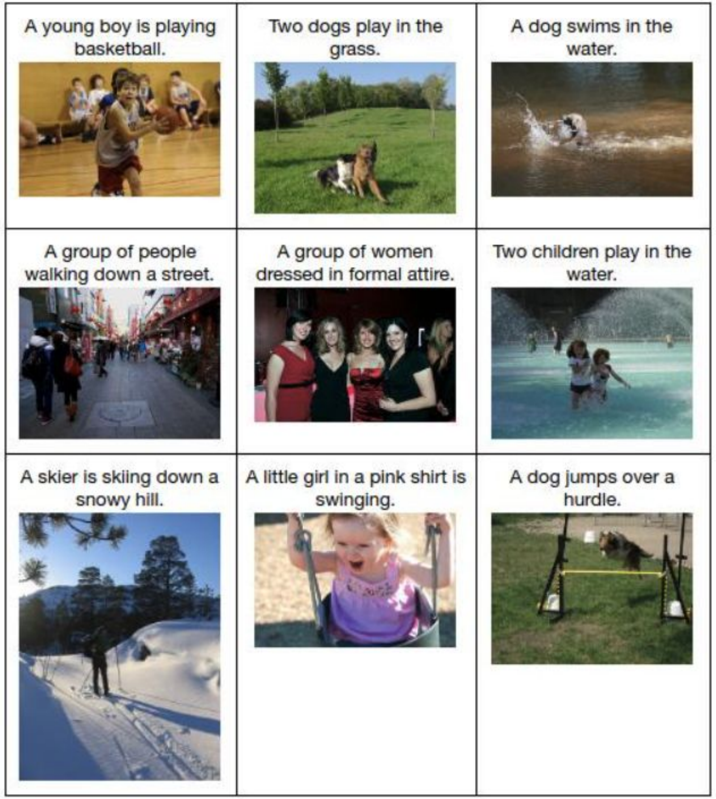
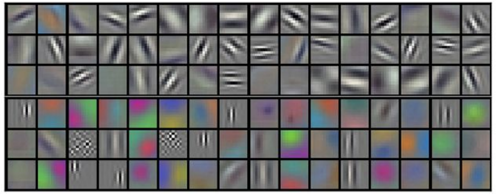
Success Stories of AI

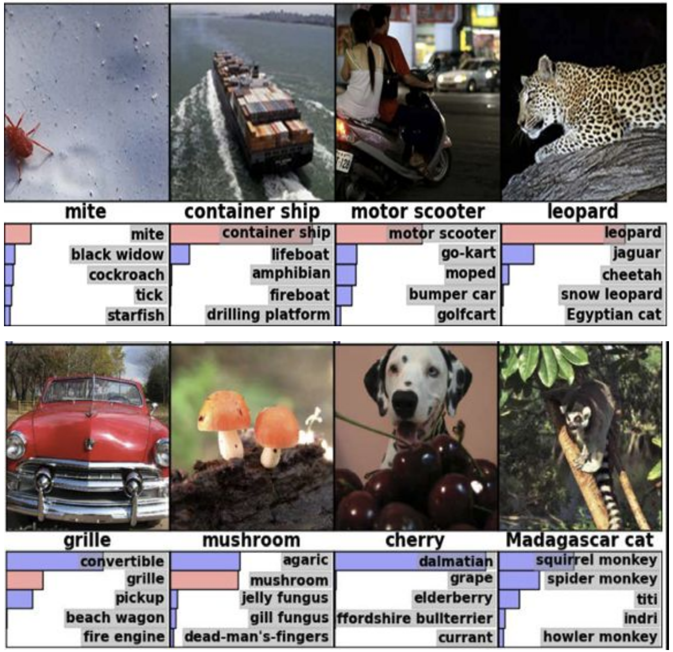
Melih Kandemir

Story 1: Computer Vision



Model	Top-1	Top-5
Sparse coding [2]	*47.1%*	*28.2%*
SIFT + FVs [24]	*45.7%*	*25.7%*
CNN	**37.5%**	**17.0%**





