Deep Learning (DL) and Protein Structure Modeling

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Why chose this paper?

- Explores a wide range of DL applications.
- Aligns with my interest in DL.
- Proposes directions to further leverage DL.

Research Background & Introduction

- Authors: Dr. Baker & Dr. Baek

- Computational structural biology was based on physically based approaches.

- Challenge: **large size of protein conformational space** and **accuracy of force fields**.

- Objective: introduce the transformative potential of DL.

DL Methods

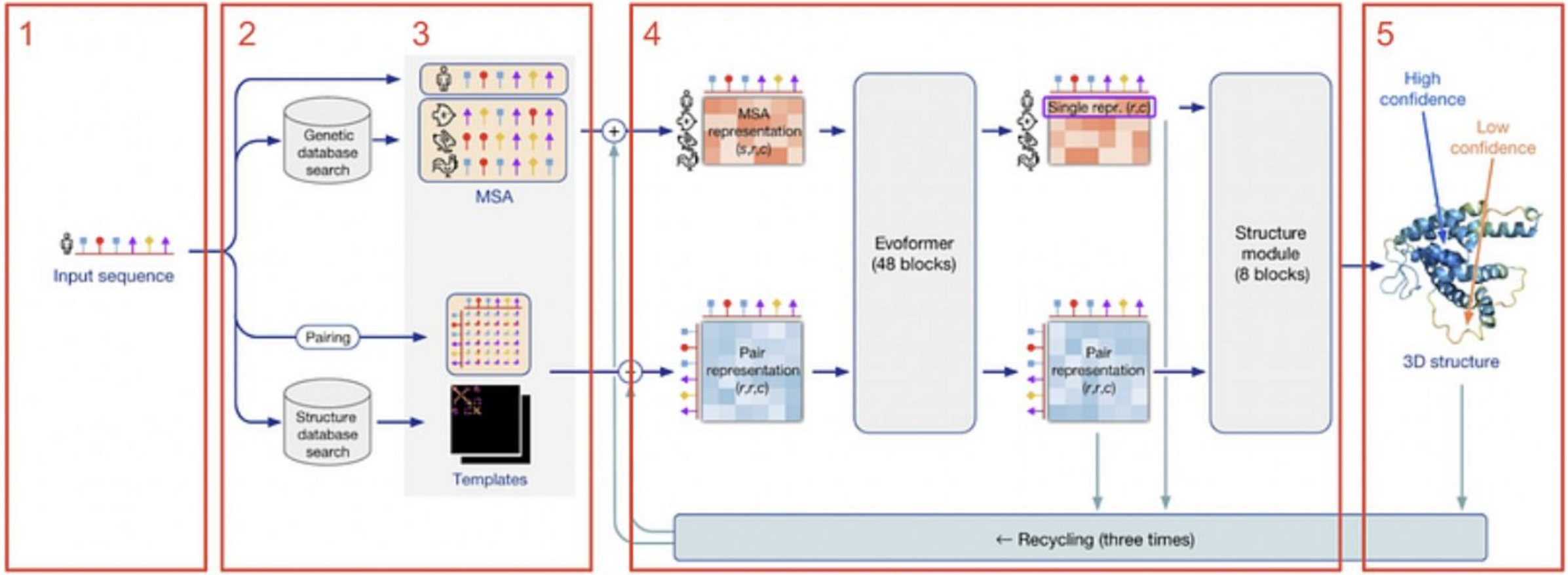
Alpha Fold2 (AF2)

- Developed by DeepMind (2020) and published in 2021.
- Predicts protein structure from its amino acid sequence.

RoseTTAFold (RF)

- Developed and published by Baker Group (2021).
- Uses “Three-track” neural network to predict protein structures from amino acids.

