Artificial Intelligence (AI) in Oncology

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MASSIVEBIO

Temple University Lewis Katz School of Medicine

St Luke's UNIVERSITY HEALTH NETWORK

Best of Oncology An ASCO Direct™ Conference

Oncology has experienced two of the greatest technological evolutions: molecular "omics" (genomics, proteomics, epigenomics) and "big data"

- A couple of decades ago, cancer was diagnosed using a combination of X-ray imaging and histopathology tests. In contrast, molecular tests can now report on changes in hundreds of genes and proteins to diagnose and determine the prognosis and treatment of cancer in an individual.
- In fact, these advances are extending survival and improving the quality of life of hundreds of thousands of patients, yet healthcare professionals face new challenges associated with the implementation of precision medicine,
- Growth of medical knowledge is exponential
- Constant specialization is required to provide highly individualized cancer care.
- This debate is not unique to highly developed countries. Providing comprehensive, state-of-the-art cancer care to millions of patients remains a significant challenge, particularly for suburban and rural populations.
- Biomedical data is heterogeneous and difficult to classify (e.g. high dimensionality, time dependence, parity, irregularity) for Artificial Intelligence applications.

Immunohistochemistry (IHC)

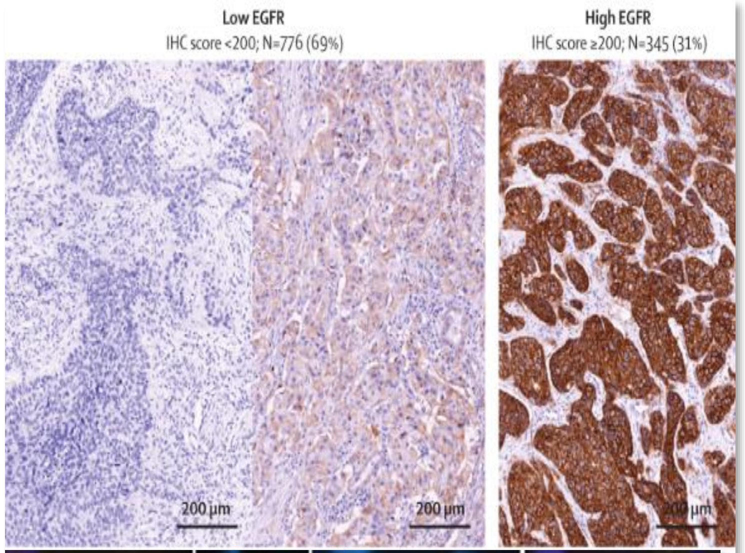
- Biomarker technique used to detect level of protein expression

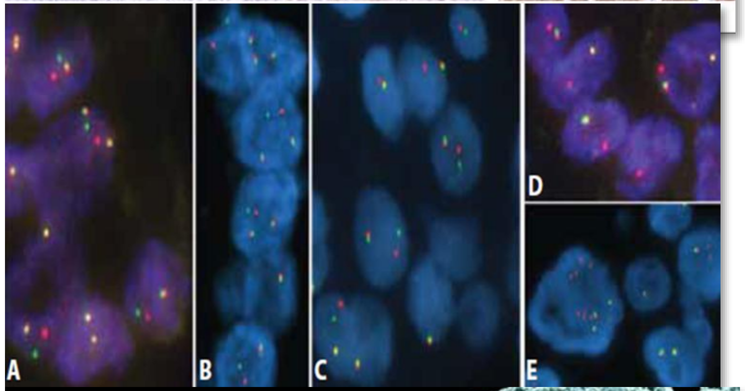
Fluorescence In Situ Hybridization (FISH)

- Biomarker technique used to detect alterations in DNA (single-gene)

Next-Generation Sequencing (NGS)

- High-throughput biomarker technique used to detect alterations in DNA (multi-gene) and to construct a comprehensive genomic profile





1. Bauman TM, et al. *J Vis Exp*. 2016;110:e53837. doi: 10.3791/53837. 2. Pirker R, et al. *Lancet Oncol*. 2012 Jan;13(1):33-42. doi: 10.1016/S1470-2045(11)70318-7. Epub 2011 Nov 4. 3. Tsao MS, et al. *IASLC Atlas of ALK and ROS1 Testing in Lung Cancer*. 2016. Reprinted courtesy of the International Association for the Study of Lung Cancer. Copyright ©2016, IASLC. 4. Bahassi and Stambrook. *Mutagenesis*. 2014 Sep;29(5):303-10. doi: 10.1093/mutage/geu031.

Aims to Push Genetics Beyond the Lab With $200 Genome

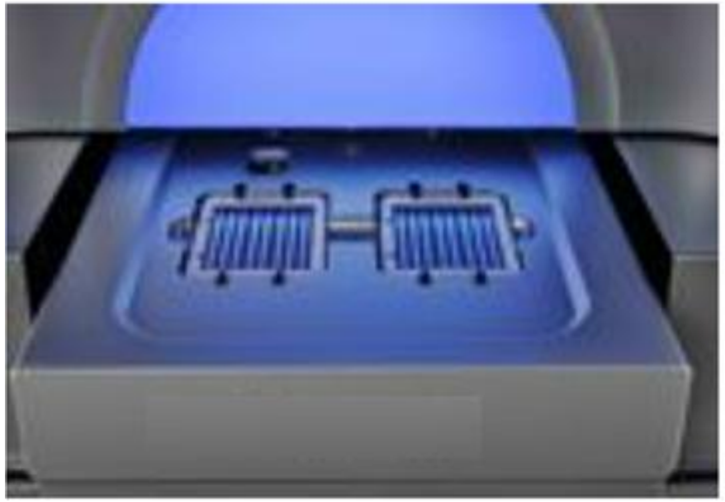
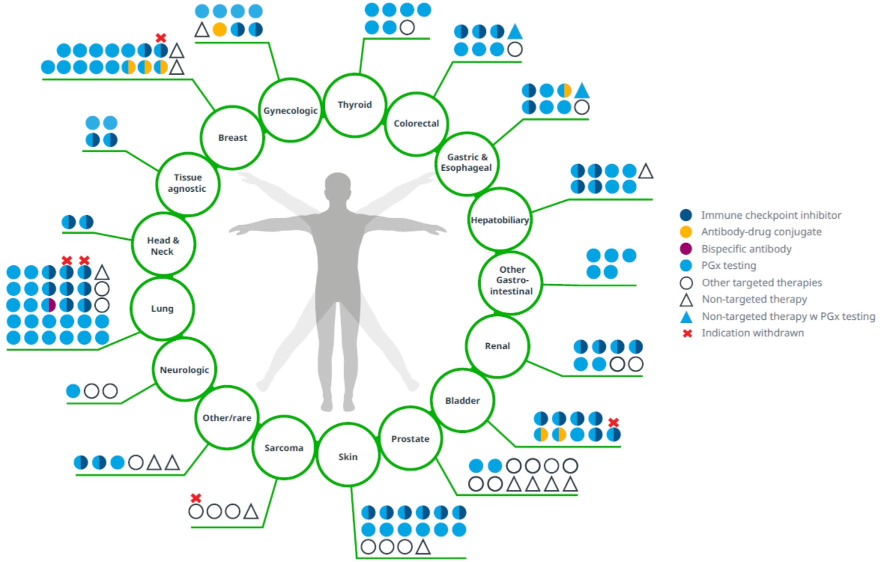


Exhibit 8: U.S. NASs in solid tumors launched 2011–2021 with indications including those granted after initial launch



Every Cancer Patient Should Be Profiled

GENERATIVE AI TO ASSIST IN TRIAL DESIGNS

Umbrella

Test impact of different drugs on different mutations in a <u>single type of cancer</u>

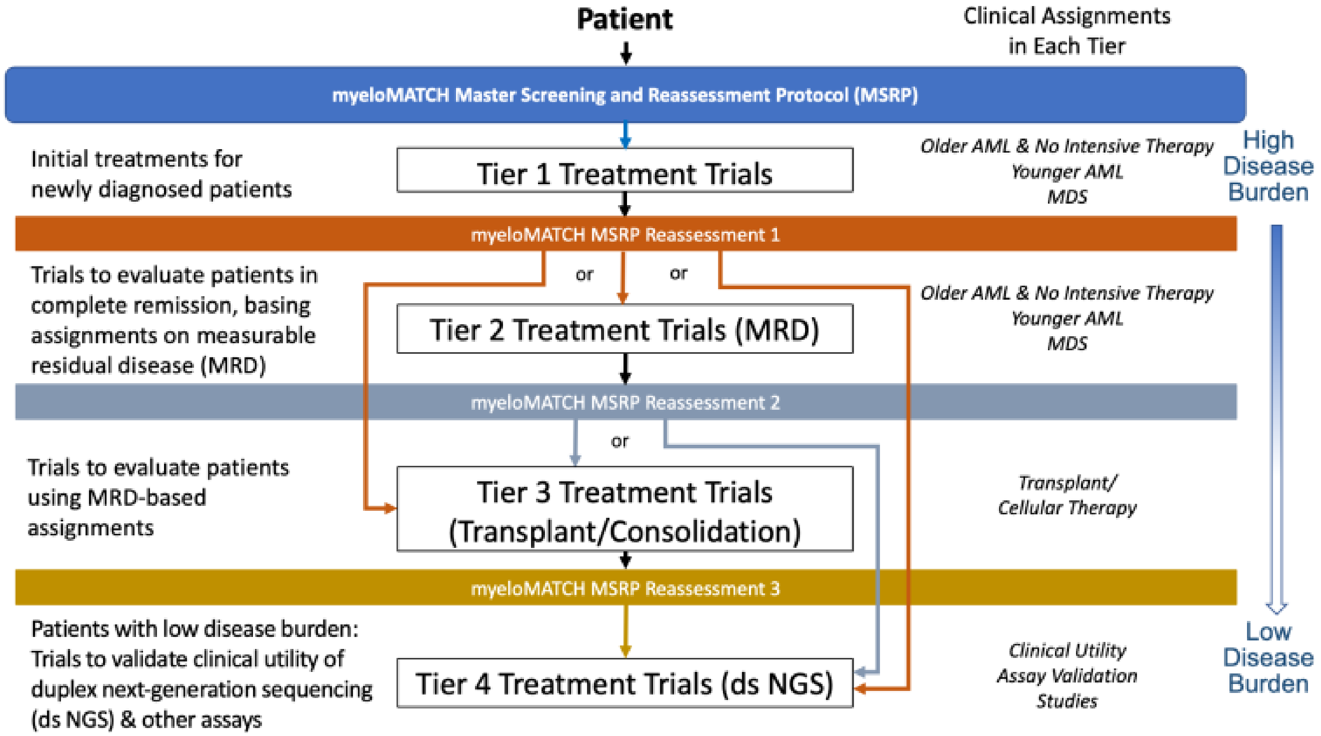
- BATTLE
- I-SPY2
- SWOG Squamous Lung Master

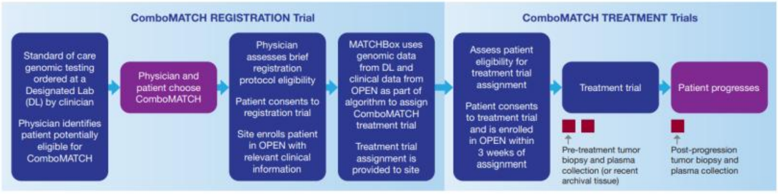
Basket

Test the effect of <u>a drug(s)</u> on a single mutation(s) in a variety of cancer types

- TAPUR
- NCI COMBO MATCH - myeloMATCH
- TAPISTRY

Kentucky Society of CLINICAL ONCOLOGY

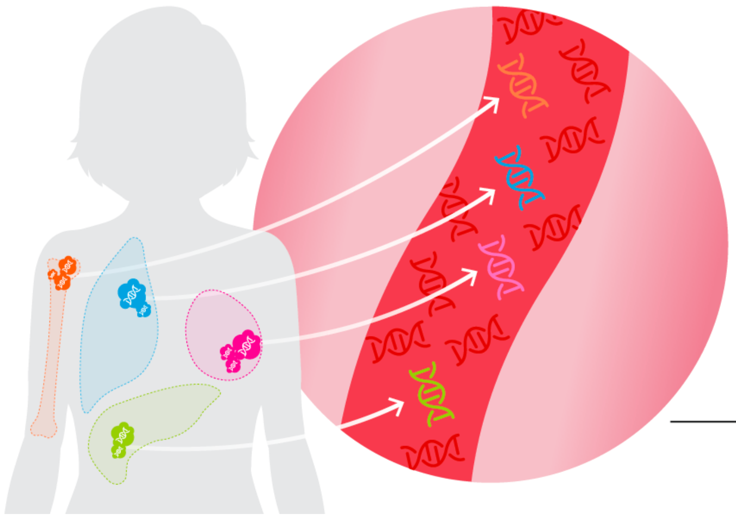




ComboMATCH is a large precision medicine initiative led by the ECOG-ACRIN Cancer Research Group and National Cancer Institute, with treatment trials by the Alliance for Clinical Trials in Oncology, Children's Oncology Group, NRG Oncology, and SWOG Cancer Research Network

