0.1 The biological process

0.2 The simulation framework

0.2.1 The simulation domain

A UV beam is shot vertically thorough the nucleus and considered to affect all chromatin in its path similarly. The simulation in therefore placed in a 2-dimensional domain. This is in-line with the experimental signal values, reported as values of a maximal z-projection [REF].

0.2.2 The polymer model

We use a cross-linked Gaussian chain [REF] of N monomers connected by harmonic springs to represent a coarse-grained model of the chromatin. Springs connecting adjacent monomers in the linear chain are assigned a minimal length L_0. Cross-linking are added randomly between pairs of monomers by a harmonic spring with minimal length zero. Cross-linking measure is given by the percentage α of non-nearest-neighbor monomers connected of the N monomers of the chain. In each realization of the simulation, a random set of non-nearest neighbor monomers is chosen for cross-linking, according to the value set for α. The cross-linked polymer is simulated up to relaxation time, at which time the UV beam is shot.

0.2.3 UV irradiation

At the end of relaxation steps, UV beam focal point is set to the polymer's center-of-mass. The damage region (DR) is represented by a 2-dimensional fixed circular region of area A_0 centered at laser's focal point. For each UV dose u, damages caused by UV are homogeneously distributed in A_0 [REF] among the polymer's monomers. Damaged monomers are chosen randomly, such that the average number of damages in A_0 increases as $k_t u$, with k_t in units of $bp/msec$.

Affect of UV irradiation on the polymer, the repair stage

To simulate crowding of repair proteins around damaged sites, a circular exclusion region is centered at the location of each damaged monomer. Ex-

clusion region is represented by an elastic spring pushing force of radius r_p, originating from each damaged monomer. The elastic force applied on any monomer within the exclusion range is thus oriented outwards. In addition to the exclusion region, all cross-links from and to damaged monomers are removed.

The system will evolve into a new steady configuration which represents the chromatin 15 minutes post UV-C. At which point, the region of interest (ROI) is defined as the circle containing 95% of the damaged monomers and centered at their center-of-mass. The ROI remains a fixed region used to track the number of damaged and undamaged monomers within it. Measurements are done off-line, such that the ROI is always centered at the center-of-mass of the monomers known to be damaged.

0.2.4   Post repair stage

As damaged monomers are repaired the exclusion region is removed from damaged monomers. Cross-links are reintroduced gradually according to the spatial distance between monomers. The amount of cross-links re-introduces is such that the initial cross-linking percentage α is restored.