ImageNet Classification with Deep Convolutional Neural Networks

Alex Krizhevsky
University of Toronto
kriz@cs.utoronto.ca

Ilya Sutskever
University of Toronto
ilya@cs.utoronto.ca

Geoffrey E. Hinton
University of Toronto
hinton@cs.utoronto.ca

Abstract

We trained a large, deep convolutional neural network to classify the 1.2 million high-resolution images in the ImageNet LSVRC-2010 contest into the 1000 different classes. On the test data, we achieved top-1 and top-5 error rates of 37.5% and 17.0% which is considerably better than the previous state-of-the-art. The neural network, which has 60 million parameters and 650,000 neurons, consists of five convolutional layers, some of which are followed by max-pooling layers, and three fully-connected layers with a final 1000-way softmax. To make training faster, we used non-saturating neurons and a very efficient GPU implementation of the convolution operation. To reduce overfitting in the fully-connected layers we employed a recently-developed regularization method called "dropout" that proved to be very effective. We also entered a variant of this model in the ILSVRC-2012 competition and achieved a winning top-5 test error rate of 15.3%, compared to 26.2% achieved by the second-best entry.

Story 2: Natural Language Understanding

Attention Is All You Need

Ashish Vaswani* Google Brain avaswani@google.com

Noam Shazeer* Google Brain noam@google.com

Niki Parmar* Google Research nikip@google.com

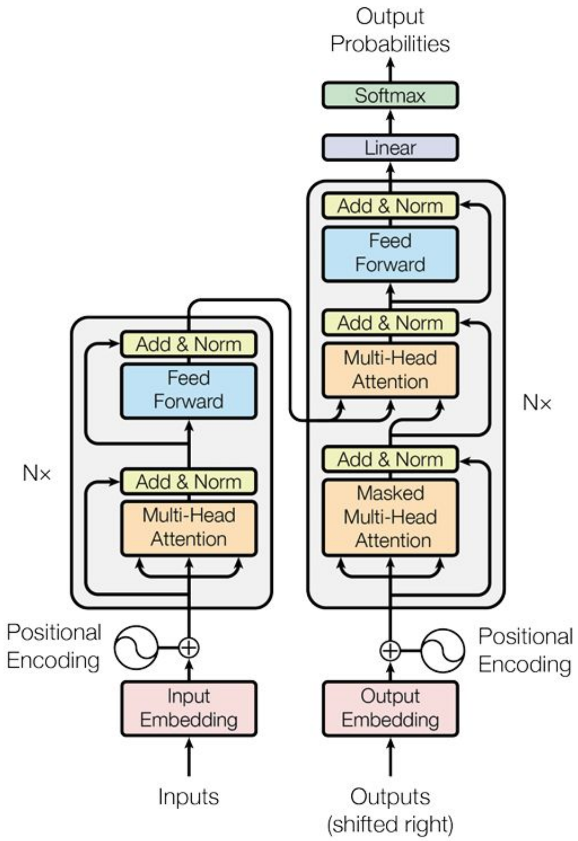
Jakob Uszkoreit* Google Research usz@google.com

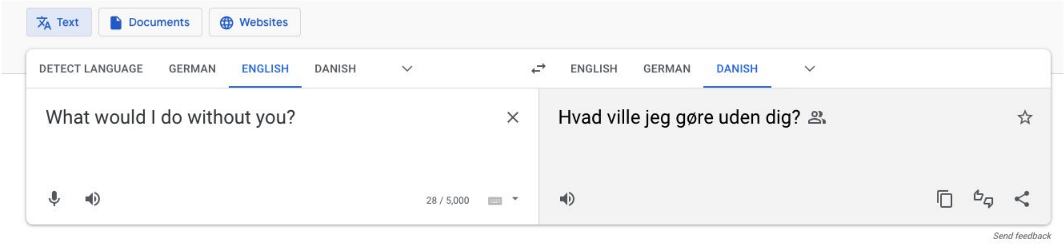
Llion Jones* Google Research llion@google.com

