Closing remarks

June 1st 2023

Ludwig Schmidt

Topics we didn't cover

Generative modeling of visual data, both 2D and 3D

Audio processing (speech, music, etc.)

Reinforcement learning (games, robotics, etc.)

Privacy & security in the context of machine learning

Ethical concerns (bias in models, societal implications,
copyright, misinformation, etc.)
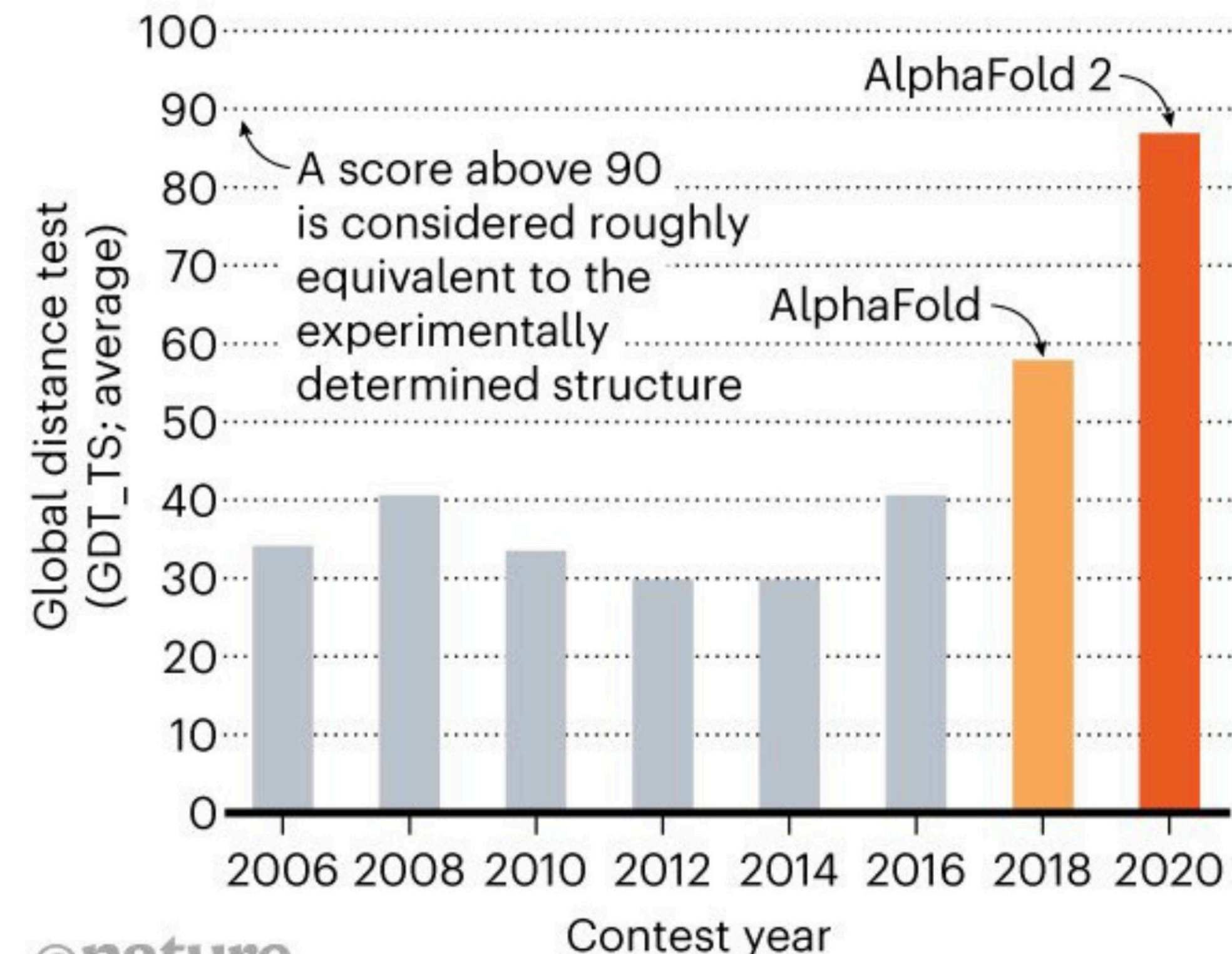
CSE 480, CSE 581, CSE 582

ML for (molecular) biology

AlphaFold2 (DeepMind, 2020)

- Deep learning approach to **protein folding**.