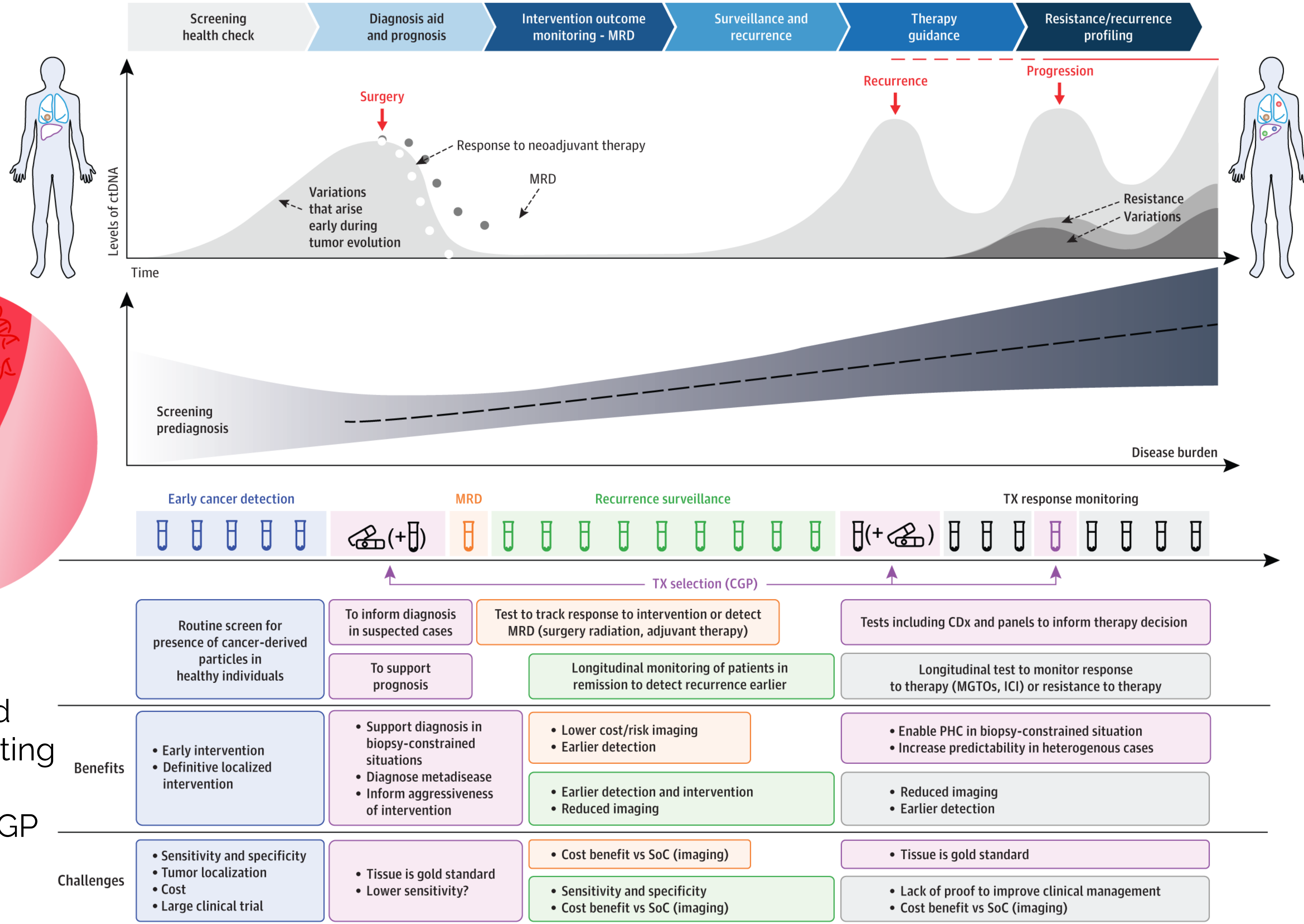
myeloMATCH
AML | MDS
Precision Medicine in Myeloid Cancer

Early profiling requires lifetime tracking



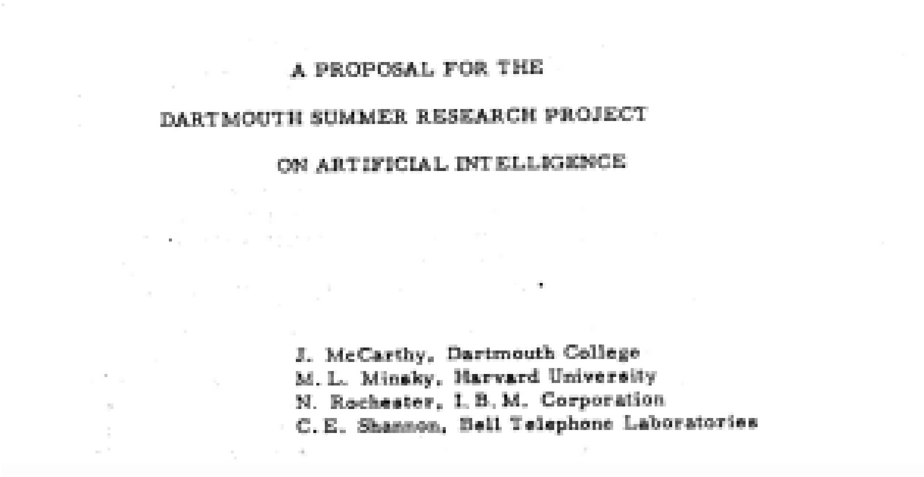
Minimally-invasive liquid biopsies capture circulating tumor (ctDNA) from the blood and offer quick CGP

Bettegowda et al., Sci Transl Med. 2014.
Lanman et al., PLOS One. 2015.



The term artificial intelligence (AI) emerged in 1956, and since then, AI has progressed tremendously

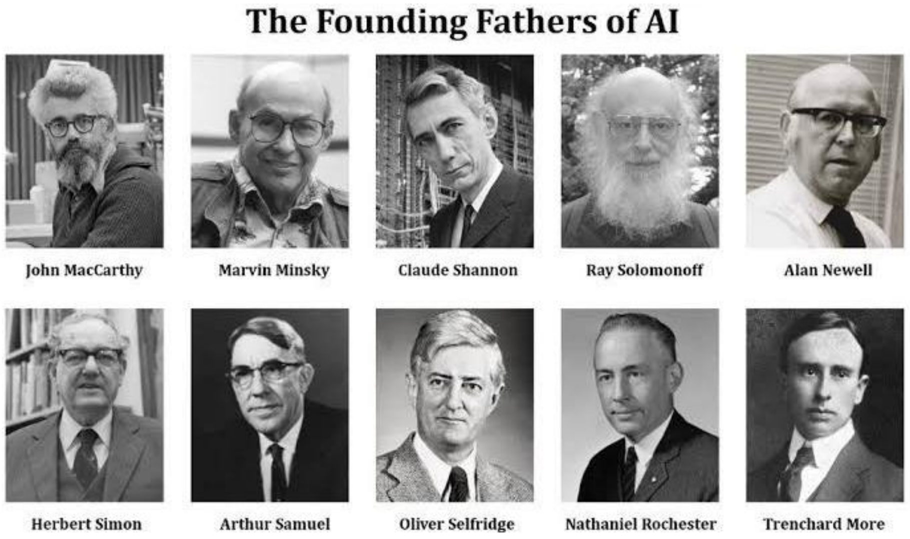
- Early advances in AI focused on building neural networks, modeled after the human brain's ability to make decisions from the given data.
- Around the 1980s, these artificial neural networks progressed to a point where "machine learning" became popular.
- Machine learning refers to a machine's ability to review data and find patterns, thus learning from the data and then applying it to problems to make informed decisions, in a process of continuous optimization.
- Then came the trend of deep learning, which is a more sophisticated subset of machine learning that requires no human intervention for the machine to progress, deducing whether they have made good predictions on their own and continuing the process of learning from these deductions.
- Today's AI machines use a mix of machine learning and deep learning, and these machines can be applied to a wide range of disciplines, including oncology.


A PROPOSAL FOR THE

DARTMOUTH SUMMER RESEARCH PROJECT

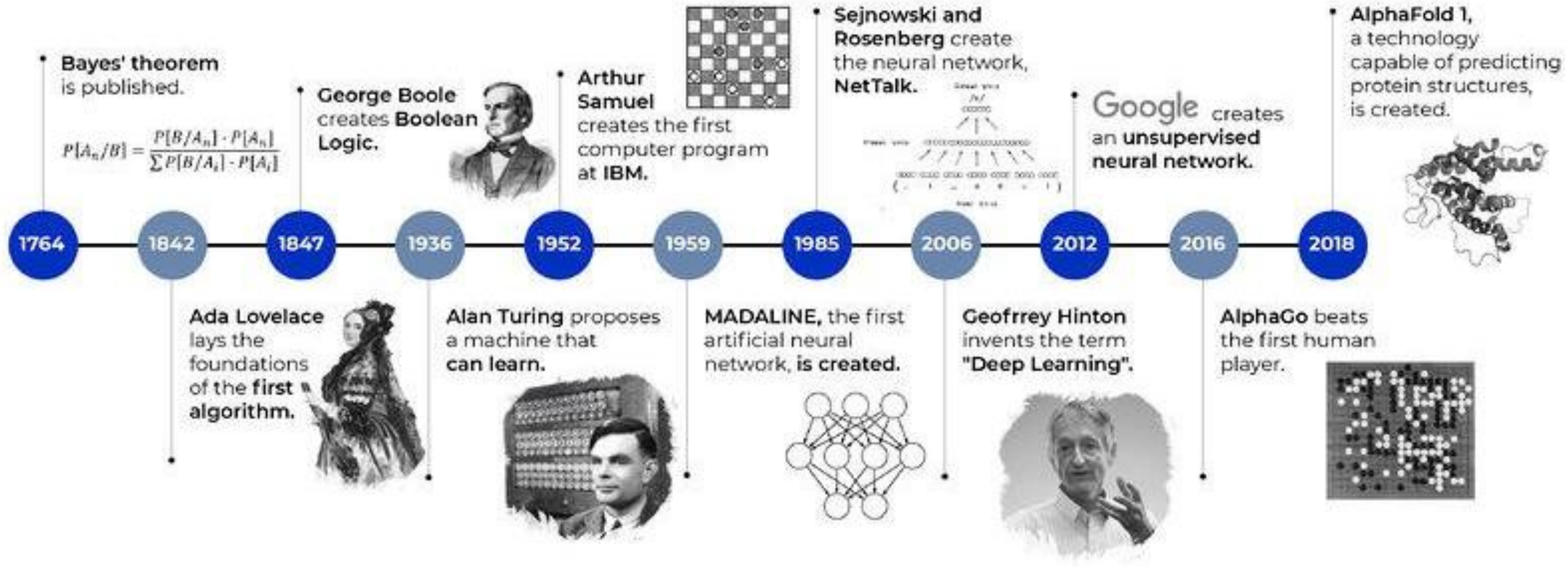
ON ARTIFICIAL INTELLIGENCE

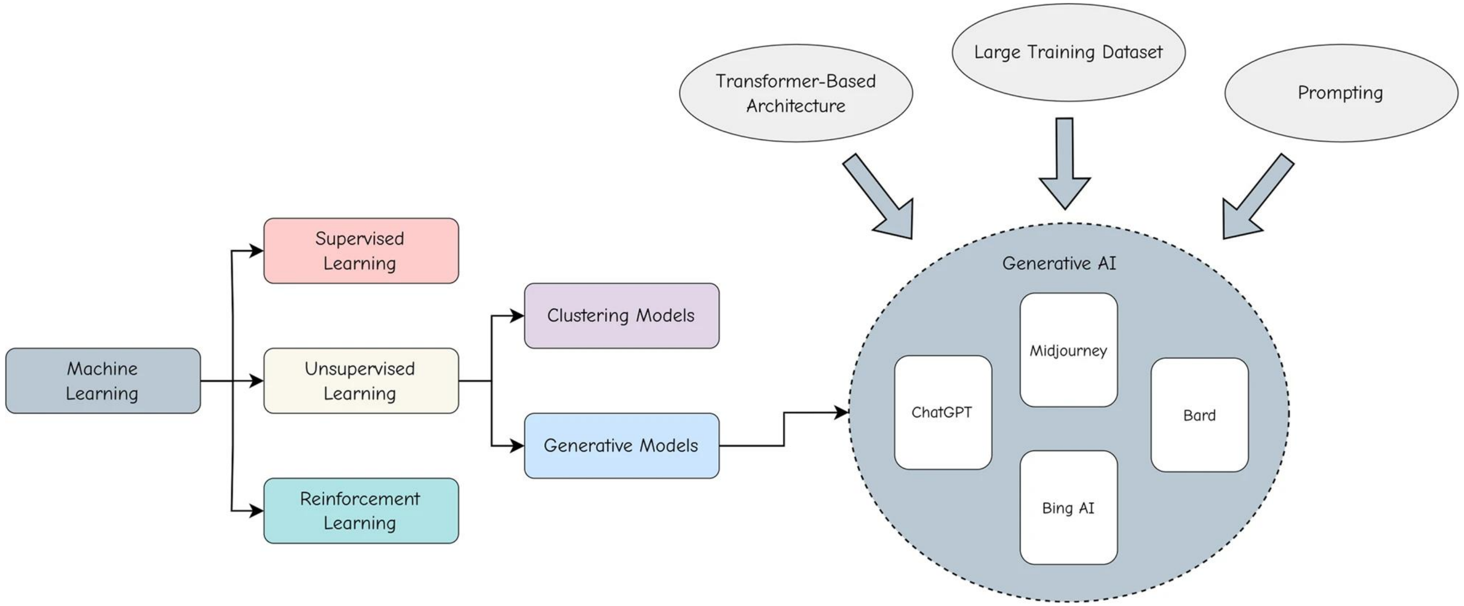
J. McCarthy, Dartmouth College
M. L. Minsky, Harvard University
N. Rochester, I. B. M. Corporation
C. E. Shannon, Bell Telephone Laboratories



MACHINE LEARNING TIMELINE

The term artificial intelligence (AI) emerged in 1956, and since then, AI has progressed tremendously





What is generative artificial intelligence (GenAI)

- Generative artificial intelligence (AI) describes algorithms (such as LLMs) that can be used to create new content (generate data), including audio, code, images, text, simulations, and videos.
- Generative AI systems fall under the broad category of machine learning.
- The increasing application of Generative AI in healthcare has the potential to revolutionize drug discovery, basic and clinical research, and patient care.