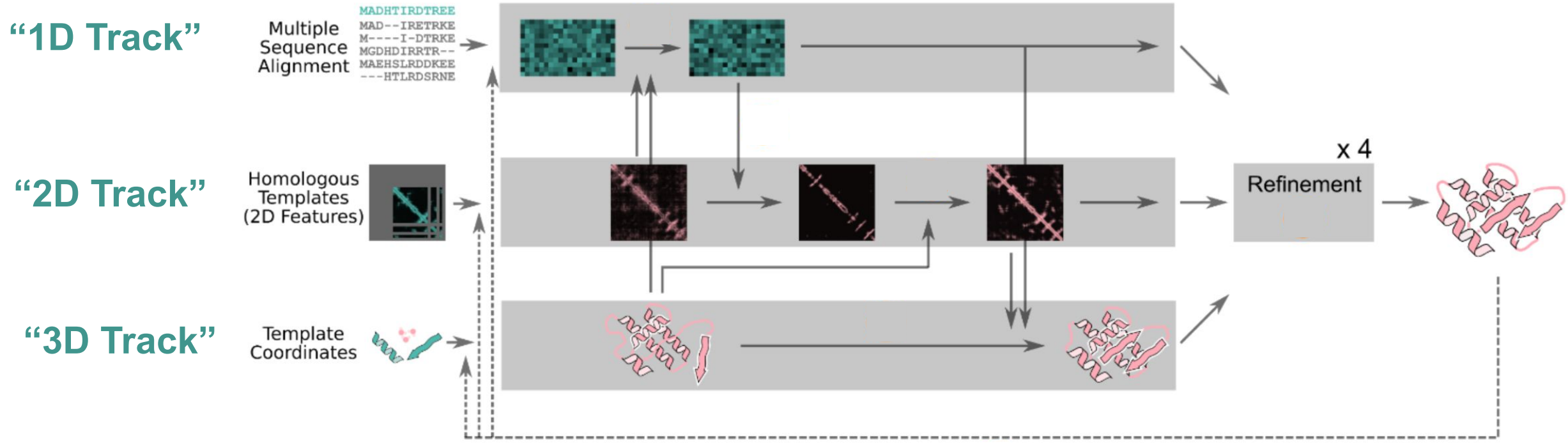
Recall: AF2 architecture



Reference

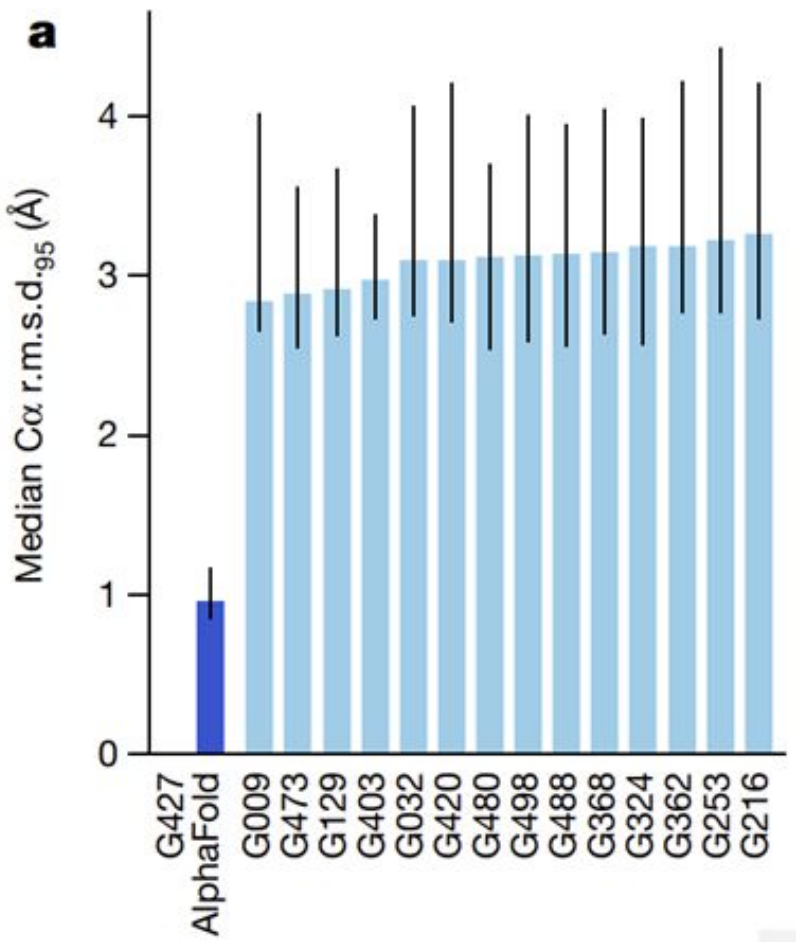
1. John Jumper et al, Highly accurate protein structure prediction with AlphaFold, 2021