Aidan N. Gomez* † University of Toronto aidan@cs.toronto.edu

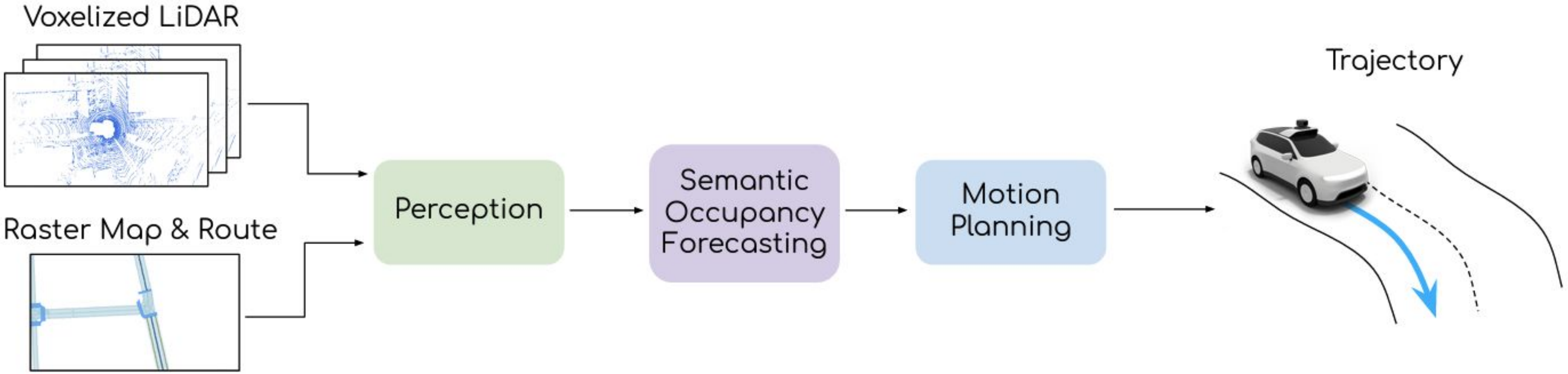
Łukasz Kaiser* Google Brain lukaszkaiser@google.com

Illia Polosukhin* ‡ illia.polosukhin@gmail.com





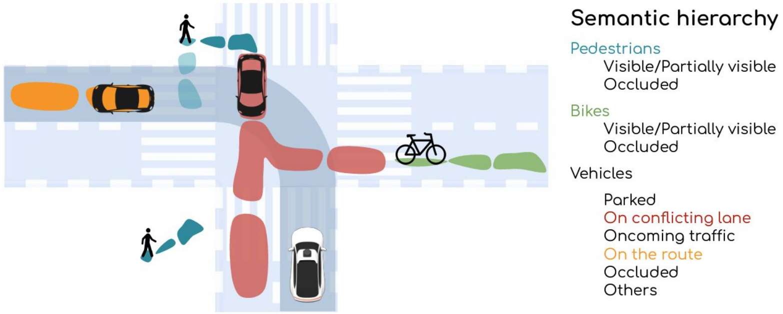
Story 3: Autonomous Driving



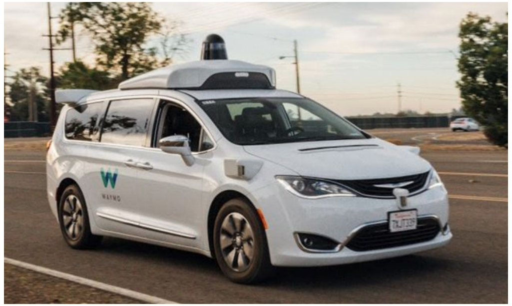
Perceive, Predict, and Plan: Safe Motion Planning Through Interpretable Semantic Representations