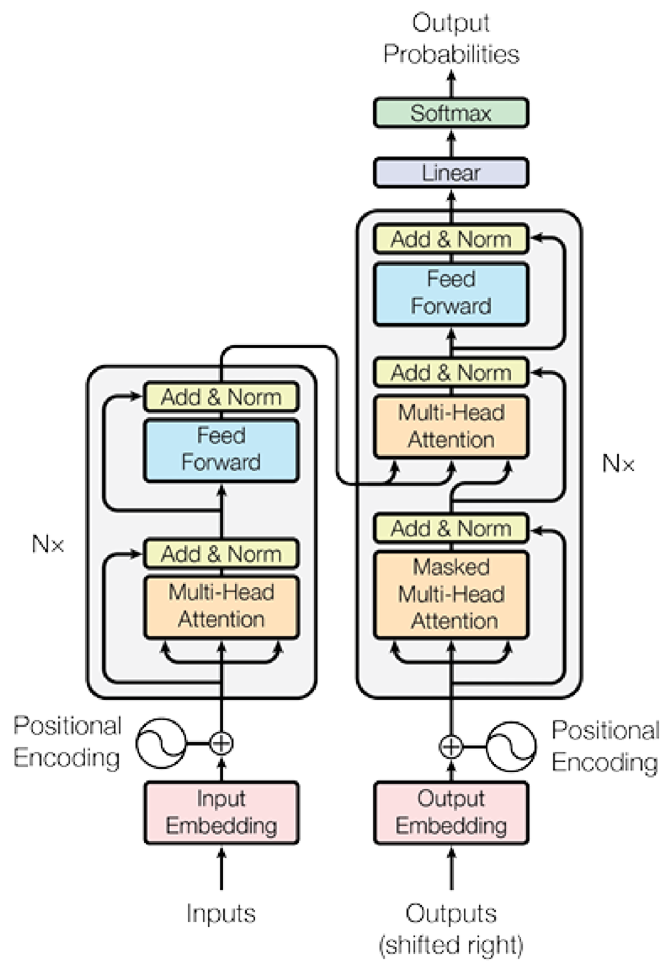


Figure 1: The Transformer - model architecture.

https://doi.org/10.48550/arXiv.1706.03762

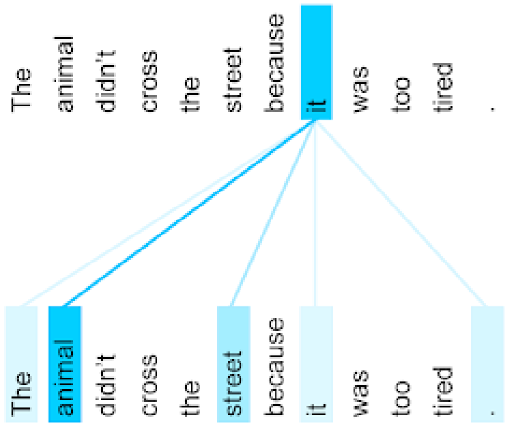
Generative AI models typically pre-trained in an unsupervised manner.

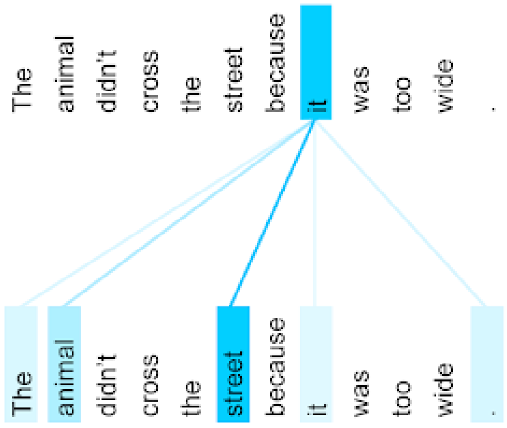
The most popular generative AI model for language generation is LLMs (Generative Pre-trained Transformer)

State-of-the-art Gen-AI models aka Large Language Models (LLMs) share a similar transformer-based architecture

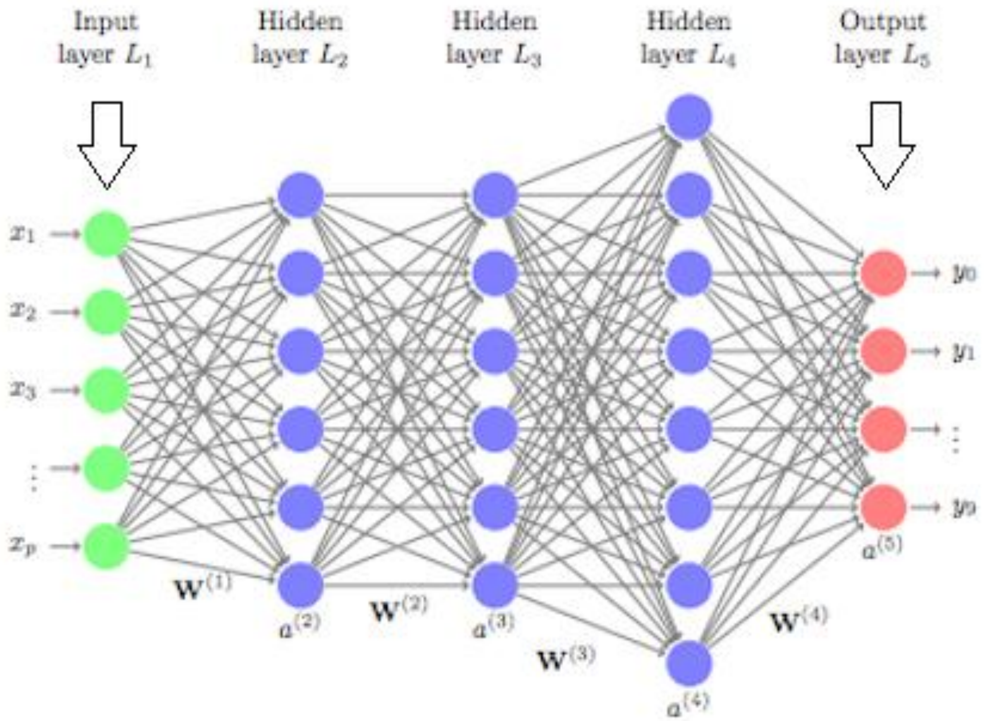
The Transformer only performs a small, constant number of steps (chosen empirically). It enabled LLMs and other large models to scale to billions of parameters

In each step, it applies a self-attention mechanism which directly models relationships between all words in a sentence, regardless of their respective position.





Artificial Neural Network



The Nobel Prize in Physics 2024

John Hopfield

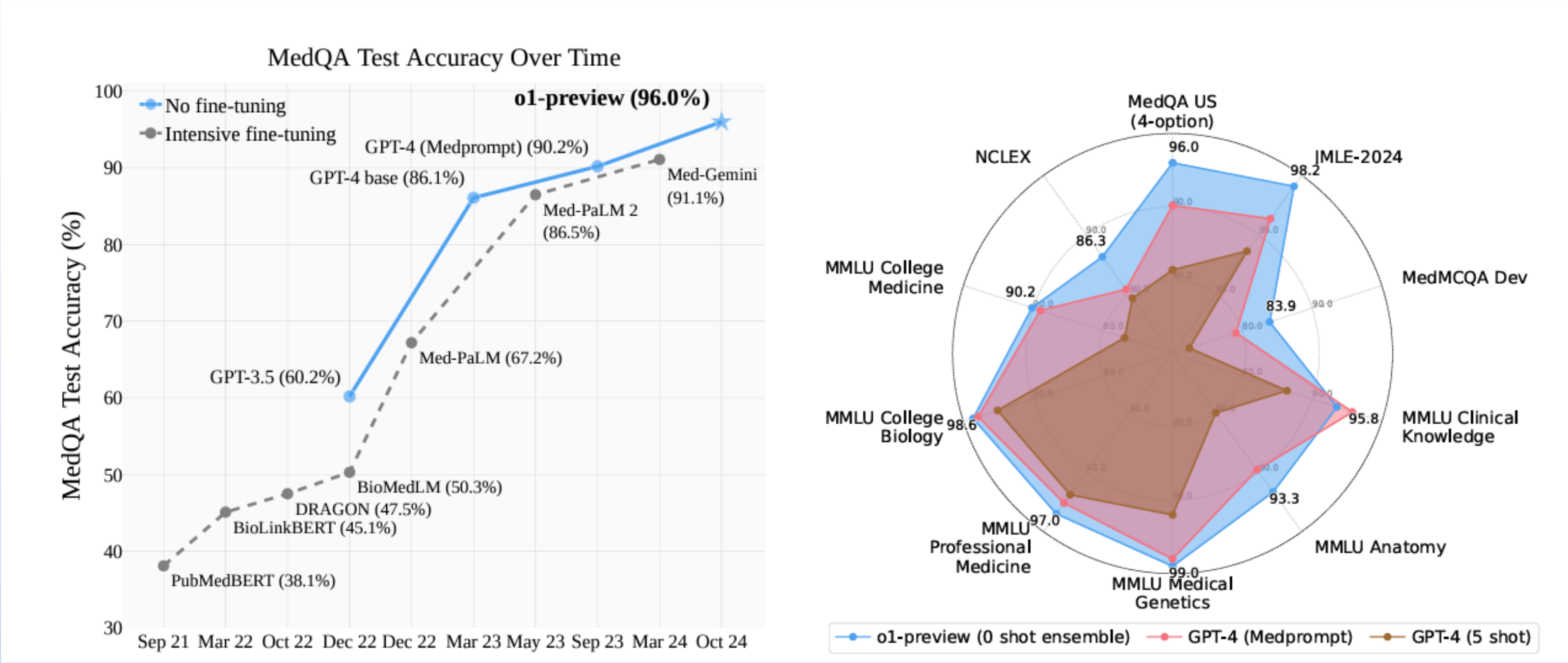
"for foundational discoveries and inventions that enable machine learning with artificial neural networks"

John Hopfield. Ill. Niklas Elmehed © Nobel Prize Outreach

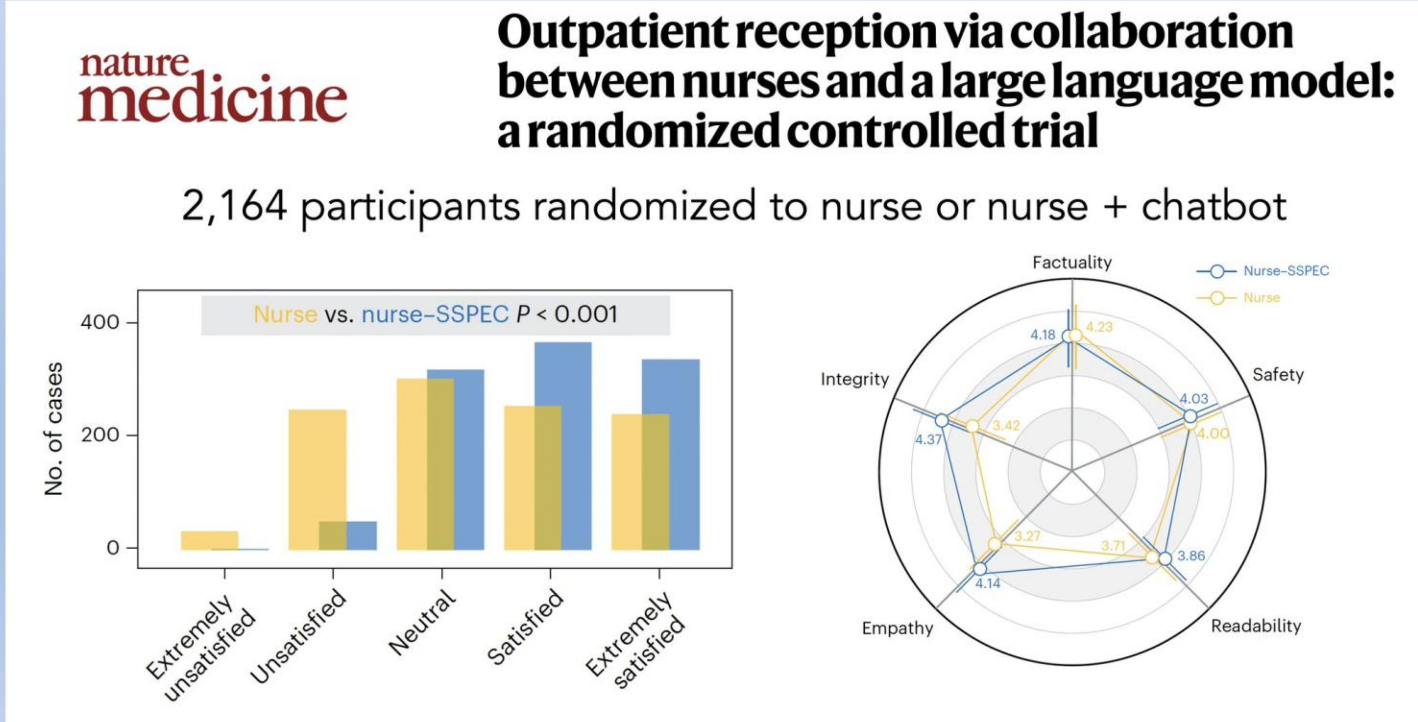
Geoffrey Hinton

"for foundational discoveries and inventions that enable machine learning with artificial neural networks"

