



COLLEGE of ENGINEERING AND PHYSICAL SCIENCES

SCHOOL OF COMPUTER SCIENCE

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ABCNet: Predicting chromosomal compartments directly from reference genomes

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ABSTRACT:

Previous research has shown that the 3D organization of a cell's genome is crucial to its functionality, directly contributing to gene regulation. Better understanding what gives rise to a genome's 3D organization, as well as the effects it has on a cell's functionality, has the potential to lead to various breakthroughs surrounding disease, cell differentiation and more. In 2009, a biochemical assay used to capture the conformation of a genome (called Hi-C) was published, allowing us to better understand how a genome might interact with itself. From this, we can categorize regions of the genome into two compartments, those that are open (A) and those that are closed (B), where A compartments are gene-rich, transcriptionally active and more loosely packed together than B compartments.

This thesis presents ABCNet, a convolutional neural network (CNN) designed to predict the A/B compartments of a genome directly from its genomic sequence. Unlike other neural networks, ABCNet does not rely on a predetermined set of extracted genomic features and/or elements to make its predictions, while still matching their accuracy. Furthermore, analysis into ABCNet's latent space hints at important genomic features indicative of its 3D genome organization.