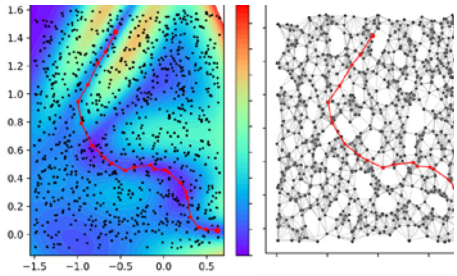

APPLICATIONS

A QUANTUM ALGORITHM FOR SIMULATING THE TRANSFORMATIONS OF PROTEINS

A study conducted by three theoretical physicists of the University of Trento, which appeared yesterday in the Physical Review Letters, demonstrates the validity and the potential for an approach founded on the use of quantum computing in simulating structural changes to which proteins are subjected in the course of their lives, biological transformations on which the synthesis and activation of the latter depends. It is a result that highlights the great advantages that can be gained from the full development of quantum technologies. Over the last few decades, enormous steps forward have been taken in characterising the processes that involve the transformations of proteins and, more generally, of biological macromolecules, making use of computer simulations. In particular, the formation (folding process) or execution of the biological functions of proteins, which are composed of amino acid chains, is regulated by specific changes in their form. Precisely analysing and succeeding in providing structural variations, in shape and trajectory, of these biomolecules are, therefore, fundamental steps for developing advanced medical treatments for many diseases. ■