A Model of Histone Sliding with UV Dose Dependency

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We start with a description of DNA and histone loss from the damage region centered at the origin. Let R_0 be the radius of the damage region, and R the radius of the ROI at which chromatin expansion has reached saturation. Due to the radial symmetry of the model, we describe the histone and DNA loss in a radial manner. A chromatin strand will is considered to start at the origin and stretch in the positive x direction. We assume that the length of the chromatin compacted from the origin up to R_0 is l, on which n_0 histones are initially embedded. The damages caused by the UV light are considered to spread up to R_0. By sliding histone over this damage point, the chromatin to the left of the exterior damage point unpacks. After expansion has reached saturation, the chromatin in the damage region has reached R by extension resulting from the loss of histone by sliding. At this point, the length of the damaged chromatin remains l but the number of histones embedded in it is n. Let the ratio $n/n_0 = g$, and the expansion factor $R/R_0 = \beta$, we will describe the fraction of histone and DNA loss as a function of the UV dose, u, by

$$d(u) \quad = \quad \frac{\beta(u) - 1}{\beta(u)} \tag{1}$$

$$h(u) \quad = \quad d(u) + \frac{n_0 - n(u)}{(R(u)/R_0)n_0} = d(u) + \frac{1 - g(u)}{\beta(u)} \tag{2}$$

with $0 \leq n(u) \leq n_0$, and $u \geq 0$.

The contribution of sliding to the total histone loss is given by

$$h(u) - d(u) = \frac{1 - g(u)}{\beta(u)} \tag{3}$$

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