



## Algorithmic Methods for Computational Molecular Biology

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submissions:

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### Message from the Guest Editor

Dear Colleagues,

Challenges for algorithmic approaches in molecular biology abound – epitomized by the thriving ISMB and ECCB. Algorithmic approaches allow us to process the data and test the hypotheses that drive forward our understanding of molecular biology.

For the future, we need better algorithms to bridge the gap from structure to function to phenotype. To handle the intrinsic flexibility of many biological systems, we need algorithms that embrace dynamic properties to predict function. Applications lie, for example, in the dynamic modelling of interaction networks; in better prediction of the impact of SNVs, in regulatory or coding regions, in structured or disordered regions of the protein, or where structure is unknown; in generating and/or processing meta-data to make our valuable data FAIR, and integrating data from various sources, platforms, or labs.

We are looking forward to receiving your contributions as research or review papers!

Dr. K. Anton Feenstra  
*Guest Editor*





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## Editor-in-Chief

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## Message from the Editor-in-Chief

Algorithms are the very core of Computer Science. The whole area has been considered from quite different perspectives, having led to the development of many sub-communities: Complexity theory (limitations), approximation or parameterized algorithms (types of problems), geometric algorithms (subject area), metaheuristics, algorithm engineering, medical imaging (applications), indicates the range of perspectives. Our journal welcomes submissions written from any of these perspectives, so that it may become a forum for exchange of ideas between the corresponding scientific subcommunities.

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