Geoffrey Hinton. Ill. Niklas Elmehed © Nobel Prize Outreach

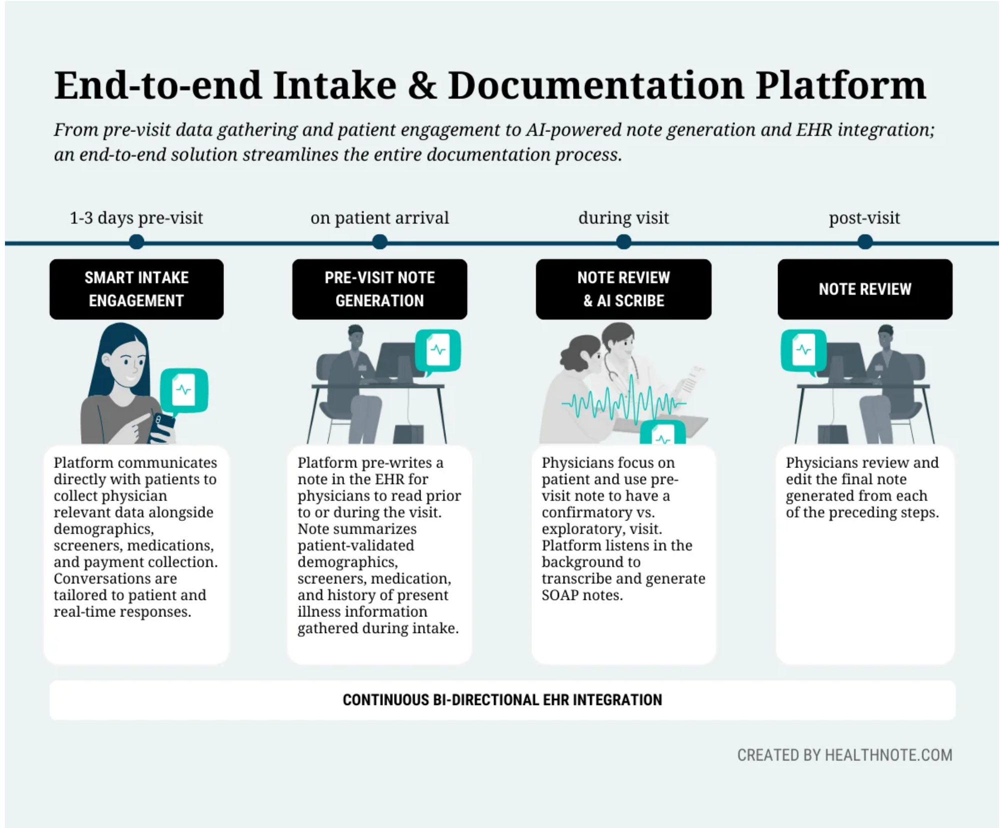


https://arxiv.org/abs/2411.03590v1



https://www.nature.com/articles/s41591-024-03148-7

Ambient AI: Medical Scribes



3M M*Modal Fluency Align	Abridge	accel-EQ	Ambience	Athelas Scribe	Augmedix Go	Augnito	Beam Health Shine AI
Chartnote	Contrast	Corti	DeepScribe	DeepCura	Eleos Health	Freed	Fusion Narrate + SOAP Health
Heidi Health	Innovaccer InScribe	iScribeHealth	Knowtex	Mariana AI	mdhub	Mentalyc	Mutuo Health
Nabla Copilot	Nuance DAX Copilot	Overnight Scribe	Playback Health	QiiQ	S10.AI	ScribeAmerica Speke	Scribeberry
ScribeMD	Simbo AI	Suki	Sully.ai	Sunoh	Tali AI	Tortus	Upheal

Data Structuring is one of the biggest challenges

- Optimized approaches to structure and standardize disparate patient-specific information (have not yet been developed.
  - Narrative text in patient medical records and clinical notes,
  - Radiological examinations,
  - Laboratory data,
  - Genomic information,
  - Pharmacogenomics
  - Drug lists
- Complicated by various medical ontologies used to generalize the data (e.g., SNOMED-CT, UMLS, ICD-9, ICD-10), introducing conflicts and inconsistencies.
- It is necessary to develop educational and case management support systems to ensure that the comprehensive, evidence-based information generated from machine learning technology is truly actionable for all patients.
- Potential solutions lie in the effective use of comprehensive electronic health information systems, including real-world data, to guide the clinical decision-making process.

https://ai.nejm.org/doi/full/10.1056/AIdbp2300110

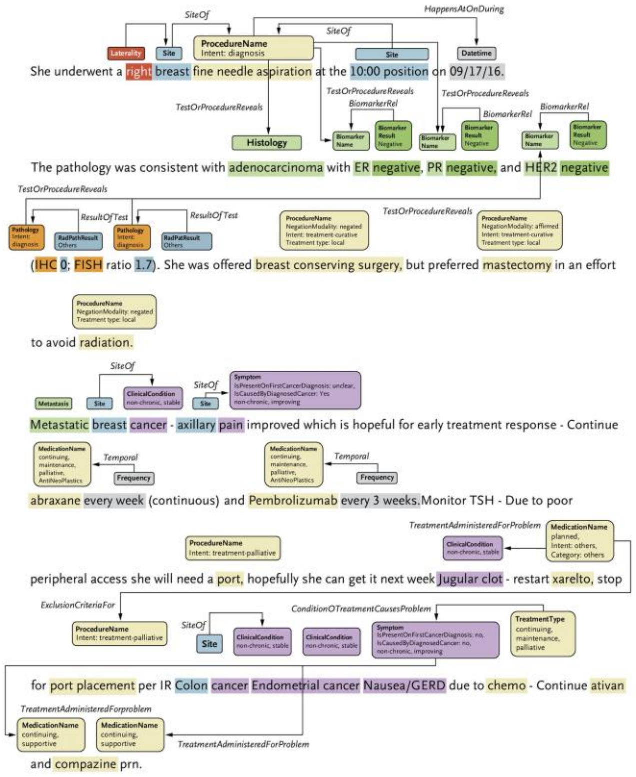
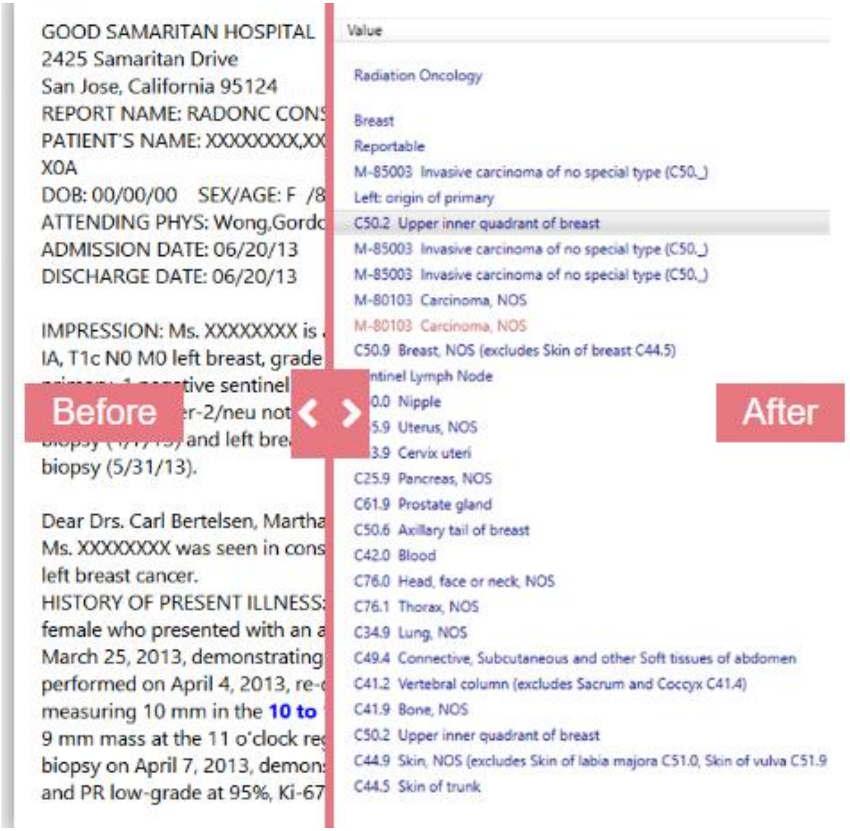
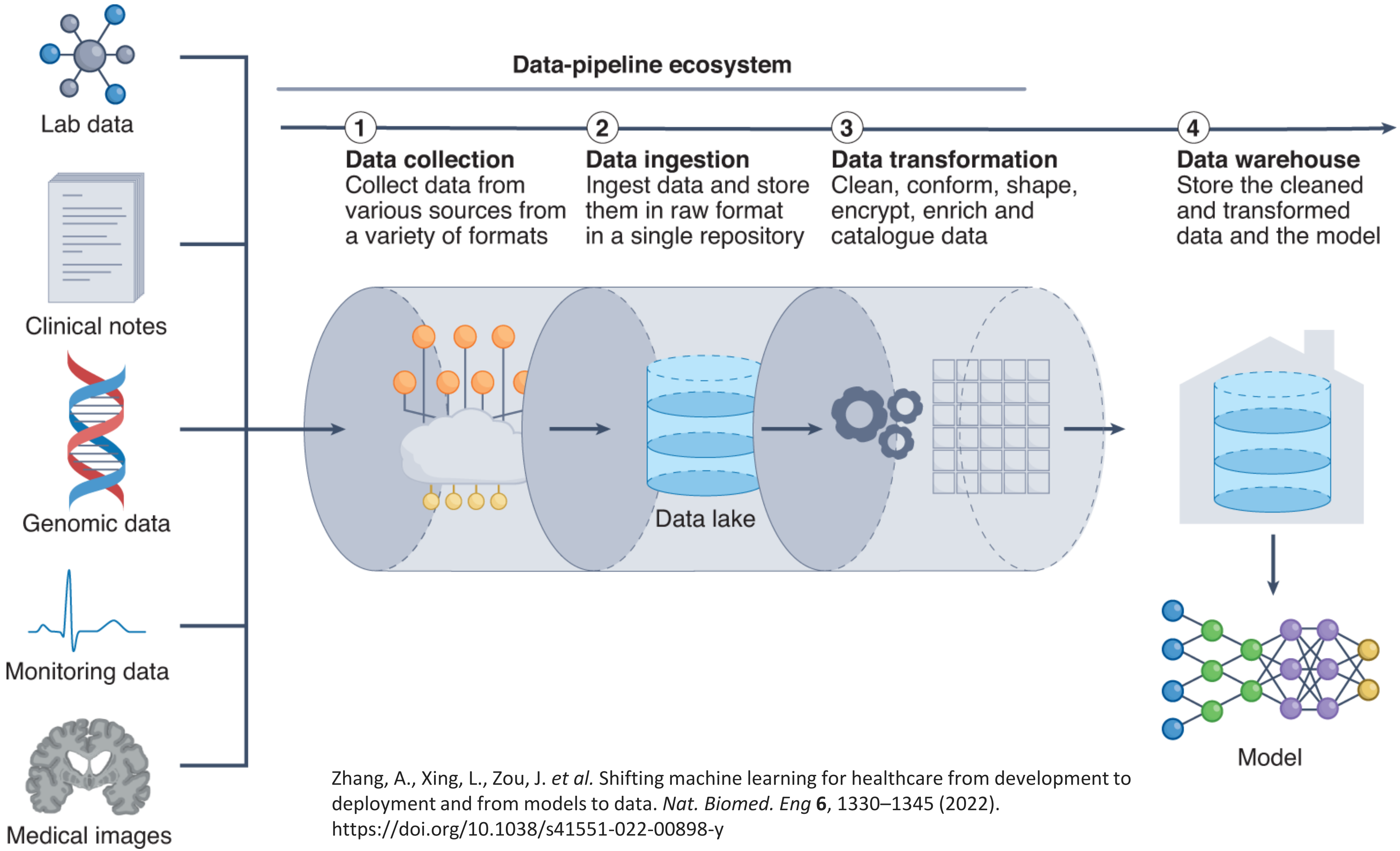


Figure 1. A Sample of the Annotated, Deidentified Medical Oncology Progress Notes.



