.E. [Kepner, 2010; Van den Heuvel, 2014]

$$\frac{(d^2y/dx^2)dx}{(dy/dx)} = N\left(\frac{dy}{y}\right) - M\left(\frac{dx}{x}\right) \qquad (6)$$

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Further considerations

$$\frac{(d^2y/dx^2)dx}{(dy/dx)} = N\left(\frac{dy}{y}\right) - M\left(\frac{dx}{x}\right)$$
(6)

 In hypoxic conditions, only low-level damage component is reduced









Electronic build-up in entrance channel



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- Otherwise, energy spectrum weakly dependent on depth









Weak depth dependence seen in proton beam



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- Weak depth dependence seen in proton beam
- Resulting difference between electron-induced complex damage yield almost constant
- Consequence: only need to measure proton spectra
- In Monte Carlo, can calculate F<sub>cd</sub>(E) on the fly for each history instead of obtaining a spectrum explicitly







 Use density functional theory (DFT) to obtain electron distribution in small (10bp) segment of B-DNA







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- Calculate electrostatic potential map
- Find cross-section from scattering through Born series
- Second term in expansion is proportional to probability of two ionisation events within 10bp. This is labelled a DSB
- Use more terms for more clustered damage







Summary of project aims

Refine physical DNA-damage model





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- Refine physical DNA-damage model
- Incorporate RBE into TPS on a voxel-by-voxel basis for proton and other particle (e.g. helium ion, carbon ion) therapies
- Provide algorithmic framework for fast IMPT optimization (PTV- and robustness-based) which includes constraints on the RBE distribution.





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