AlphaFold changes everything (and nothing)

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The ability to create an AlphaFold model for any sequence in a few minutes changes every protein crystal structure determination into a molecular replacement problem and every protein cryo-EM structure determination into a docking problem. Making this even more transformative is the ability to iteratively improve AlphaFold modeling by docking an AlphaFold model into density, rebuilding it, and using the rebuilt model as a template for further AlphaFold model generation (Terwilliger et al., 2022). These features of AlphaFold will make structure determination by crystallography and cryo-EM easier and more powerful than ever before, but do not fundamentally change the importance of the experiment. Anyone can carry out these steps easily using Phenix and free cloud-based Google Colab notebooks.

Terwilliger, et al. (2022). Improved AlphaFold modeling with implicit experimental information. bioRxiv 2022.01.07.475350; https://doi.org/10.1101/2022.01.07.475350