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Biology entered a new era, with bioinformatics producing biological data that are impossible nowadays to obtain with wet experiments. Soon scientists and clinicians will use new DNA technologies to detect mutations driving cancer and other diseases, identify new strains of pathogens, map the physiological effects of the microbial communities residing in our organs, track subtle changes in our immune repertoire, predict drug response, and make innumerable other contributions to our health and knowledge of complex biological systems. The scale and complexity of the data will vastly exceed anything the biological and medical community has faced before. Tackling these questions with advanced engineering, new computer algorithms and novel computational approaches is a challenge that will lead to revolutionize biology and medicine through deeper, ubiquitous use of DNA information. Among different examples, we shall present a computational approach to protein-protein interactions that we developed within a project on neuromuscular diseases. The project demands a high computational power to test billions of interactions, it run on the machines of the World Community Grid for more than 3 years, and provided a huge amount of information on the interaction of human proteins. High Performance Computing helped to obtain an unprecedented amount of information on protein-protein interactions between real partners but also, and most importantly, between non-partners.

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D'après une photo de Philippe Servent







