AI against COVID-19

An overview of AI during COVID-19's time and some researches and examples

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AI against COVID-19

- Overview
- Research
- Examples

Overview

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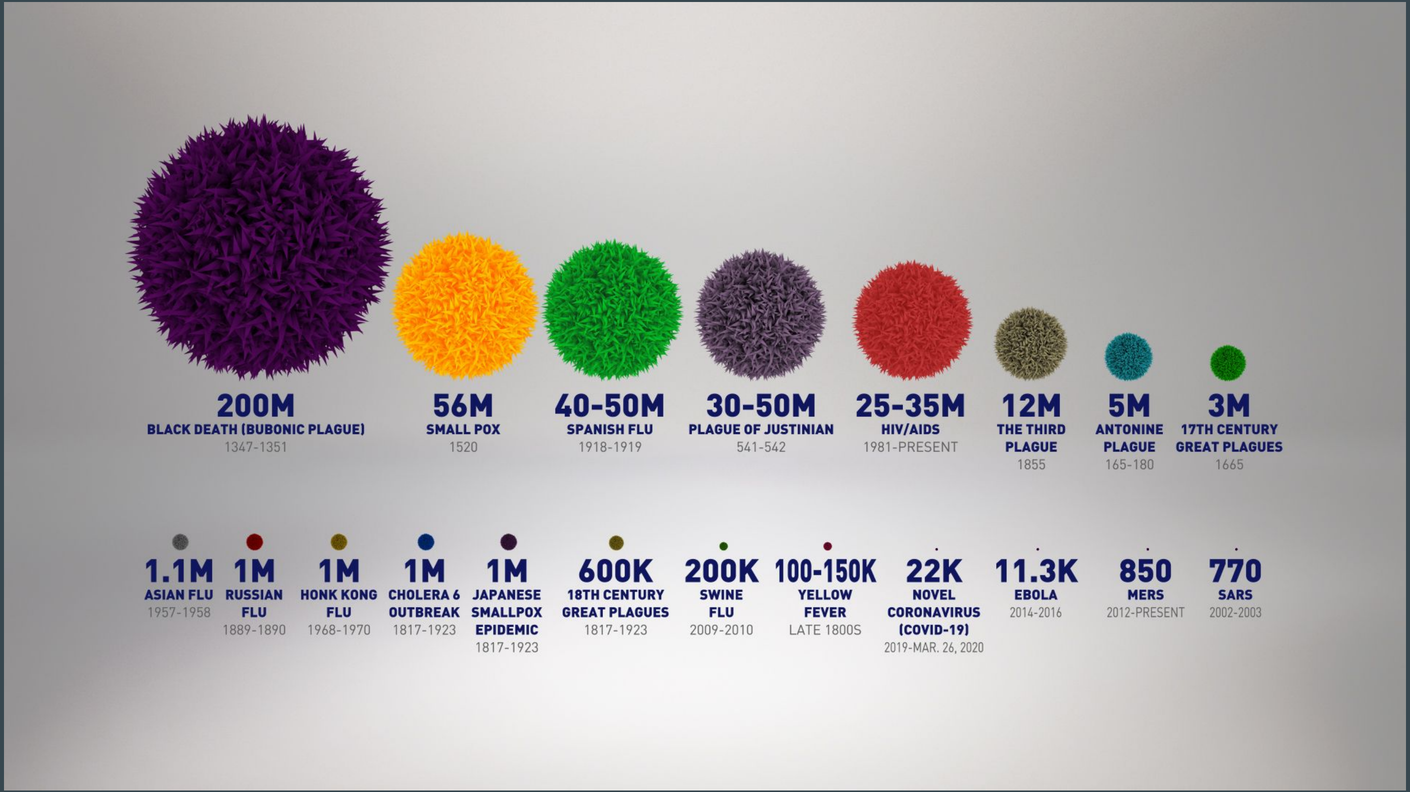
200M
BLACK DEATH (BUBONIC PLAGUE)
1347-1351
56M
SMALL POX
1520
40-50M
SPANISH FLU
1918-1919
30-50M
PLAGUE OF JUSTINIAN
541-542
25-35M
HIV/AIDS
1981-PRESENT
12M
THE THIRD PLAGUE
1855
5M
ANTONINE PLAGUE
165-180
3M
17TH CENTURY GREAT PLAGUES
1665
1.1M
ASIAN FLU
1957-1958
1M
RUSSIAN FLU
1889-1890
1M
HONK KONG FLU
1968-1970
1M
CHOLERA 6 OUTBREAK
1817-1923
1M
JAPANESE SMALLPOX EPIDEMIC
1817-1923
600K
18TH CENTURY GREAT PLAGUES
1817-1923
200K
SWINE FLU
2009-2010
100-150K
YELLOW FEVER
LATE 1800S
22K
NOVEL CORONAVIRUS (COVID-19)
2019-MAR. 26, 2020
11.3K
EBOLA
2014-2016
850
MERS
2012-PRESENT
770
SARS
2002-2003

