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Highly accurate protein structure prediction with AlphaFold

vendredi 29 avril 2022 09:00 (45 minutes)

Proteins are essential to life, and understanding their structure can facilitate a mechanistic understanding of their function. Predicting the three-dimensional structure that a protein will adopt based solely on its amino acid sequence —the structure prediction component of the 'protein folding problem'—has been an important open research problem for more than 50 years. AlphaFold, a novel machine learning approach developed at DeepMind, demonstrated accuracy competitive with experimental structures in a majority of cases and greatly outperformed other methods, and has since been recognized as "Method of The Year 2021" by Nature Methods. In this talk I will outline the problem, describe the AlphaFold method and our engineering approach, discuss applications in biology, and sketch possible future directions and connections.
https://www.nature.com/articles/s41586-021-03819-2
https://www.nature.com/articles/s41586-021-03828-1

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Classification de Session: AI and physics conference