**Title**: Multiscale modelling meets machine learning: leveraging deep learning and friends to investigate soft and biological matter systems

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One of the outstanding challenges in the computer-aided investigation of biological macromolecules, such as proteins and DNA, is represented by the intrinsic multiscale nature of several processes and phenomena; these range from large conformational changes induced by ligand binding to the epigenetic regulation of gene expression, and beyond. A single framework for the in silico study of such phenomena is impossible and inadequate, as different properties take place at distinct characteristic length- and time-scales; consequently, models and representations at various resolutions are needed, which address each property specifically. A large amount of work has been devoted in the past few decades to develop methods to tackle this issue, on the modelling as well as on the analysis side. More recently, however, machine learning techniques have entered the field of multiscale modelling, demonstrating also here their usefulness and power in addressing old and new problems. In this talk I will review some of the most prominent cases in which deep learning and other ML techniques have been successfully employed in the investigation of biologically relevant macromolecules, and discuss what appear (to me) to be the most promising avenues for their application in this field.