The Relation between the Gene Network, Gene Expression and the Physical Structure of Chromosomes Modelling and Simulation

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Abstract: Remarkably little is known about the higher-order folding motifs of the chromatin fibre inside the cell nucleus during interphase. Folding depends among others on local gene density and transcriptional activity and plays an important role in gene regulation. Strikingly, at fibre lengths above 5 to 10 Mb the measured mean square distance between any two points on the chromosome fibre is independent of genomic distance along the chromosome while for lengths below 1Mb there is a strong dependence. We propose a polymer model that can explain this levelling-off by means of looping probabilities, i.e., interaction between genes. A detailed investigation of this model as well as a model for the 30nm chromatin fibre that we will present shows that loops on all scales are necessary to explain the experimental data. Thus we can link the interaction between genes in the gene regulatory and interaction network to the physical structure as well as the gene expression opening new inroads to our understanding. I will also describe the Monte Carlo alogrithms that were used.

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