Using Optical Character Recognition + Natural Language Processing + Gen-AI to solve data structuring

- Gen-AI can take unstructured data sets—information that has not been organized according to a preset model, making it difficult to analyze—and analyze them,
- This is a potential breakthrough for healthcare operations, which are rich in unstructured data such as clinical notes, diagnostic images, medical charts, and recordings.
- These unstructured data sets can be used independently or combined with large, structured data sets, such as insurance claims.



Zhang, A., Xing, L., Zou, J. *et al.* Shifting machine learning for healthcare from development to deployment and from models to data. *Nat. Biomed. Eng* **6**, 1330–1345 (2022). https://doi.org/10.1038/s41551-022-00898-y

Convolutional Neural Networks (CNN)

Algorithms based on artificial intelligence (AI) represent a promising avenue to simultaneously improve the accuracy of diagnostic images, as well as to help radiologists become more, giving them more time to focus on patient care.
Academic Radiology: average radiologist must interpret an image every 3-4 seconds to maintain the daily workflow

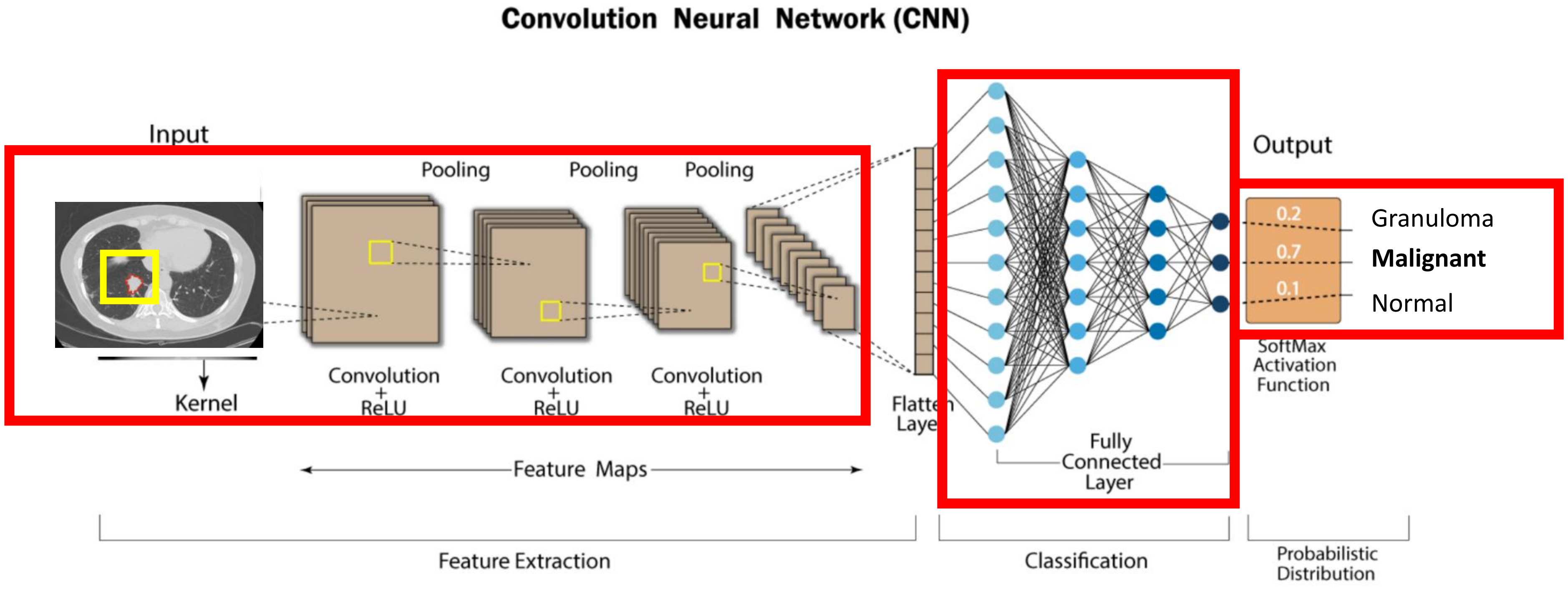
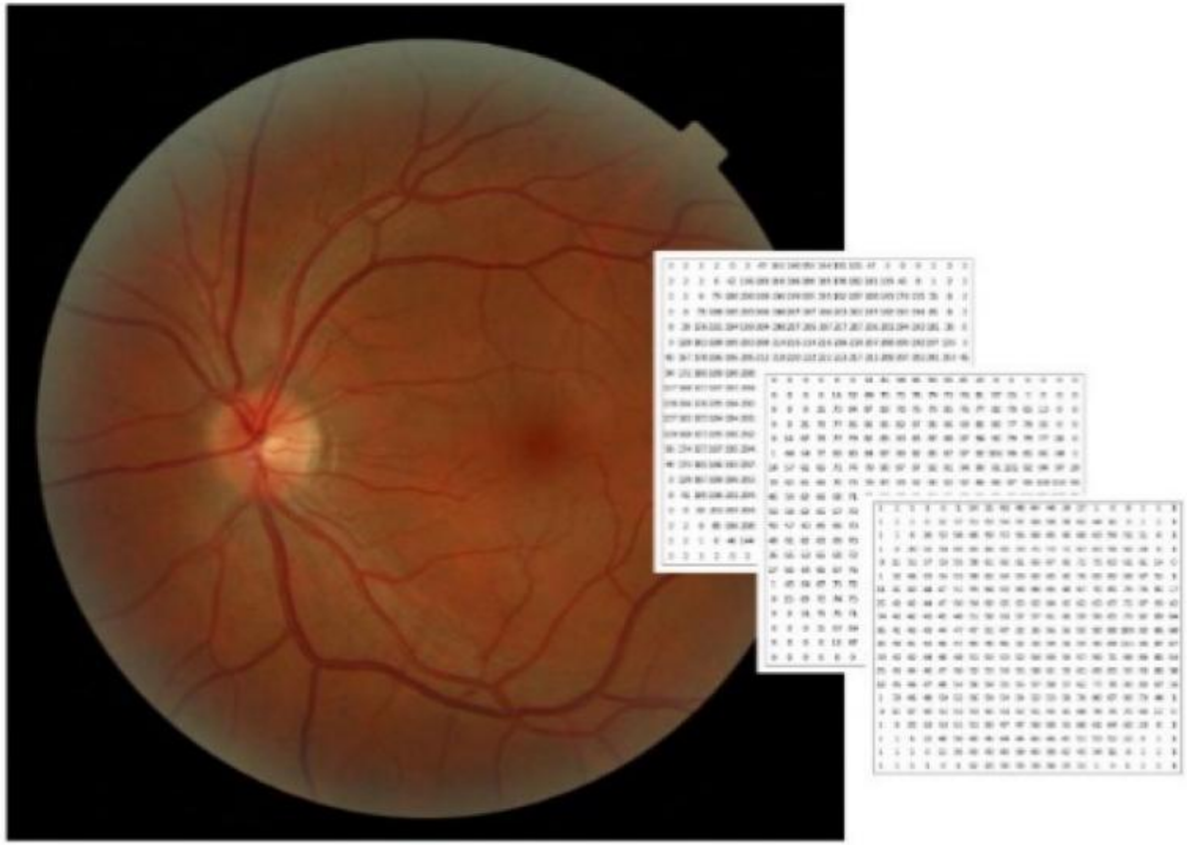
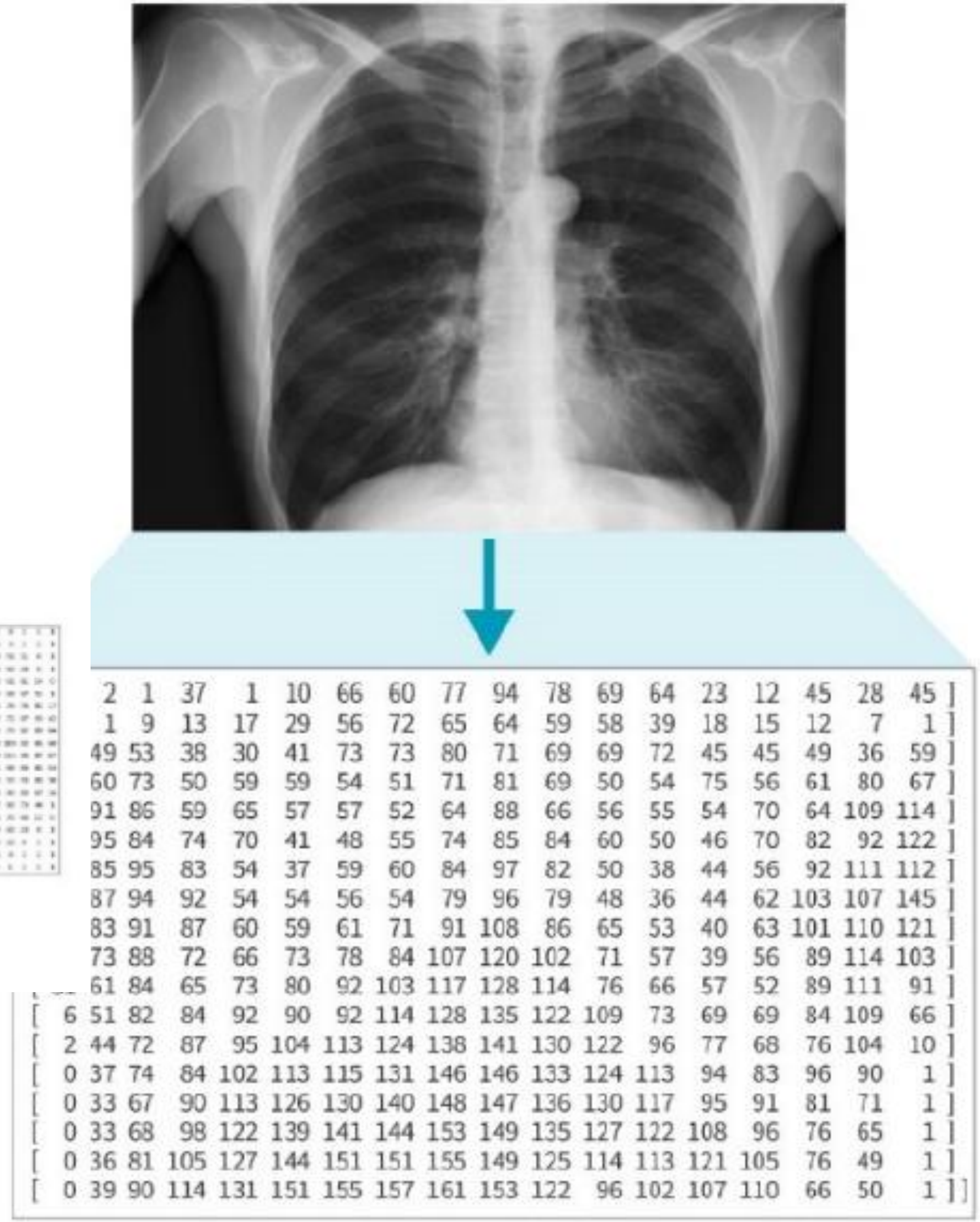


Image Source: Internet and Adapted by Dr. Nikhil Thaker

224X224 COLORED IMAGE → **150,528 FEATURES**





Fundamentals of Machine Learning for Healthcare - SOM-XCHE0010 Stanford School of Medicine, Stanford Center for Health Education. Study guide (1):27-28

Possibilities: Using Cancer Screening and AI Models for AEs

nature

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nature > letters > article

Published: 25 January 2017

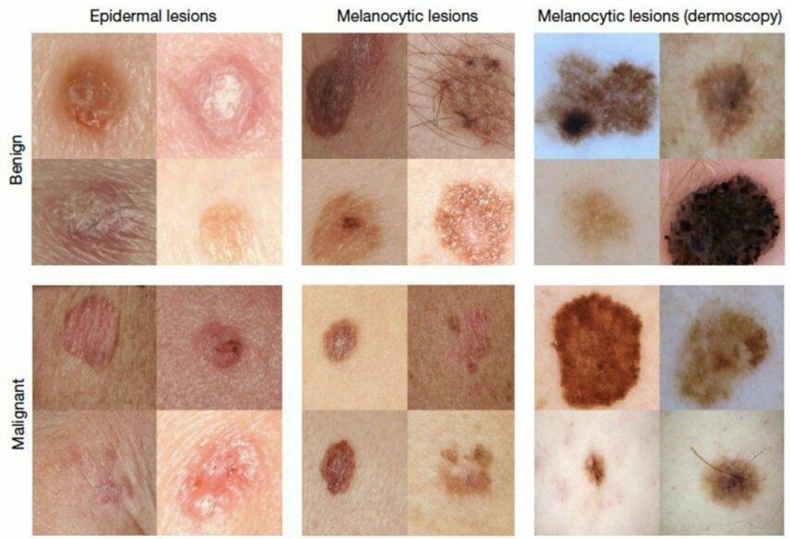
Dermatologist-level classification of skin cancer with deep neural networks

