



Computational Analysis of Proteomes and Genomes

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Message from the Guest Editor

The world is in urgent need of new cutting-edge computational tools that can create useful knowledge from information that is being published quickly and in a fragmented manner, delivering more tailored therapies against key multifactorial diseases. Despite the vast scientific and technological advances in drug research and development (R&D), as well as the amount of time and funding involved, we are witnessing a steady decline in pharmaceutical productivity in the last decades due to: i) lack of safety; ii) patient-related constraints; iii) target-related issues. We need better-informed decisions in drug development, which means more robust and faster identification of the best targets and drug candidates to advance to preclinical and clinical trials. It is time to take advantage of the big boom of data availability, as well as the existence of powerful and cheaper software/hardware that allows the high performance of top in silico algorithms to enhance and accelerate scientific discoveries in this area.





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Message from the Editor-in-Chief

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