- First method to reach **accuracy similar to experimental data** (X-ray crystallography).

- Sophisticated **problem-specific architecture**, inspired by transformers / attention.

- Biology went **from ≈ 100k to ≈ 100M** protein structures.

Also: direct **language modeling of proteins** (ESM)

STRUCTURE SOLVER

DeepMind's AlphaFold 2 algorithm significantly outperformed other teams at the CASP14 protein-folding contest — and its previous version's performance at the last CASP.

A score above 90 is considered roughly equivalent to the experimentally determined structure

AlphaFold 2

AlphaFold

Global distance test (GDT_TS; average)

Contest year

©nature

Assignment deadlines / late day policy

Project deadline: Friday, June 2, 11:59pm

HW2 deadline: Sunday, June 4, 11:59pm

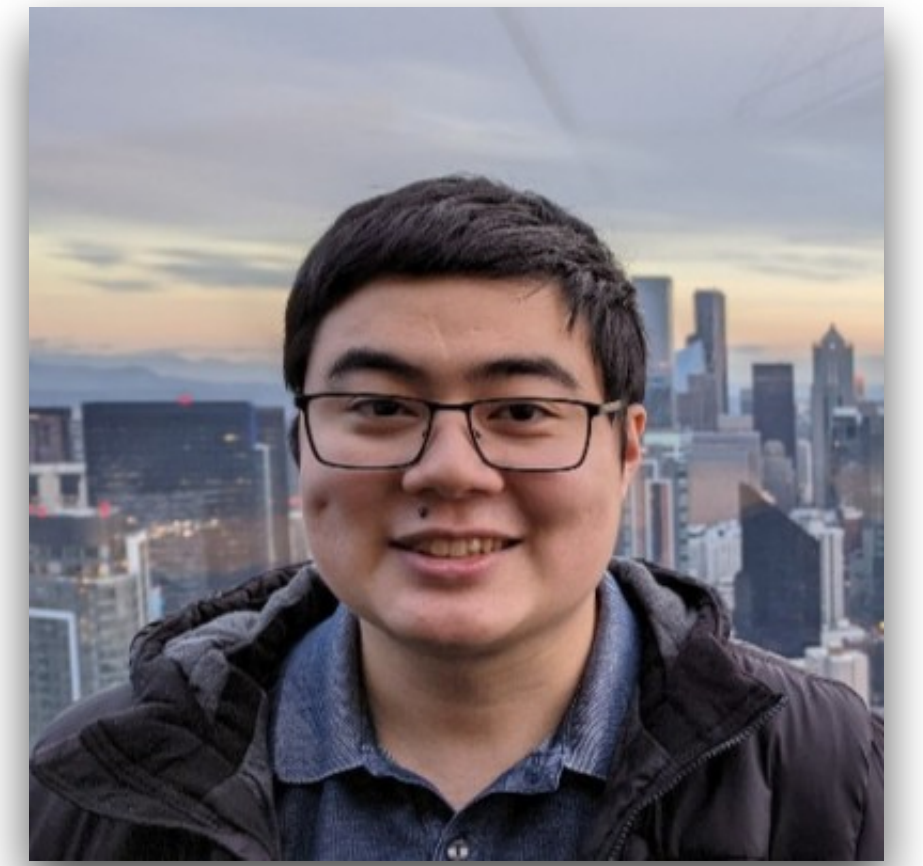(HW1 grades released by Monday, June 5)

Late day policy:

- **Two days** to be used across both the project and HW2.

- If you use a late day on an assignment, we do not guarantee that we will handle regrade requests before the grade submission deadline (June 13).

Please submit the course evaluation! (Deadline Sunday, June 4, 11:59 pm)

Thank you!

Tim Dettmers

Jonathan Hayase

Gabriel Ilharco

Mitchell Wortsman

Thank you!