Andre Esteva, Brett Kuprel, Roberto A. Novoa, Justin Ko, Susan M. Swetter, Helen M. Blau & Sebastian Thrun

Nature **542**, 115–118 (2017) | Cite this article

194k Accesses | **5289** Citations | **2938** Altmetric | Metrics

21 Board Certified Stanford Dermatologists
129,450 images of 2,032 diseases
1.41 million AI training images



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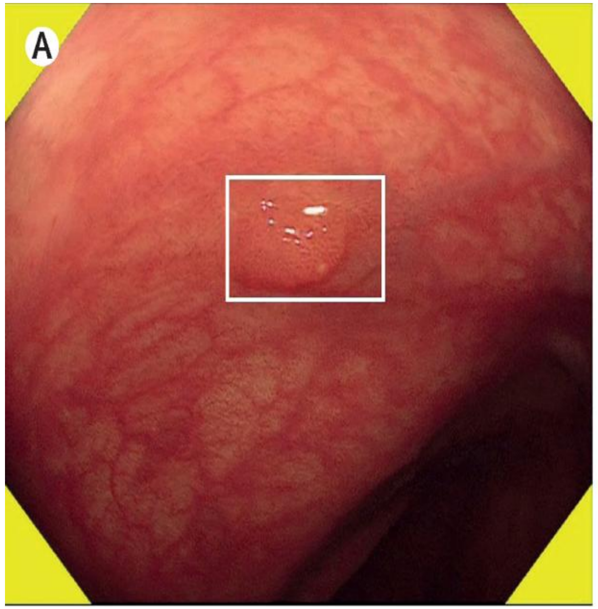
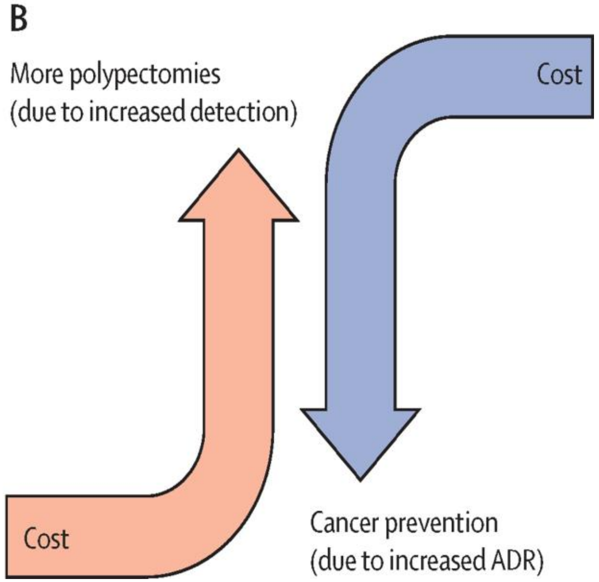
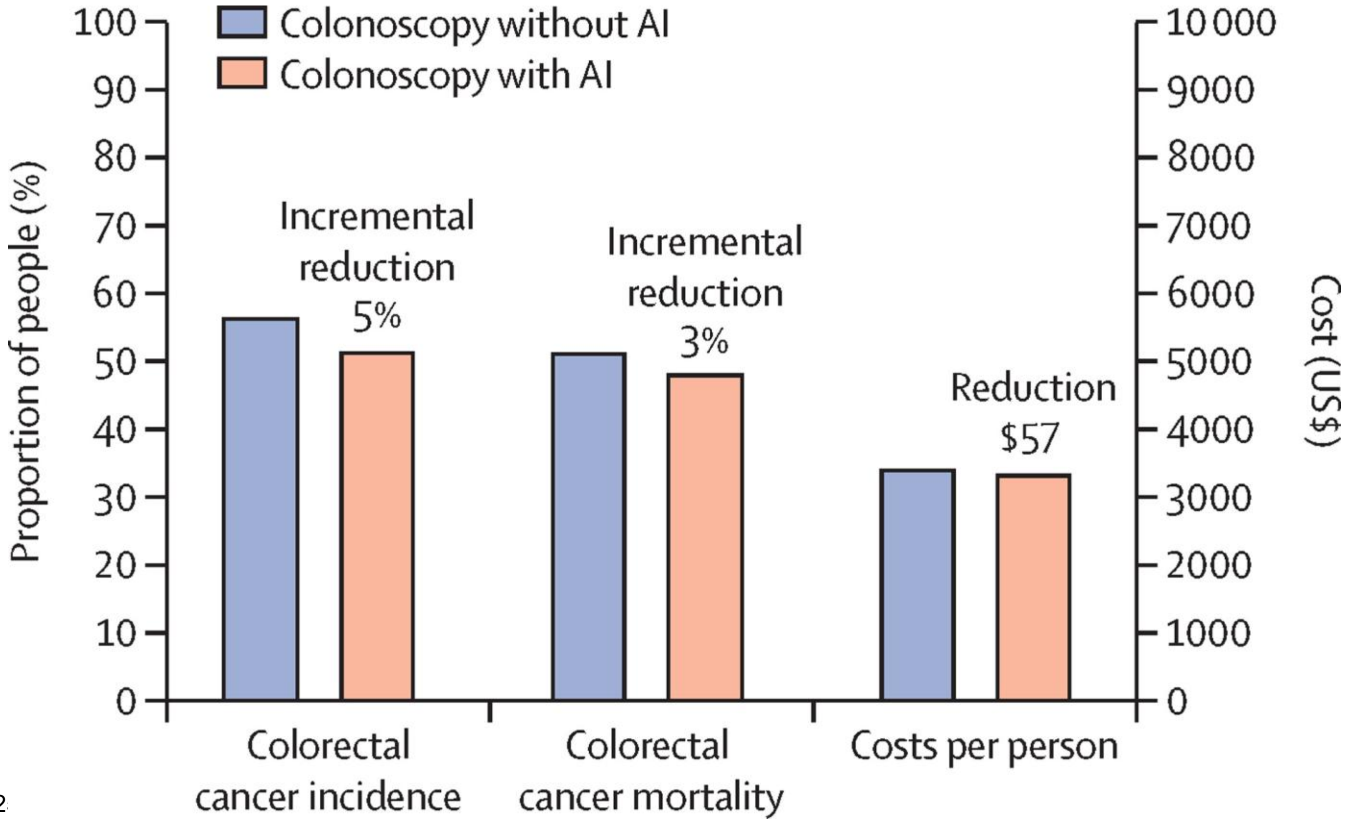




Cost-effectiveness of artificial intelligence for screening colonoscopy: a modelling study

Prof Miguel Areia, MD, Yuichi Mori, MD, Loredana Correale, PhD, Prof Alessandro Repici, MD, Prof Michael Bretthauer, MD, Prof Prateek Sharma, MD, Filipe Taveira, MD, Marco Spadaccini, MD, Giulio Antonelli, MD, Alanna Ebigbo, MD, Prof Shin-ei Kudo, MD, Julia Arribas, MD, Ishita Barua, MD, Prof Michal F Kaminski, MD, Prof Helmut Messmann, MD, Prof Douglas K Rex, MD, Prof Mário Dinis-Ribeiro, MD, Prof Cesare Hassan, MD

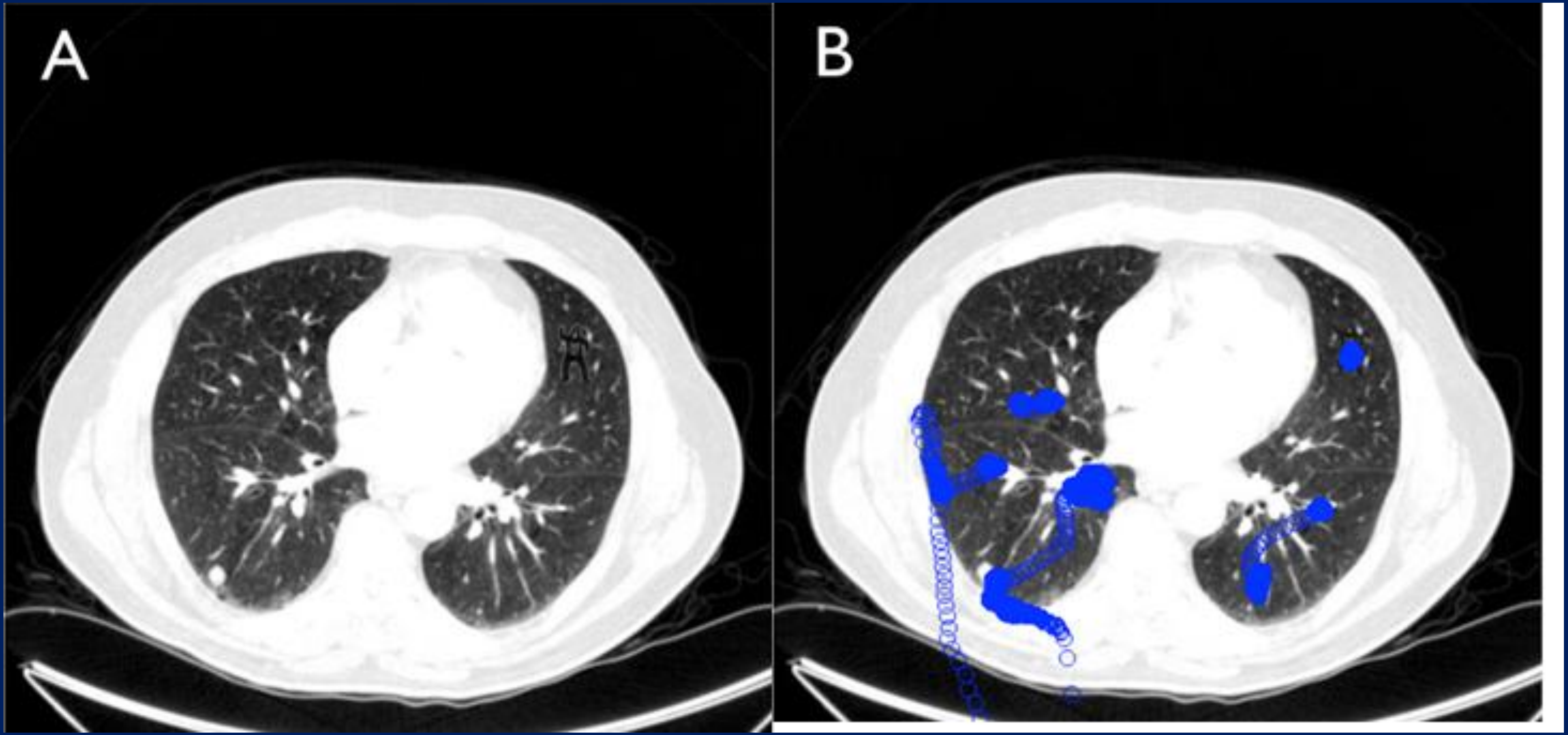
The Lancet Digital Health
Volume 4 Issue 6 Pages e436-e444 (June 2022)
DOI: 10.1016/S2589-7500(22)00042-5



AI in cancer detection and diagnostic optimization:
Algorithms and Computer Vision

- Algorithms based on artificial intelligence (AI) represent a promising avenue to simultaneously improve the accuracy of diagnostic images, as well as to help radiologists become more, giving them more time to focus on patient care.
- Academic Radiology: average radiologist must interpret an image every 3-4 seconds to maintain the daily workflow
- AI components in radiology and image analysis would drive greater efficiency in this field, by generating access to a greater amount of data than their human counterparts.
- Sustained inattentional blindness even in expert observers is a documented phenomenon, and AI with computer vision can overcome those challenges.
- In addition, unnecessary diagnostic procedures can also be reduced by leveraging these innovative tools.
- AI technologies able to detect pixel-level changes in tissue invisible to the human eye, while humans used forms of reasoning not available to AI. The ultimate goal will be to find the best way to combine the two to transform the future of radiology.

Sustained inattentional blindness



S4ND: Single-Shot Single-Scale Lung Nodule Detection

- As an additional example, a deep learning algorithm in Computer Vision, using 1,000 AI CT scans to teach you how to analyze lung tissue for abnormalities, found that AI could identify lung cancer with 30% more accuracy than humans (state of the art).