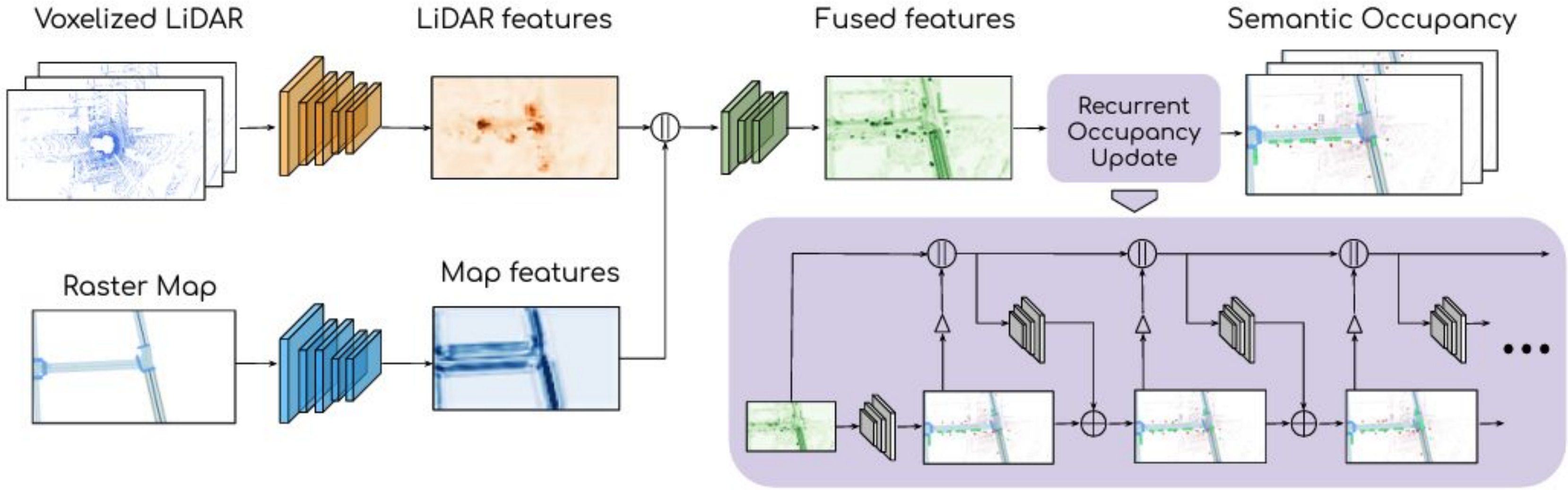
Abbas Sadat*[1], Sergio Casas*[1,2],
Mengye Ren[1,2], Xinyu Wu[1], Pranaab Dhawan[1], Raquel Urtasun[1,2]

Uber ATG[1], University of Toronto[2]
{asadat, sergio.casas, mren3, xinyuw, pdhawan, urtasun}@uber.com

