

Assessing AlphaFold predictions

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Protein structure prediction is becoming an increasingly important tool in biology, with applications ranging from molecular replacement, to modelling complexes, to proteome-scale bioinformatics. As the use of structure prediction grows, it will be important to develop best practices such that experimentalists' confidence in model predictions adheres closely to the accuracy of individual predictions. In this talk, I will discuss what I consider to be best practices for reporting and analysing AlphaFold predictions. I will also provide some advice on creating benchmarking sets for assessing novel applications of AlphaFold.