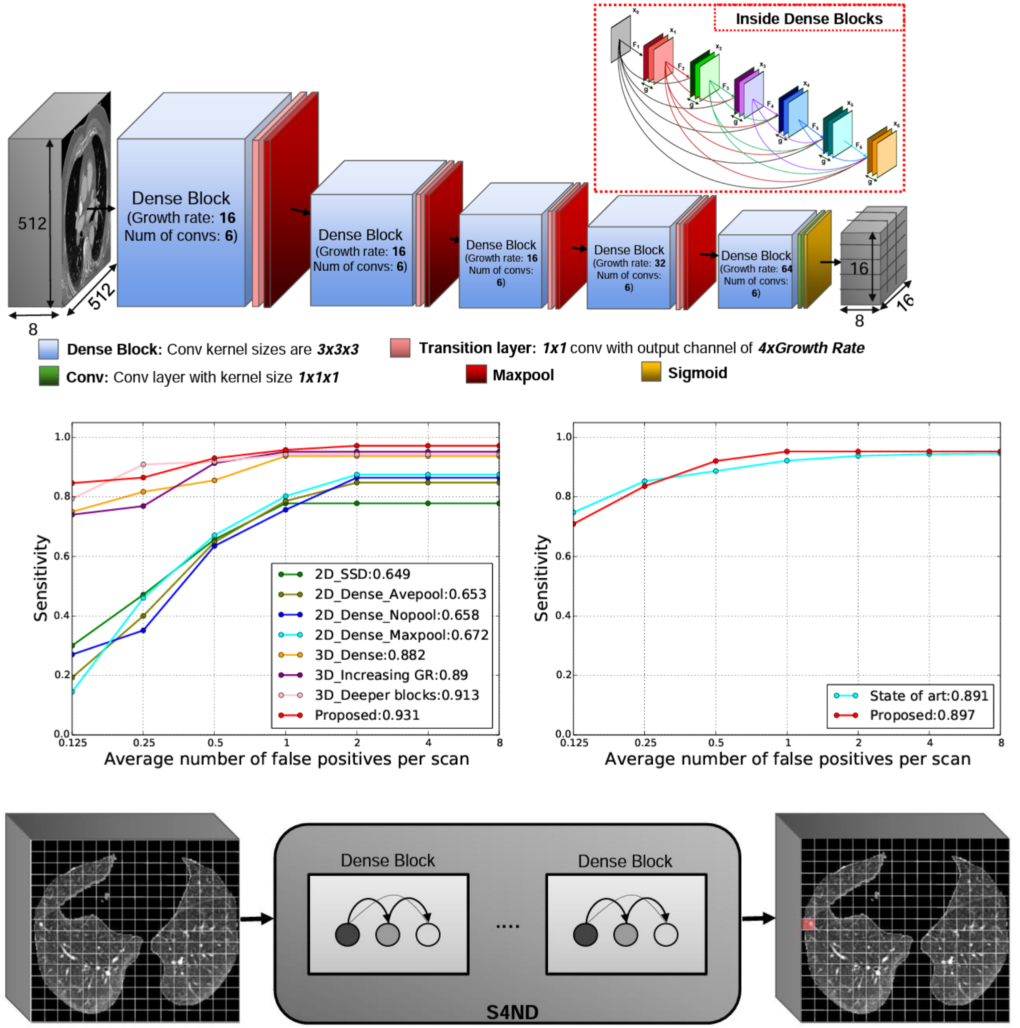
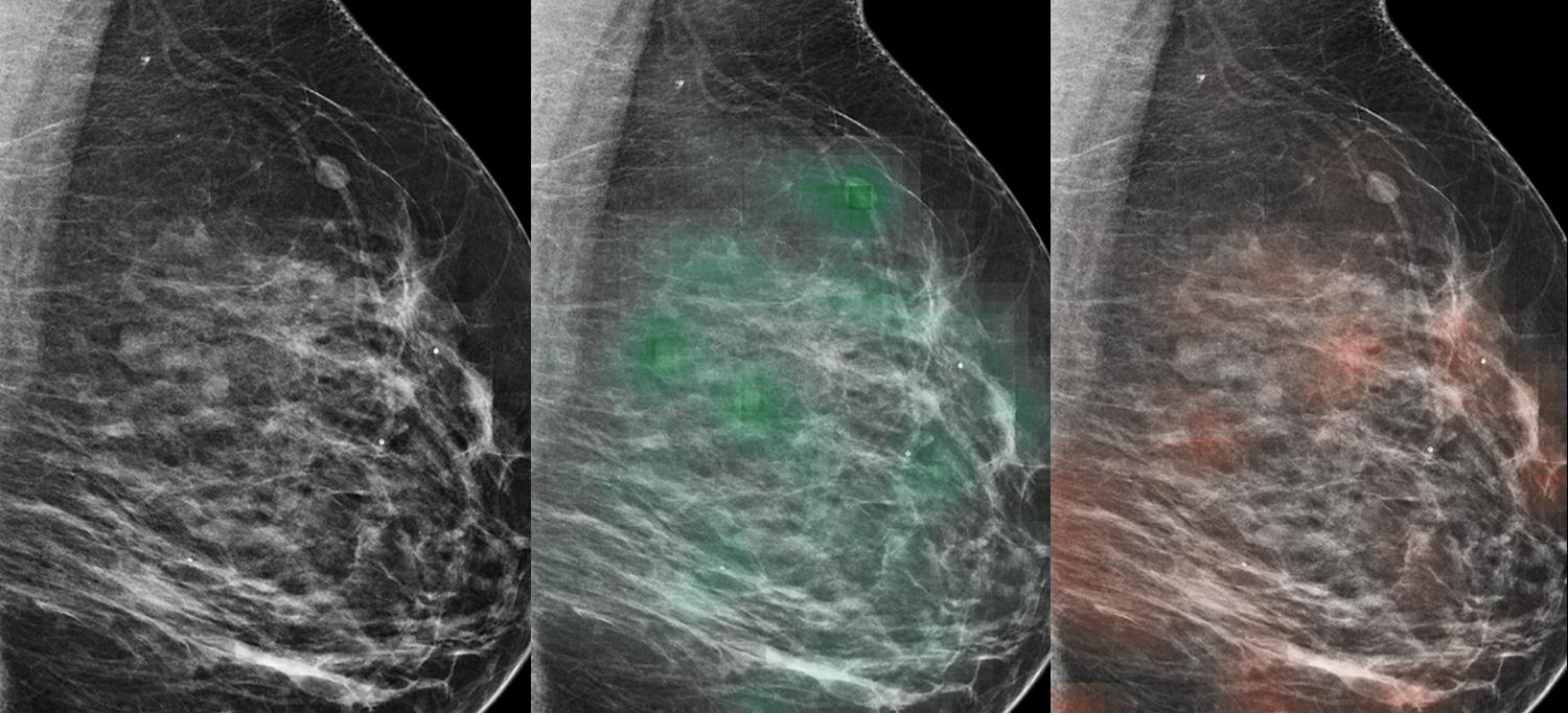


Fig. 1. Our framework, named S4ND, models nodule detection as a cell-wise classification of the input volume. The input volume is divided by a 16 × 16 × 8 grid and is passed through a newly designed 3D dense CNN. The output is a probability map indicating the presence of a nodule in each cell.

Khosravan N., Bagci U. (2018) S4ND: Single-Shot Single-Scale Lung Nodule Detection. In: Frangi A., Schnabel J., Davatzikos C., Alberola-López C., Fichtinger G. (eds) Medical Image Computing and Computer Assisted Intervention – MICCAI 2018. MICCAI 2018. Lecture Notes in Computer Science, vol 11071. Springer, Cham. https://doi.org/10.1007/978-3-030-00934-2_88



An AI tool learned to predict which lesions were likely malignant (red heat map) or likely benign (green heat map), with potential to aid radiologists in the diagnosis of breast cancer.

IMAGES COURTESY OF NYU SCHOOL OF MEDICINE

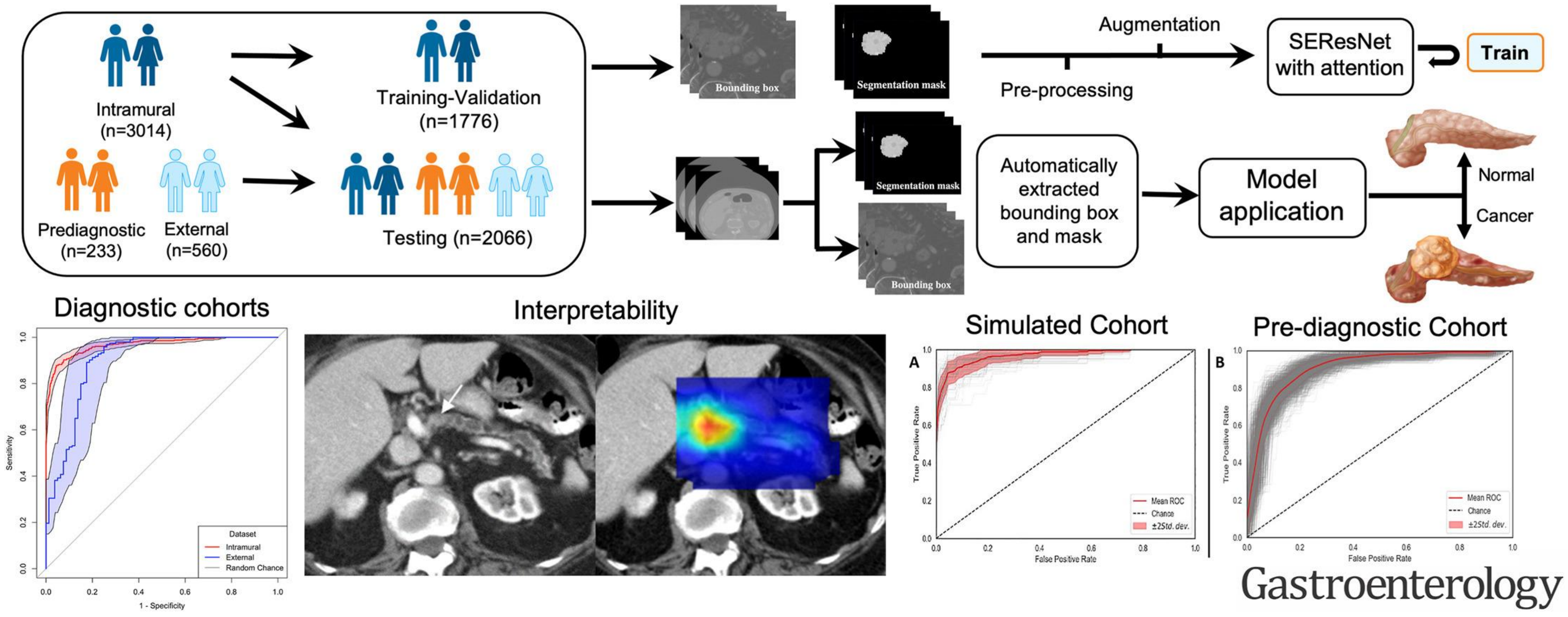
Mammography Screening with Artificial Intelligence trial (MASAI): a clinical safety analysis of a randomised, controlled, non-inferiority, single-blinded, screening accuracy study

R	Detection Rate	Recall	PPV
AI-integrated Mammography ***(39,996 women)***	6.1/1000	2.2%	28.3%
Conventional Mammography ***(40,024 women)***	5.1/1000	2.0%	24.8%

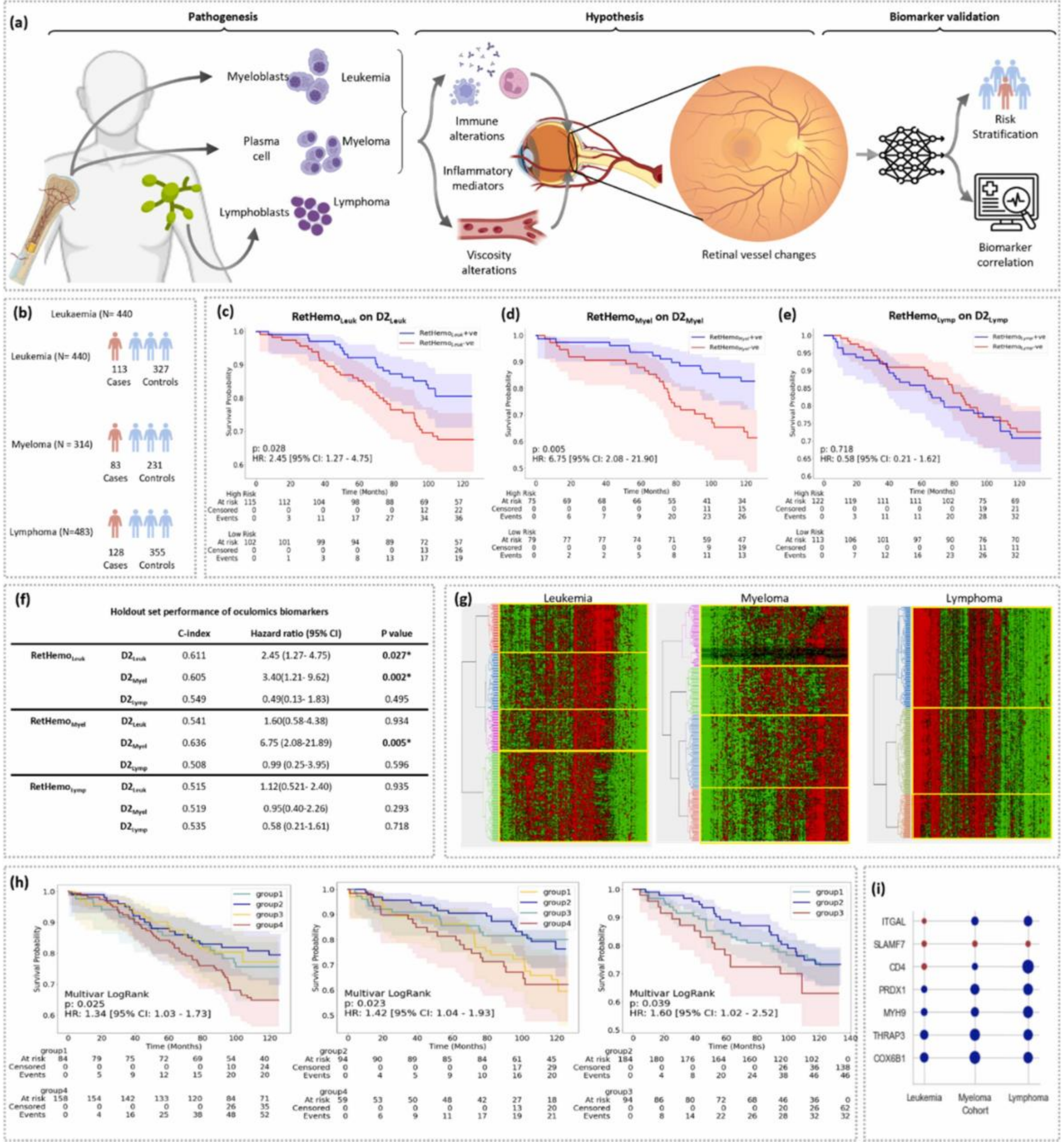
- 80,033 women randomized
- 44.3% reduction in screen-reading radiologist workload
- **Conclusion**: *AI-supported screening resulted in a similar cancer detection rate compared with standard double reading, with a substantially lower screen-reading workload*