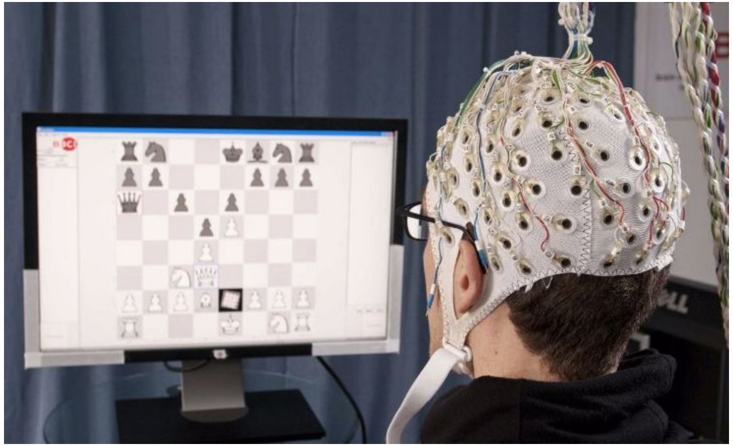


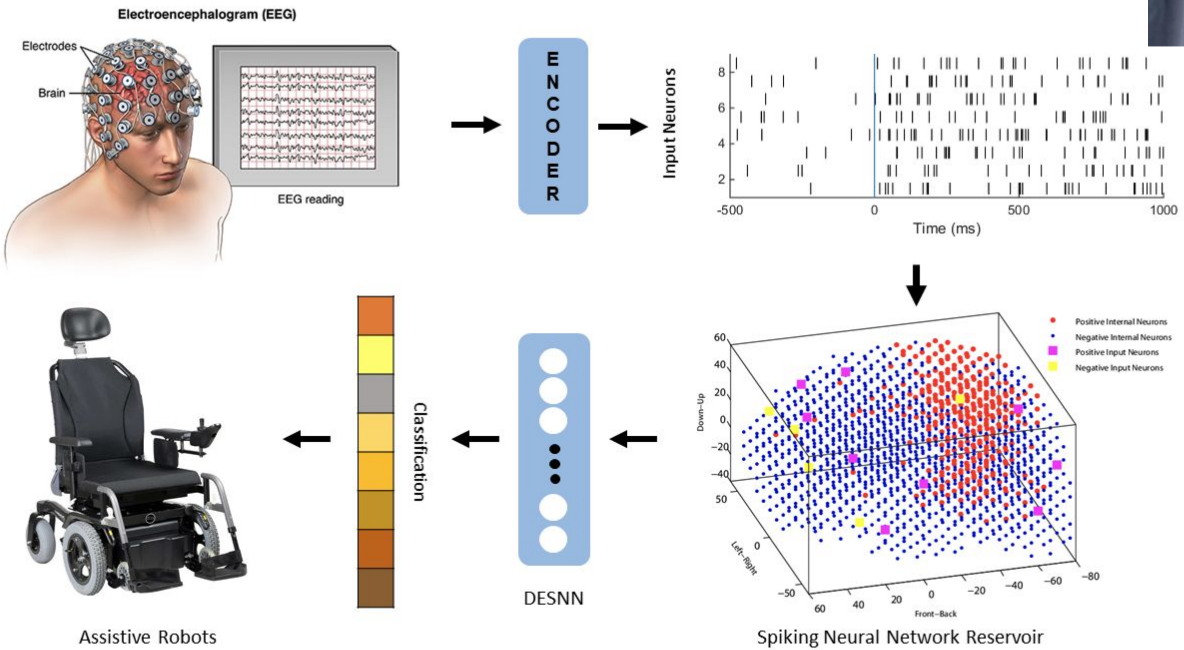
Story 3: Autonomous Driving

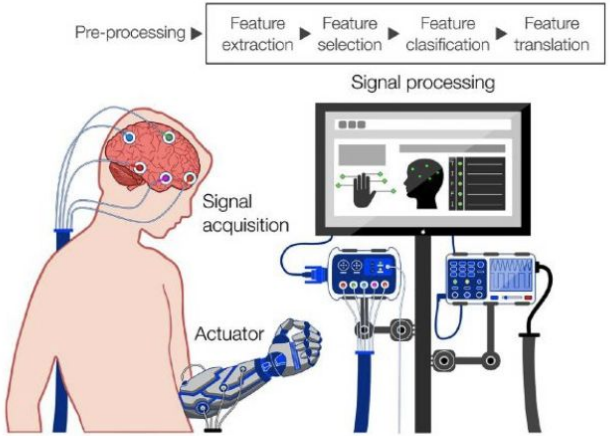




Story 4: Brain-Computer Interfaces







Story 5: Human-Robot Interaction

a) Skill transfer
b) Cobots

Is imitation learning the route to humanoid robots?

Stefan Schaal

This review investigates two recent developments in artificial intelligence and neural computation: learning from imitation and the development of humanoid robots. It is postulated that the study of imitation learning offers a promising route to gain new insights into mechanisms of perceptual motor control that could ultimately lead to the creation of autonomous humanoid robots. Imitation learning focuses on three important issues: efficient motor learning, the connection between action and perception, and modular motor control in the form of movement primitives. It is reviewed here how research on representations of, and functional connections between, action and perception have contributed to our understanding of motor acts of other beings. The recent discovery that some areas in the primate brain are active during both movement perception and execution has provided a hypothetical neural basis of imitation. Computational approaches to imitation learning are also described, initially from the perspective of traditional AI and robotics, but also from the perspective of neural network models and statistical-learning research. Parallels and differences between biological and computational approaches to imitation are highlighted and an overview of current projects that actually employ imitation learning for humanoid robots is given.

