

The effect of chromosome-nuclear envelope attachments on 3D genome organization

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We build computational models of the polytene chromosomes from *Drosophila* salivary gland nuclei. The chromosomes, bounded by the nuclear envelope, are modeled as random self-avoiding walks under confinement. We use three ensembles of computational nuclei to determine the effects of chromosome-nuclear envelope (Chr-NE) attachments on the 3D organization of the genome: each ensemble includes approximately 3000 nuclei with 0, 15, and 48 Chr-NE attachments respectively. Both the number and distribution of Chr-NE attachments in these three ensembles bring about changes in the 3D organization of chromosomes. Increasing the number of Chr-NE attachments drastically decreases the probability of inter-arm chromosome contacts with a more modest decrease in the probability of intra-arm chromosome contacts. Changing the distribution of Chr-NE attachments repositions the chromosomes with respect to the NE: chromosome regions with the fewest Chr-NE attachments are repositioned toward the center of the nucleus while those with the most Chr-NE are repositioned toward the periphery. A simple lattice model is used to explain why Chr-NE attachments induce these changes in our computational nuclei.