Investigating ionisation cluster size distribution due to sub-1 keV electrons in view of Heisenberg’s Uncertainty

B Li\textsuperscript{1,2,\ast}, H Palmans\textsuperscript{1}, L Hao\textsuperscript{1} and A Nisbet\textsuperscript{2,3}

\textsuperscript{1} National Physical Laboratory, Teddington, Middlesex TW11 0LW, U.K.
\textsuperscript{2} The Department of Physics, University of Surrey, Guildford GU2 7XH, U.K.
\textsuperscript{3} Royal Surrey County Hospital, Guildford, Surrey GU2 7XX, U.K.

E-mail: bo.li@surrey.ac.uk

Abstract. As the wavelengths of low energy electrons become comparable with the length scale of the mean ionisation step size, each event particle should be treated with care as the condition outlined in Heisenberg’s uncertainty principle (HUP) should also be satisfied. Within this quantum-classical regime, spatial delocalisations of individual ionisation event sites that are generated outside the target region are calculated, and particular attention is given to the validity of using classical transport methods in simulations of nanodosimetric parameters such as mean cluster size, first and second moments, variance and cumulative frequency of ionisation cluster-size probability distributions. This paper presents the comparison between conventionally calculated nanodosimetric quantities and the ones where interacting particles are treated semi-classically with spatial uncertainties satisfied by HUP. The simulated primary charged particles are electrons of energies between 100 eV and 1 keV in DNA equivalent target aqueous water volumes using GEANT4-DNA.

1. Introduction

High levels of cellular damages upon exposure to irradiation are thought to be initiated by low energy secondary electrons, typically of energies of a few hundreds eV [5, 13]. In view of radiation induced initial damage to biologically sensitive targets, typical studied volumes are of biological equivalence to segments of DNA of 10 base pairs [3, 7] has shown that electrons of a few hundreds eV yield the highest number of double-strand breaks in the DNA, which can be explained as the probability of electron-induced ionisation clusters greater than 2 also peaks for initial electron energies of a few hundred eV [6].

In the frame of radiation transport modelling, methods that are generally used for macroscopic target sizes such as condensed theory methods are no longer applicable for target sizes approaching the biological sensitive volumes, typically of a few nanometres. When the target volume of interest is reduced, the occurrences of particle interactions are considered as stochastic. Most computational studies of radiation track structure are achieved by event-driven simulations based on Monte Carlo methods, such as GEANT4-DNA, where each particle is treated as a classical object with precisely known position and energy. In contrary to the multiple scattering theories used in condensed history methods, each particle in the track-structure simulations is treated individually with discretisation of interaction events. However, care should be taken in the use of these ‘classical’ track-structure codes

\ast To whom any correspondence should be addressed.
as dimensions of the target volume approach nanoscale, as well as energies of interest (i.e. ionisation energies of liquid water) enter the sub-1keV range [1,15]. This is due to spatial delocalisation in the location of the interaction sites, which is dependent on the velocity and the energy loss of the interacting particle [10].

2. Background
2.1. Quantum limit of classical mechanics
In the quantum limit of classical mechanics, the product of Δx and Δp will approach the quantum limit at $\hbar$ [4], where quantum quantities Δx and Δp are the delocalisation in position and uncertainty in momentum respectively. For singular events such as the individually calculated interaction event by the Monte Carlo methods, the associated position uncertainty depends on the interacting particle’s initial velocity $v_x$ and the energy deposition $\Delta E$ of the associated interaction event. This relation is shown by Kaplan and Miterev [10] as, 

$$\Delta x \geq \frac{\hbar v_x}{\Delta E}$$

(1)

Two conditions must be simultaneously satisfied for the classical treatment of particles to remain as valid. First, the particle’s associated spatial delocalisation must be greater or equal to $\Delta x_c$. And second, $\Delta x_c$ must be small with respect to the mean free ionisation (the interaction of interest for radiobiological studies) path length $\lambda_{ion}(T)$ of electrons in aqueous water, at a given energy $T$ of interest. I.e. $\Delta x_c < \lambda_{ion}(T)$. Typical electron ionisation path lengths in liquid water $\lambda_{ion}(T)$ increase steadily from ~1.5 nm at electron energy of 100 eV to ~3.8nm for 1 keV electrons. A small local minimum occurs at electron energy of ~150 eV at step length of ~1.4 nm.