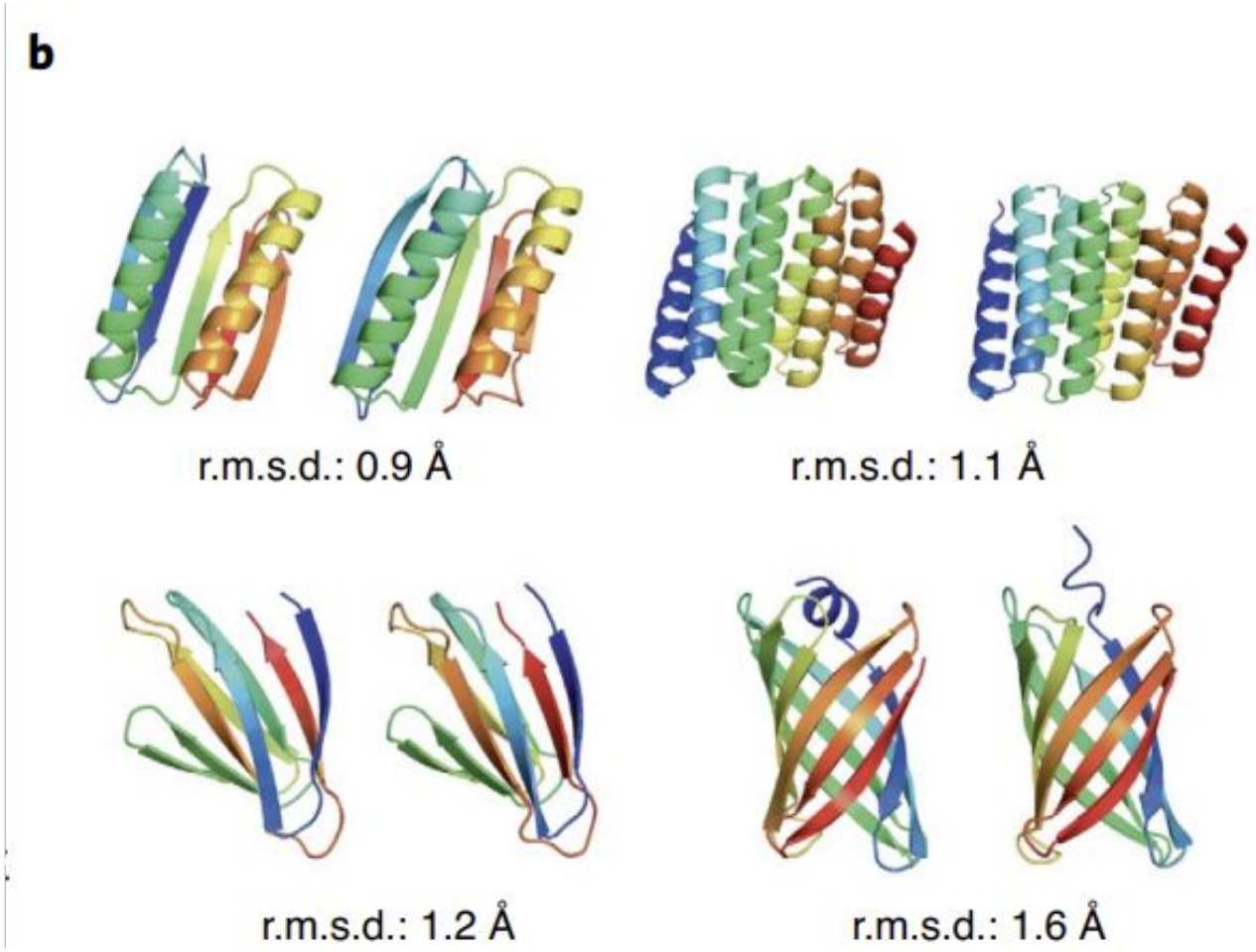
Recall: RF architecture



Slide Credit: David Juergens

Results





References:

1. John Jumper et al, Highly accurate protein structure prediction with AlphaFold, 2021
2. Baker and Baek., Deep learning and protein structure modeling, 2021/

Accomplishments

- Prediction of Protein-Protein Complexes
- Foundational role for further extensions
- Recovers sequences from structures in addition to structures from sequences.
- Performs high accuracy on fields that the available datasets are much smaller, and many of them are not publicly available.

Challenges

- DL methods require large and information-rich datasets for accurate model training.

Conclusion + Future work

- Protein-Protein Interaction (PPI)
- Assembly modeling
- Protein Design
- Small-molecule drug discovery

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