AI against COVID-19

Main applications

- Early detection
- Predict the spread
- Predict the future course of the disease
- Predict the number of cases and deaths
- Development of drugs and vaccines
- Reduce workload of healthcare workers
- Prevention of the disease

Research

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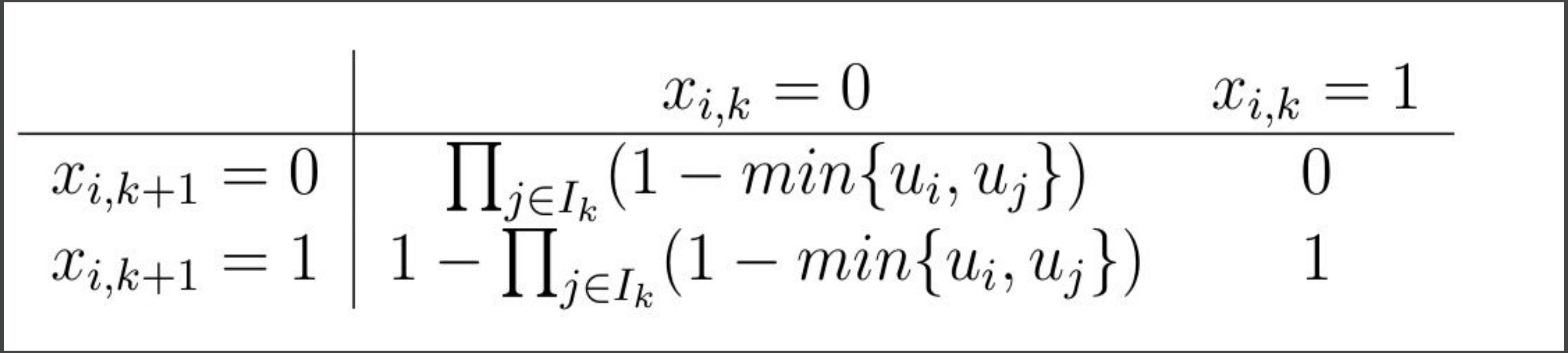
Microscopic Epidemic model and
Multi-Agent Reinforcement Learning

Microscopic Epidemic model based on Multi-Agent system

As defined in “A Microscopic Epidemic Model and Pandemic Prediction Using Multi-Agent Reinforcement Learning” by Dr. Changliu Liu:

- *1..M* agents
- Activity level on a *k* day: $u_{i,k} \in [0,1]$
- Chance of 2 agents to meet on *k* day: $min\{u_{i,k}, u_{j,k}\}$
- $x_i = 1\ (infected)\ and\ x_i = 0\ (healthy)$
- Set of infected agents on a *k* day: $I_k := \{i : x_{i,k} = 1\}$



	$x_{i,k} = 0$	$x_{i,k} = 1$
$x_{i,k+1} = 0$	$\prod_{j \in I_k} (1 - min\{u_i, u_j\})$	0
$x_{i,k+1} = 1$	$1 - \prod_{j \in I_k} (1 - min\{u_i, u_j\})$	1

Table of state transition probability from A Microscopic Epidemic Model and Pandemic Prediction Using Multi-Agent Reinforcement Learning”

