ABSTRACT

THESIS: Genome-wide analysis of the 30nm chromatin fiber

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Positioning of nucleosomes within the 30nm fiber is fundamental in understanding how DNA compaction regulates gene expression. Numerous studies have focused on determining the structure, however; no studies have assessed the structure genome-wide. In this study, a new *in silico* methodology for genome-wide nucleosome arrangement was assessed through the use of randomly generating *in silico* datasets for the solenoid, solenoid-interdigitated, cross-linker (with odd and even n), twisted ribbon, and twisted ribbon-interdigitated. A PERL script was written to generate six *in silico* datasets from the human genome based on patterns and probabilities of close proximity nucleosomes, and align various length terminal ends of the sequences to the genome. A graphical representation was used to assess the genome-wide pattern of paired sequence alignments for each model. Whole genome sequence data from formaldehyde fixed HeLa cells were filtered, aligned, and compared to the models. Lack of sufficient experimental alignments yielded inconclusive model determination.