Title: Modelling Electrostatic Interactions and Solvation in Chromatin

Abstract: Chromatin is a complex of proteins and DNA found in the nuclei of eukaryotic cells. It reinforces the DNA and its topology tunes DNA transcription and gene expression. We analyse chromatin compaction from an electrostatic perspective and focus on the role of electrostatics and solvation as determinants of the topology of chromatin. We examine the effect of the histone tails and propose a methodology to connect electrostatic calculations to the structural and functional features of protein-DNA systems. This methodology can also be combined with coarse-grained representations to investigate the electrostatic origins of effects such as different stages in DNA unwrapping, nucleosome destabilisation upon histone tail truncation, and the role of specific arginines and lysines undergoing Post-Translational Modifications. We present a comprehensive study of the electrostatic interactions between nucleosome pairs sampling different translations and rotations. Our analysis aims to provide a cohesive description of nucleosome electrostatic interactions in the chromatin fibre, combining information on the energetics of different relative positions of nucleosomes. We also conduct an analysis of the porosity of nucleosomes and related to the importance of solvation phenomena. We complement and support our computational findings on nucleosome electrostatic interactions experimental Zeta Potential and Dynamic Light Scattering measurements on single nucleosomes under varying ionic concentrations, providing information on the surface charge and the size of nucleosomes.