Examples

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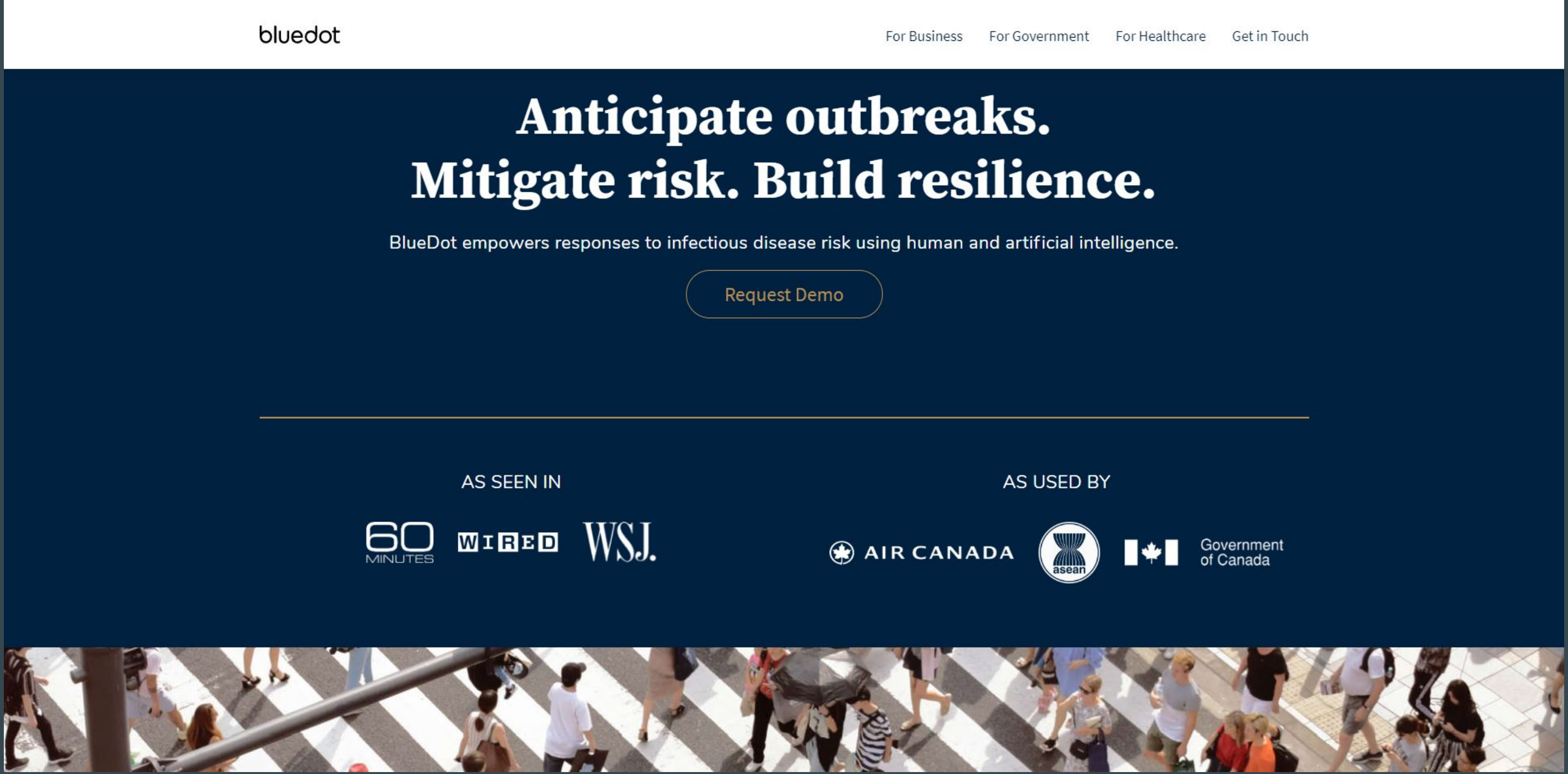
BlueDot - AlphaFold System

BlueDot



bluedot

**Anticipate outbreaks.
Mitigate risk. Build resilience.**

BlueDot empowers responses to infectious disease risk using human and artificial intelligence.