Story 6: Ad Placement

How do search engines make money?

Counterfactual Reasoning and Learning Systems

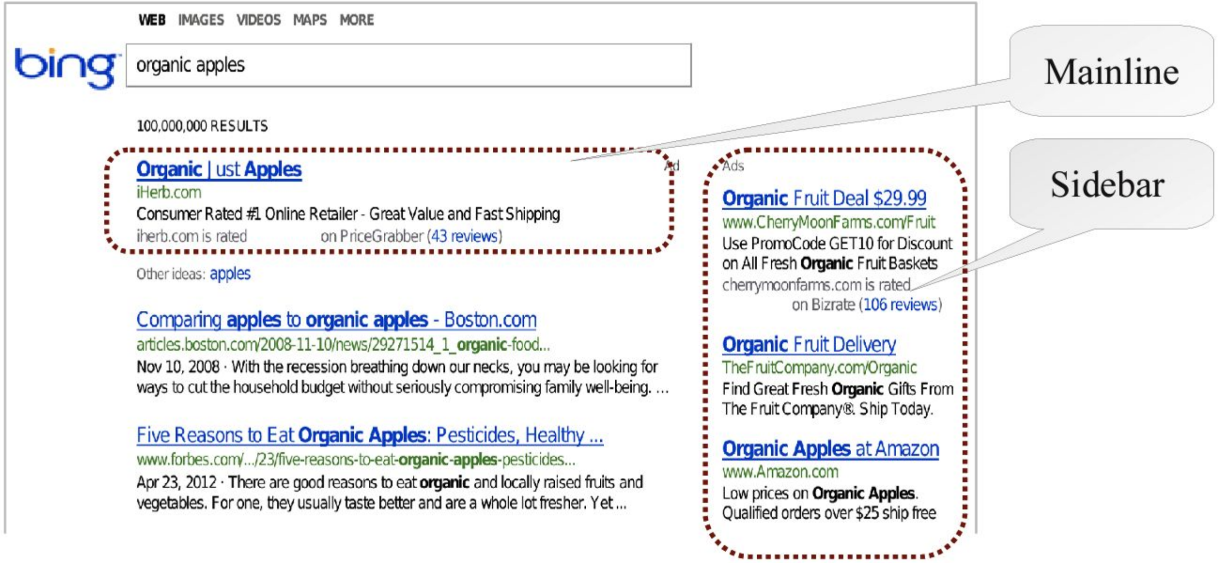
Léon Bottou
LEON@BOTTOU.ORG
Microsoft Research, Redmond, WA.

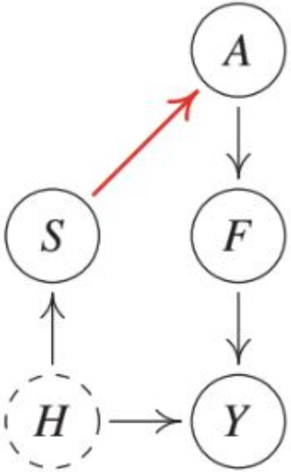
Jonas Peters[†]
JONAS.PETERS@TUEBINGEN.MPG.DE
Max Planck Institute, Tübingen.

