DNA Structure and Dynamics: Two Successful Stories using HPC

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In this contribution, we will present two examples in Computational Biophysics where we performed extensive Molecular Dynamics simulations using HPC resources granted by PRACE Call 12 and 15. In the first example, we analysed the basic mechanisms of signal transmission in DNA and the origins of the allostery exhibited by systems such as the ternary protein-DNA-protein complex BAMHI-DNA-GRDBD. We found that perturbation information generated by a primary protein binding event travels as a wave to distant regions of DNA following a hopping mechanism. However, such a structural perturbation is transient and mediated by a subtle entropy mechanism, which does not lead to permanent changes in the DNA geometry and interaction properties at the secondary binding site [1,2]. In the second example, we analysed all the crystal forms determined experimentally of the Drew-Dickerson DNA dodecamer to understand the physical properties leading to stable crystals. We revealed the nature of the intermolecular forces leading to crystal stabilization by exploring the effects of crystallizing agents and the solvent environment. In particular, we highlighted the role of spermine in the stabilization of specific symmetry groups and compared its dynamical behaviour at atomic detail with free DNA in solution [3].

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2. A. Balaceanu, P.D. Dans, M. Orozco. Wave of perturbation: Protein-DNA binding allostery. Success stories: PRACE Annual Report 2017. http://www.prace-ri.eu/IMG/pdf/Prace-Annual-Report2017_LOWRES.pdf (pp. 20).
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