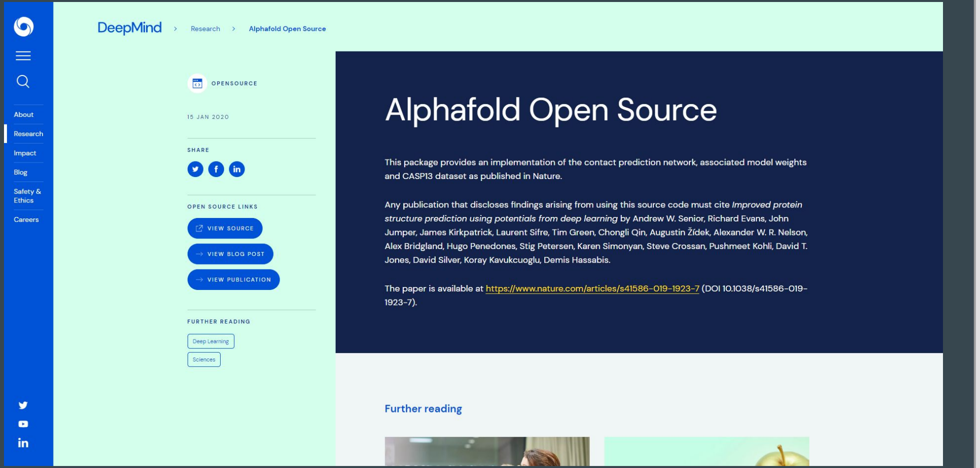
AS SEEN IN

60 MINUTES WIRED WSJ.

AS USED BY

AIR CANADA asean Government of Canada

AlphaFold System



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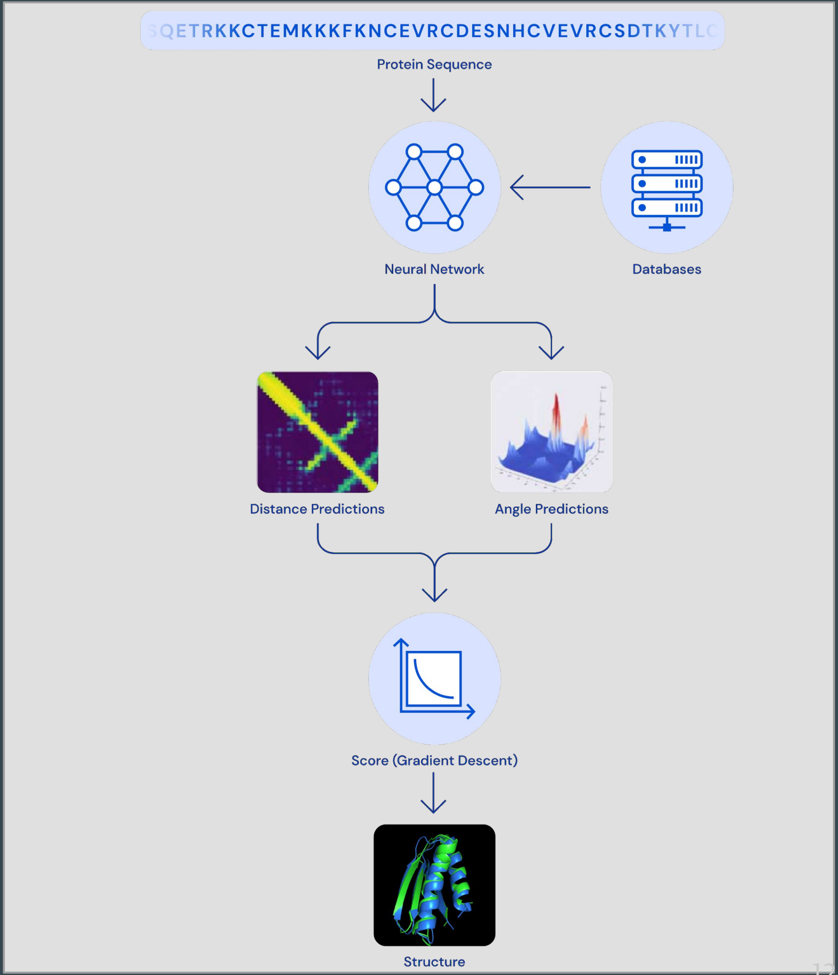
Alphafold Open Source

This package provides an implementation of the contact prediction network, associated model weights and CASP13 dataset as published in Nature.