Joaquin Quiñonero-Candela,[a‡] **Denis X. Charles,**[b] **D. Max Chickering,**[b]
Elon Portugaly,[a] **Dipankar Ray,**[c] **Patrice Simard,**[b] **Ed Snelson**[a]

[a] *Microsoft Cambridge, UK.*
[b] *Microsoft Research, Redmond, WA.*
[c] *Microsoft Online Services Division, Bellevue, WA.*

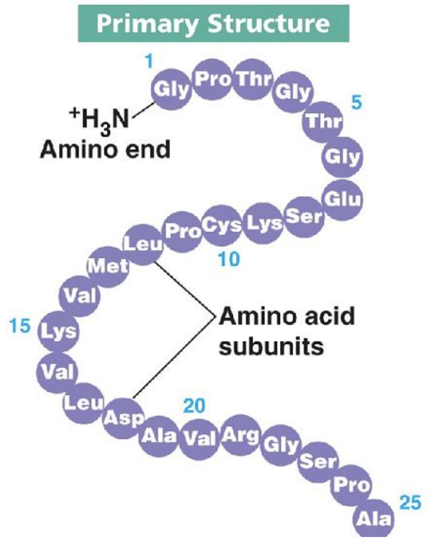
Y: Whether user clicked
A: mainline reserve
F: number of ads in the mainline
S: User status and statistics
H: Hidden user state





Story 7: Protein Folding

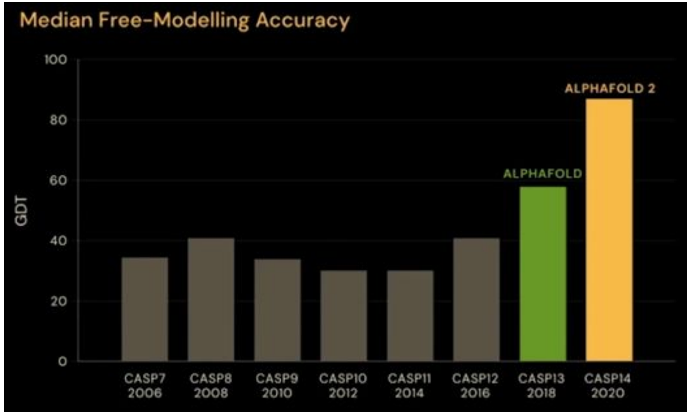
- Biggest advancement in structural biology since 20+ years
- Proteins are structure providers, mover, reaction catalyst, etc. of living things
- Proteins are chains of 21 elementary molecules called “amino acids”
- The problem:
  - Given the 1D chain, predict the 3D structure
- Why care?
  - 3D structure determines its function



Amino Acid	Abbreviations
Alanine	Ala; A
Arginine	Arg; R
Asparagine	Asn; N
Aspartic acid	Asp; D
Cysteine	Cys; C
Glutamic acid	Glu; E
Glutamine	Gln; Q
Glycine	Gly; G
Histidine	His; H
Isoleucine	Ile; I
Leucine	Leu; L
Lysine	Lys; K
Methionine	Met; M
Phenylalanine	Phe; F
Proline	Pro; P
Serine	Ser; S
Threonine	Thr; T
Tyrosine	Tyr; Y
Tryptophan	Trp; W
Valine	Val; V

The CASP Competition

- 200 million proteins as AA sequences
- Ground-truth 3D structures for 170000 proteins
  - Super-expensive data! Requires X-ray crystallography
  - 120000$ and take one year “per protein”
- 10^{143} possibilities (compared to 10^{80} atoms in the universe)



