DCC Simulation Modelling

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It has been shown that gene expression is greatly impacted by the chromatin conformation in a cell's nucleus. The chromatin conformation in the nucleus is therefore not random but is subject to regulatory elements in the nucleus. One family of chromatin interacting proteins is suspected to play an important role in this process; the condensins. Condensins are classified as Structural Maintenance Complexes (SMC's) and have been shown to play a role in chromatin compaction. The exact mechanism it uses however remains unclear and is the subject of interest of our work. To further investigate the modus operandi of condensins, we chose C. elegans as a model organism and used an in silico simulation engine to test different models we envisioned for C. elegans's condensin I^{DC}, which is also known as the Dosage Compensation Complex (DCC). In this report we will show that our results imply the presence of a single DNA-extruding domain in the DCC and that boundary elements on the chromatin are a necessity for proper DCC function and especially loop formation. We will also show that previously suggested recruitment elements alone don't suffice to produce simulations that show good correspondence to our in vivo Hi-C data.

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