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On the Transcription-Based Solenoidal Model of Chromosomes Epigenomics of Molecular Networks

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The organization of transcription within the eukaryotic nucleus or the prokaryotic nucleoid may be expected to both depend on and determine the structure of the chromosomes. In yeast and bacteria, genes that are controlled by the same sequence-specific transcription factor tend to be either clustered or regularly spaced along the chromosomes. The same spacing is found for most transcription factors within a chromosome. Furthermore, in bacteria, the gene encoding the transcription factor locates at identical regular intervals from its targets. This periodicity is consistent with a solenoidal epi-organization of the chromosome, which would dynamically gather the interacting partners into foci. Binding at genuine regulatory sites on DNA would thus be optimized by locally increasing the concentration of transcription factors and their binding sites. As many transcription factors are simultaneously active and some share targets, the resulting collection of foci provides a potent self-organizational principle for the chromosome, and consequently for the functional nuclear architecture. The transcription-based solenoidal model of chromosomes allows predictions of unprecedented accuracy, in particular on the functional three-dimensional structure of chromosomes.