Recent Advances in Protein Bioinformatics

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Deadline for manuscript submissions:
closed (5 May 2021)

Message from the Guest Editors

Bioinformatics, or the development of computational methods for understanding biological data, has seen a surge of energy in recent years. The understanding of protein structure and function has vastly benefitted from new models, methods, and tools. This revolution has mainly been fueled by an ever-increasing computational power, giving access to previously unthinkable calculations as in the case of molecular dynamics pushing the boundaries of microseconds; advanced machine-learning techniques modeling complex problems, as in the case of AlphaFold, Google's deep-neural-network algorithm for de novo prediction of protein folding; and mathematical approaches applied to complex problems from a different perspective, as in the case of RING, which analyzes amino-acid contacts exploiting graph theory. The added value deriving from the combined approach of biochemistry and computer science reflects the deep interdisciplinarity of the problems arising in the field of protein biochemistry, and the rise in mixed approaches is a trend destined to soar in the coming years.

SpecialIssue

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Message from the Editor-in-Chief

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