2.2. Nanodosimetric parameters of track structure
The propagation of a charged particle at initial energy $T$ through a target volume of given geometry dimension and composition $G$, the ionisation cluster-size probability distribution can be written as $P_\nu(T;G)$. This describes the probability that exactly $\nu$ number of ionisations is produced within a predefined target volume, where $\nu$ is defined as the number of ionisation event counts per single track of a primary charged particle. The mean ionisation cluster number of the distribution $P_\nu(T;G)$ is known as the first moment $M^1_{\nu}(T;G)$, and will be referred to as the mean cluster size hereforth. This can be calculated according to the generic equation, where $\zeta$ denotes the order of moment, as shown in equation 2.

$$M^\zeta_{\nu}(T;G) = \sum_{\nu=0}^{\infty} \nu^\zeta P_\nu(T;G)$$

(2)

The stochastic fluctuations on the number of ionisation formation within microscopic target volumes can be characterised by the variance $V_{rel}(T;G)$ of the distribution $P_\nu(T;G)$. This is proposed by Fano as the quotient of the variance and the mean of the cluster-size distribution, shown in equation 4.

$$V_{rel}(T;G) = \frac{M^2_{\nu}(T;G) - M^2_{\nu}(T;G)}{M^2_{\nu}(T;G)}$$

(3)

Another nanodosimetric parameter that is examined in this paper is the cumulative probability $F_2(T)$. This is defined as the probability for the primary electron to undergo at least two ionisation interactions within the target volume. It is thought that this quantity could be related to the probability of the formation of double strand breaks within DNA segments [8,14].

$$F_2(T) = \sum_{\nu=2}^{\infty} P(\nu|T;G)$$

(4)
3. Methods

3.1. Simulation of ionisation cluster formation in biologically equivalent DNA target volumes

Low electromagnetic package GEANT4-DNA version 10.0.0 is used to obtain ionisation cluster distributions in this paper. Detailed description of the simulation packages can be found in the literature \[9,11\].

The simulated environment consisted of a cube of liquid-filled world volume. The side length of the cube is chosen to be greater than the electron total interactions range at given primary particle energy levels. A target cylindrical volume consisted of liquid water, which is biologically equivalent to a DNA segment of 10 base pairs, has dimensions of 2.3 nm diameter and 3.4 nm height. The target volume is placed in the center of the world volume. The use of nanodosimetric cylindrical liquid water environment to study nanodosimetric parameters has been a common practice \[5,12,13\].

Primary particles are initiated from the center of the target volume with momentum towards the positive z-direction (along the principal axis of the target cylinder). The center is defined as the point of half height of the target cylinder and at the origin with respect to its base plane.

Ionisation cluster-sizes are recorded per primary particle within the target volume in two ways. First, without the consideration of the spatial delocalisation constraint due to HUP, a bench mark ionisation cluster-size distribution is collected with well-defined target volume boundaries. In a second case, ionisation events that occur outside the defined target volume are also considered if their delocalised spatial range overlaps or enters the target region. The boundaries of the delocalised position are determined according to equation 1 given the coordinates of the interaction event and the initial velocity of the interacting particle. This will be referred to as HUP-cluster-size distributions.

4. Results and discussions

The average spatial delocalisations associated with ionisation events within the DNA-equivalent target region are calculated from equation 1 as 0.2615 nm and 0.726 nm for 100 eV and 1 keV electron primaries respectively. Despite the average increases in the ionisation energy deposition within the DNA equivalent target volume: from 12.55 eV to 13.73 eV for primary electrons of 100 eV and 1 keV respectively, the average velocity of the interacting particles at the ionisation sites has increased by a much larger proportion: from 4.81 mm/ns (for 100 eV primaries) to 14.33 mm/ns (for 1 keV primaries). This has resulted in the average increase in spatial uncertainties in ionisation interaction sites as electron primary energies increase from 100 eV to 1 keV, within the predefined nano-target volume. Mean free ionisation path length of electrons in liquid water is ~1.5 nm and ~3.8 nm for electron energy of 100 eV and 1 keV respectively. The spatial uncertainties associated with both energy levels are smaller, however, and are comparable, with respect to the mean ionisation free path length. This suggests that the simulated environment is in the quantum-classical regime and the constraint posed by HUP should also be satisfied for the classical treatments of particles to hold.

Figure 1 shows the cluster-size distribution of primary electrons due ionisation events in liquid water at two different initial energies T: 100 eV and 1 keV. In the case when T=100 eV, only 5% of the electron primaries as simulated in the HUP-cluster-size distribution received additional counts of ionisations from outside of the target volume. Within the total 5% of the affected primaries, the majority at 4.76% had an increase shift in cluster-size by one. The remaining 0.2% and 0.01% were contributed from two and three additional counts respectively. As seen from figure 1 the shape of the two cluster size distributions coincides very almost perfectly. The percentage difference between the two distributions with respect to the well-defined target boundaries (i.e. the conventional method of cluster-size definition) is also represented. It can be seen that their differences over most cluster sizes are below 0.1%. The slight increase in the tail at higher cluster size number is due to the skewed amplification of the difference from small sample sizes as larger cluster sizes become less probable. Similar results are seen for electron primaries of 1 keV. Here, the general shape of the probability distribution becomes logarithmic. This can be explained by the increase in ionisation mean free path for increase in electron energy in liquid water. As the ionisation mean free path becomes larger than the half height (primary electron is initiated from the half height) of the target volume, it is expected.
that most of the primary electrons do not undergo ionisation events and thus energy is transported out of the target region via primaries. The percentage discrepancies between the conventionally defined target volume simulation and the HUP-cluster-size distribution are also shown in figure 1. Again, it is seen that the two distributions overlay almost perfectly. Percentage differences between the two are even smaller than the case with 100 eV primary electrons.

