INVITED SPEAKER

FEEDBACK ON THE USE OF ALPHAFOLD FOR PROTEIN INTERACTION PREDICTION AND MODELING

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The prediction of protein-protein interactions and the characterization of their structural organization provide essential information to elucidate the molecular mechanisms underlying cross-talks between cellular pathways. The advent of machine learning has culminated in recent months with the development of the Alphafold method, which pushes back many of the methodological limits encountered so far in exploiting evolutionary information to predict the mode of recognition between proteins. Combining predictive approaches and experimental methods should dramatically help understand how large networks of proteins work together. In this discussion, we will share our experience and understanding of Alphafold's performance and limitations on different types of protein interactions.