DeepMind’s solution

Article

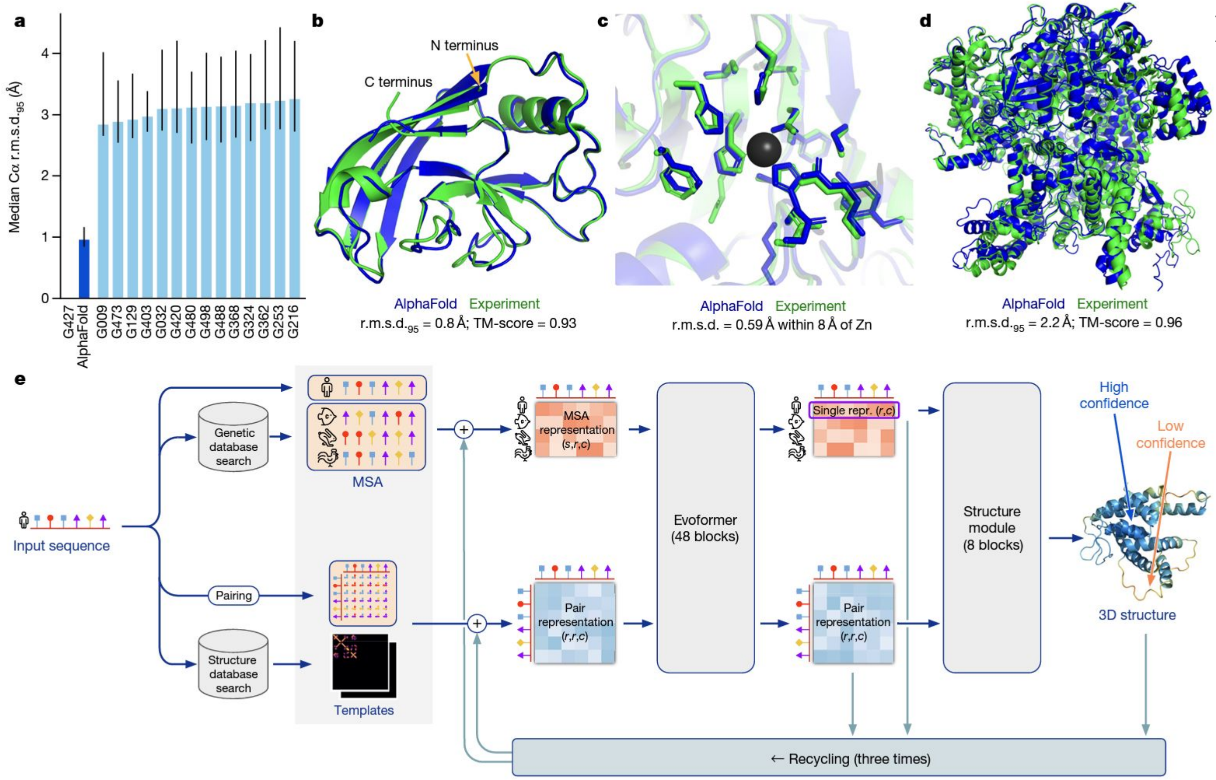
Highly accurate protein structure prediction with AlphaFold

https://doi.org/10.1038/s41586-021-03819-2

Received: 11 May 2021

Accepted: 12 July 2021

John Jumper[1,4✉], Richard Evans[1,4], Alexander Pritzel[1,4], Tim Green[1,4], Michael Figurnov[1,4], Olaf Ronneberger[1,4], Kathryn Tunyasuvunakool[1,4], Russ Bates[1,4], Augustin Žídek[1,4], Anna Potapenko[1,4], Alex Bridgland[1,4], Clemens Meyer[1,4], Simon A. A. Kohl[1,4], Andrew J. Ballard[1,4], Andrew Cowie[1,4], Bernardino Romera-Paredes[1,4], Stanislav Nikolov[1,4], Rishub Jain[1,4], Jonas Adler[1], Trevor Back[1], Stig Petersen[1], David Reiman[1], Ellen Clancy[1], Michal Zielinski[1], Martin Steinegger[2,3], Michalina Pacholska[1], Tamas Berghammer[1], Sebastian Bodenstein[1], David Silver[1], Oriol Vinyals[1], Andrew W. Senior[1], Koray Kavukcuoglu[1], Pushmeet Kohli[1] & Demis Hassabis[1,4✉]



Impact: Accurate physics-based simulation of biological systems

- Discovery of unknown functions of the human genome
- Understanding both genetic and environmental causes of many diseases
- Quick design of new proteins that alter the function of existing ones that would enable
  - New treatment methods
  - New agriculture solutions (green, more nutritious, and better protected food production)
  - New preventive health and anti-aging solutions
  - New biomaterials (e.g. textile)