Any publication that discloses findings arising from using this source code must cite *Improved protein structure prediction using potentials from deep learning* by Andrew W. Senior, Richard Evans, John Jumper, James Kirkpatrick, Laurent Sifre, Tim Green, Chongli Qin, Augustin Žídek, Alexander W. R. Nelson, Alex Bridgland, Hugo Penedones, Stig Petersen, Karen Simonyan, Steve Crossan, Pushmeet Kohli, David T. Jones, David Silver, Koray Kavukcuoglu, Demis Hassabis.

The paper is available at https://www.nature.com/articles/s41586-019-1923-7 (DOI 10.1038/s41586-019-1923-7).

Further reading



SQETRKKCTEMKKKFKNCEVRCDESNHCVEVRCSDTKYTLC

Protein Sequence

Neural Network

Databases

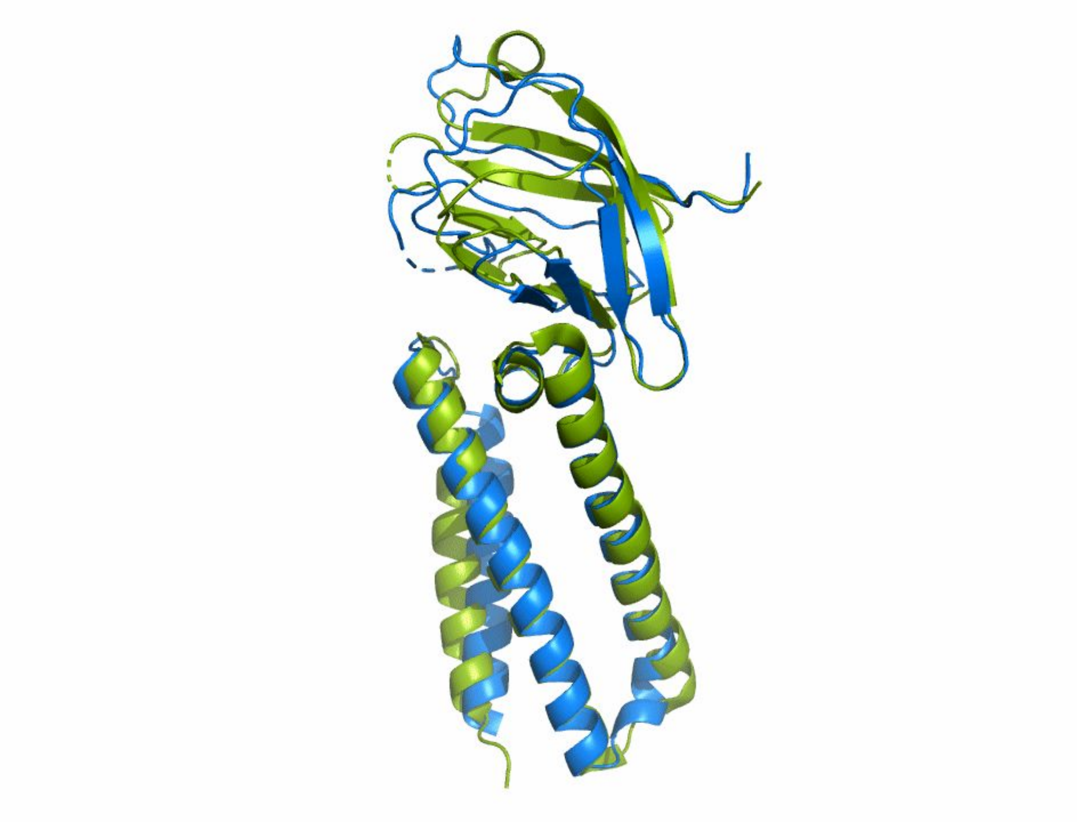
Distance Predictions

Angle Predictions

Score (Gradient Descent)

Structure

AlphaFold System



Conclusion & Questions

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