

A multicolour polymer model for the prediction of 3D structure and transcription in human chromatin

Monday, 19 December 2022 18:35 (20 minutes)

Within each human cell, three types of RNA polymerases and a panoply of different types of transcription factors bind chromatin to simultaneously determine 3D chromosome structure and transcriptional programme. Experiments suggest that, in some cases, different types of proteins segregate to form specialised transcription factories, while in others they mix and gather together, binding the same chromatin regions. Here, we use coarse grained molecular dynamics simulations to study the coupled 3D structure and transcriptional dynamics of chromatin fibers and whole human chromosomes, via a polymer model which accounts for multiple types – or “colours” – of DNA-binding proteins, mimicking complexes containing RNA polymerase I, II, and III, or cell-type-invariant and cell-type-specific transcription factors.

Our simulations show the appearance of both segregated and mixed clusters, depending on their size, with larger clusters being more likely mixed: this is suggestive a transition between the two types of clusters based on simple biophysical parameters. Second, the model leads to non-trivial spatio-temporal correlations between different transcription units, dependent on the underlying chromosome structure. Finally, it predicts transcriptional data better than previously considered models.

Primary author: Dr NEGRO, Giuseppe (University of Edinburgh)

Co-authors: Prof. MARENDUZZO, Davide (University of Edinburgh); Prof. GONNELLA, Giuseppe (University of Bari); Dr SUMA, Antonio (University of Bari); Mr SEMERARO, Massimiliano (University of Bari)

Presenter: Dr NEGRO, Giuseppe (University of Edinburgh)

Session Classification: Session 4 B