Figure 2 shows the mean cluster sizes for the two methods in energy ranges from 100 eV to 1 keV. Discrepancies between the two distributions are below 3.5%. Furthermore, it is seen that these differences are not significant to change the general shape of the distributions. This can be seen in figure 3 as the percentage of variance difference fluctuates at ~1.5%. Similarly, there are no significant differences found in other nanodosimetric parameters: $M_2$, and cumulative frequency (figure 4). All of the above nanodosimetric parameters, including $M_1$ and ionisation cluster-size distributions show good agreement with other published results using the classical treatments [7,12].

**Figure 1.** This is the ionisation cluster-size probability distribution $P_\nu(T;G)$ for primary electrons at initial energy of 100 eV and 1 keV for both cases: conventional cluster-size distribution and HUP-cluster-size distributions.

**Figure 2.** shows the mean ionisation cluster size of primary electrons with energy $T$ from 100 eV to 1 keV.

**Figure 3.** This is the relative variance as calculated by equation 3 for primary electron energies from 100 eV to 1 keV.

**Figure 4.** The cumulative frequency $F_3(T)$ is shown (calculated from equation 4) for primary electron energies from 100 eV to 1 keV.
5. Results and discussions
It has been demonstrated in this paper that for electron primaries of energy between 100 eV -1 keV special care needs to be taken when studying their track structure at nanometer scale, using classical mechanics. This can be seen as the mean free ionisation path length is comparable with the spatial uncertainties of the particles that are involved with ionisation interactions in the defined DNA-equivalent target regions. Given the non-violation of Heisenberg’s uncertainty principle (HUP), which proposes constraints on the spatial and momentum uncertainties, nanodosimetric quantities are simulated using the Monte Carlo codes GEANT4-DNA. In particular, the studied nanodosimetric quantities are mean ionisation cluster-size distribution, first and second ionisation moment, and the ionisation variance as well as the cumulative frequency of the ionisation cluster-size distribution. The effect on the ionisation cluster-size based on the determination of each interaction’s associated spatial delocalisation (as given by HUP), as opposed to the conventional consideration of well-localised position is examined in this paper. It has been found that the ionisation cluster-size distributions for electrons of energy 100-1k eV do not show significant variation due to the inclusion of HUP, as their significant (discarding larger, improbable cluster sizes) percentage differences are only within 5%. It also follows that the other studied nanodosimetric parameters are relatively unaffected by the inclusion of HUP.

6. Acknowledgement
This work is funded by Biologically weighted Quantities in RadioTherapy (BioQuaRT), a Joint Research Project within the European Metrology Research Programme EMRP, Engineering and Physical Sciences Research Council U.K. (EPSRC) and NHS Invention for Innovation U.K. (i4i).

7. References
[1] Emfietzoglou D, Papamichael G, Kostarelos K, & Moscovitch M. 2000 Physics in Medicine and Biology, 45(11), 3171
[2] Fano U. 1947 Physical Review, 72(1), 26.
[3] Friedland W, Jacob P, Paretzke H G and Stork T. 1998 Radiation research, 150(2), 170-182.
[4] Gottfried K and Yan T M 2003. Springer Science & Business Media.
[5] Grosswendt B 2002. Radiation and environmental biophysics, 41(2), 103-112.
[6] Grosswendt B 2005. Radiation protection dosimetry, 115(1-4), 1-9.
[7] Grosswendt B 2006. Radiation protection dosimetry, 122(1-4), 437-445.
[8] Grosswendt B, Pszona S and Bantsar A. 2007 Radiation protection dosimetry, 126(1-4), 432-444.
[9] Incerti S, Baldacchino G, Bernal M, Capra R, Champion C, Francis Z, and Zacharatou C 2010 International Journal of Modeling, Simulation, and Scientific Computing, 1(02), 157-178.
[10] Kaplan I G and Miterev A M. 1985 Radiation Physics and Chemistry (1977), 26(1), 53-56.
[11] Ivanchenko V N, Incerti S, Francis Z, Tran H N, Karamitros M, Bernal M A, and Guèye P. 2012 Nuclear Instruments and Methods in Physics Research Section B: Beam Interactions with Materials and Atoms, 273, 95-97.
[12] Lazarakis P, Bug M U, Gargioni E, Guatelli S, Rabus H and Rosenfeld A B. 2012 Physics in medicine and biology, 57(5), 1231.
[13] Nikjoo H and Goodhead D T. 1991 Physics in medicine and biology, 36(2), 229.
[14] Rabus H and Nettelbeck H. 2011 Radiation Measurements, 46(12), 1522-1528.
[15] Thomson, R. M., & Kawrakow, I. 2011 Medical physics, 38(8), 4531-4534.