THE LANCET
Oncology

Automated Artificial Intelligence Model Trained on a Large Data Set Can Detect Pancreas Cancer on Diagnostic Computed Tomography Scans As Well As Visually Occult Preinvasive Cancer on Prediagnostic Computed Tomography Scans



Published: August 30, 2023 DOI:https://doi.org/10.1053/j.gastro.2023.08.034



ELSEVIER

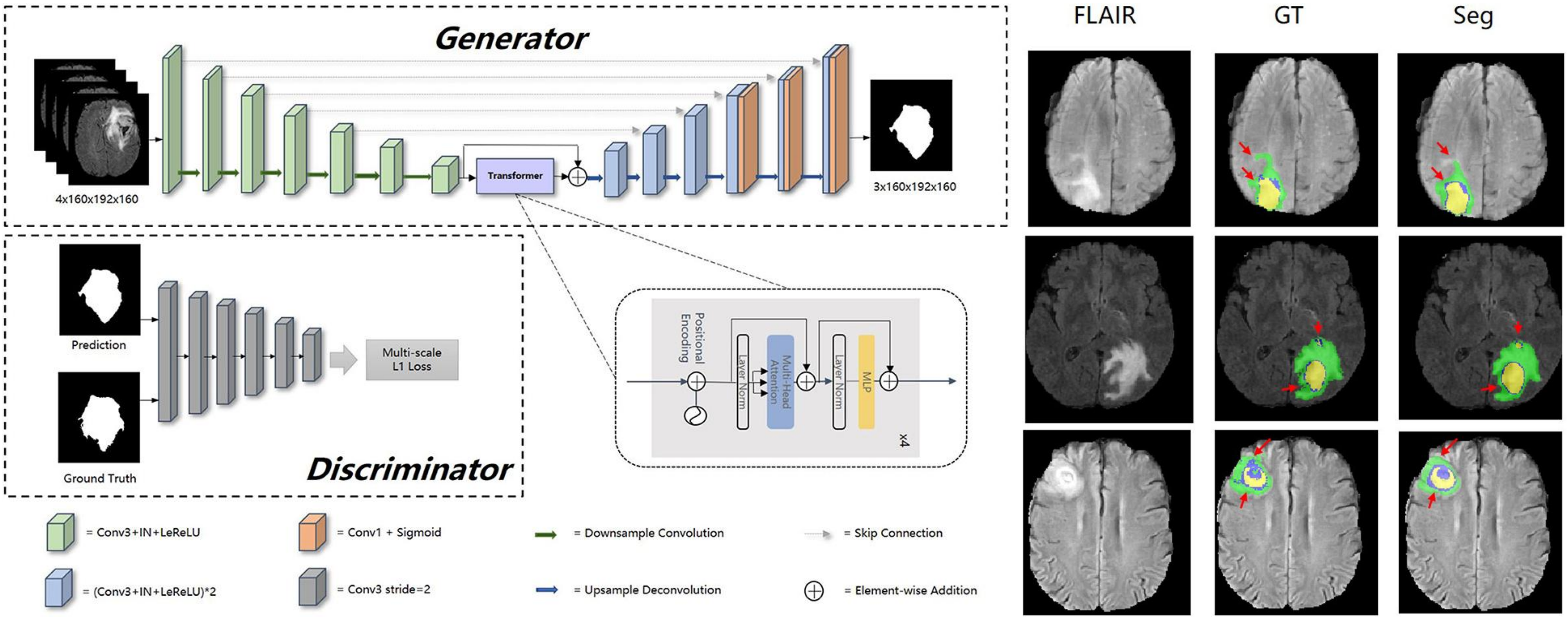
European Journal of Cancer
Volume 229, 16 October 2025, 115752

Original research

AI-informed retinal biomarkers predict 10-year risk of onset of multiple hematological malignancies

Amritpal Singh [a], Ajay K. Nooka [b], Gourav Modanwal [c], Nieraj Jain [d], Madhav V. Dhodapkar [b], Sruthi Arepalli [d], Sagar Lonial [b], Anant Madabhushi [a c e]

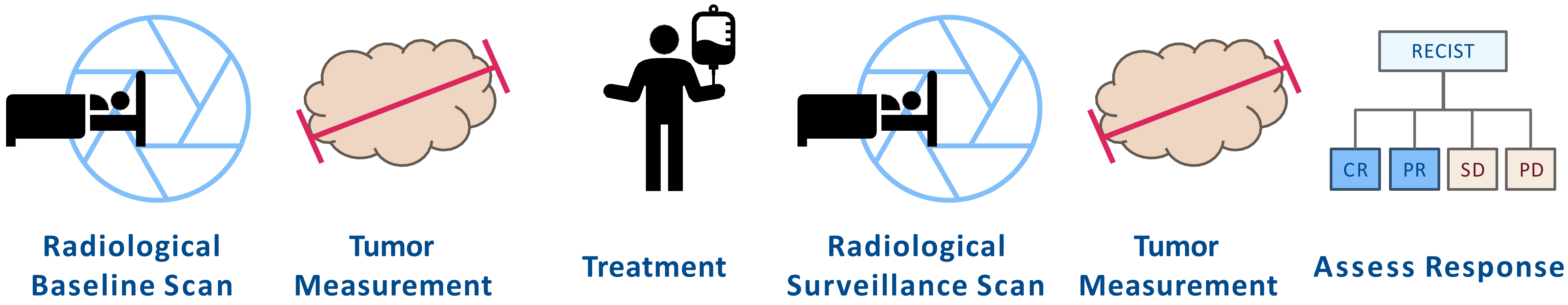
- RetHemo AI predicts hematological cancer risk up to 10 years early.
- RetHemo predictions show significant associations with hematological risk.
- Retinal features cluster into high-risk groups with different disease progressions.
- RetHemo+ individuals show altered serum proteins, hinting at inflammation.
- RetHemo offers non-invasive, cost-effective cancer risk stratification via retina.
- Unique signatures identified for the leukemia, myeloma and were not prognostic when applied to different cancers
- This suggests that retinal changes in myeloma from increased abnormal protein are unique and not found in leukemia.
- However, leukemia-induced features are found in both, possibly due to a common inflammatory pathway.



A transformer-based generative adversarial network for brain tumor segmentation

Tumor Scans Support an Understanding of Treatment Response

FRIENDS of CANCER RESEARCH



Traditionally in clinical trials, radiologists measure tumors at the local sites and later, the measurement is confirmed by a blinded independent central review (BICR).

There is potential to incorporate AI tools that measure tumors to streamline this process.

FRIENDS of CANCER RESEARCH

New Project: ai.RECIST

QUESTION: Can AI-based imaging tools improve tumor measurement?

- **Phase 1: Evaluating the Feasibility of AI Tools for Supporting RECIST Measurements in Clinical Trials**
- **Determine AI tool capabilities.**
- **Align on image characteristics and**
- **metadata.**
- **Compare AI tools and human readers using a**
- **common dataset to assess variability.**

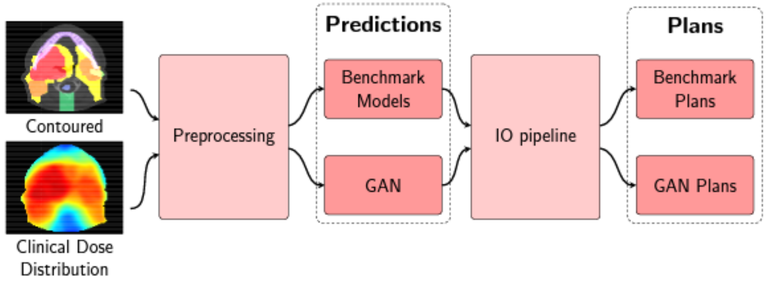
Phase 2: Refining RECIST Using AI-Based Imaging Tools

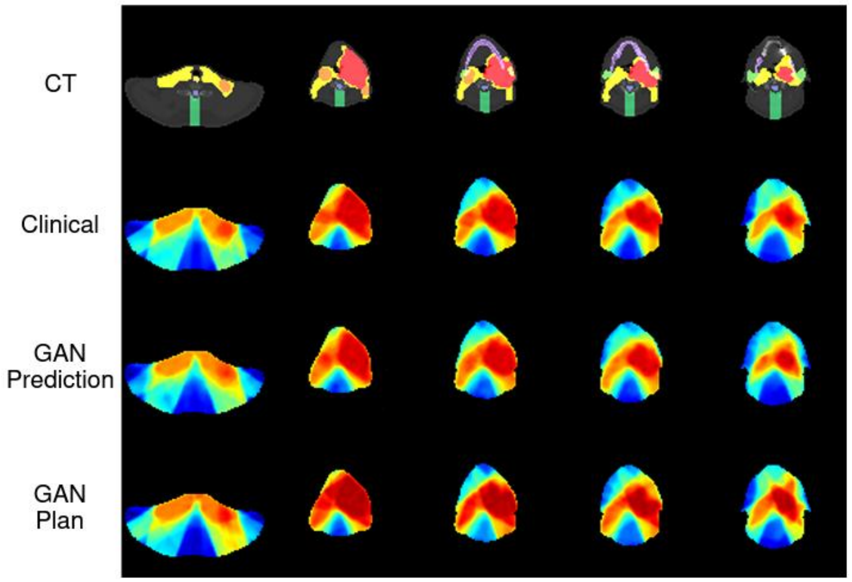
- Consider alternative approaches for measuring tumor burden (e.g., kinetics, metabolomics).
- Establish a standardized approach for integrating AI-based imaging tools into clinical trials.

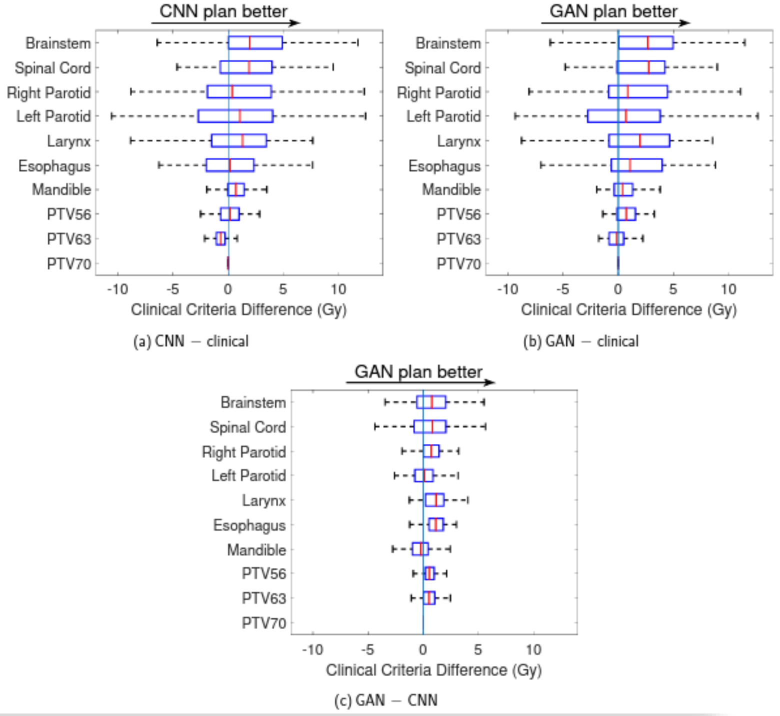
This project is kicking off now – stay tuned for updates!

Radiation Oncology – Adaptive Planning

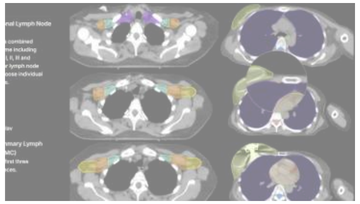
- **Ethos** – AI driven rapid re-planning of radiation treatment while the patient is on the radiation table
- **CBCT**: 17 seconds
- **Segmentation**: 30 seconds
- **Re-Plan**: 2.5 minutes
- **QA**: 2 minutes



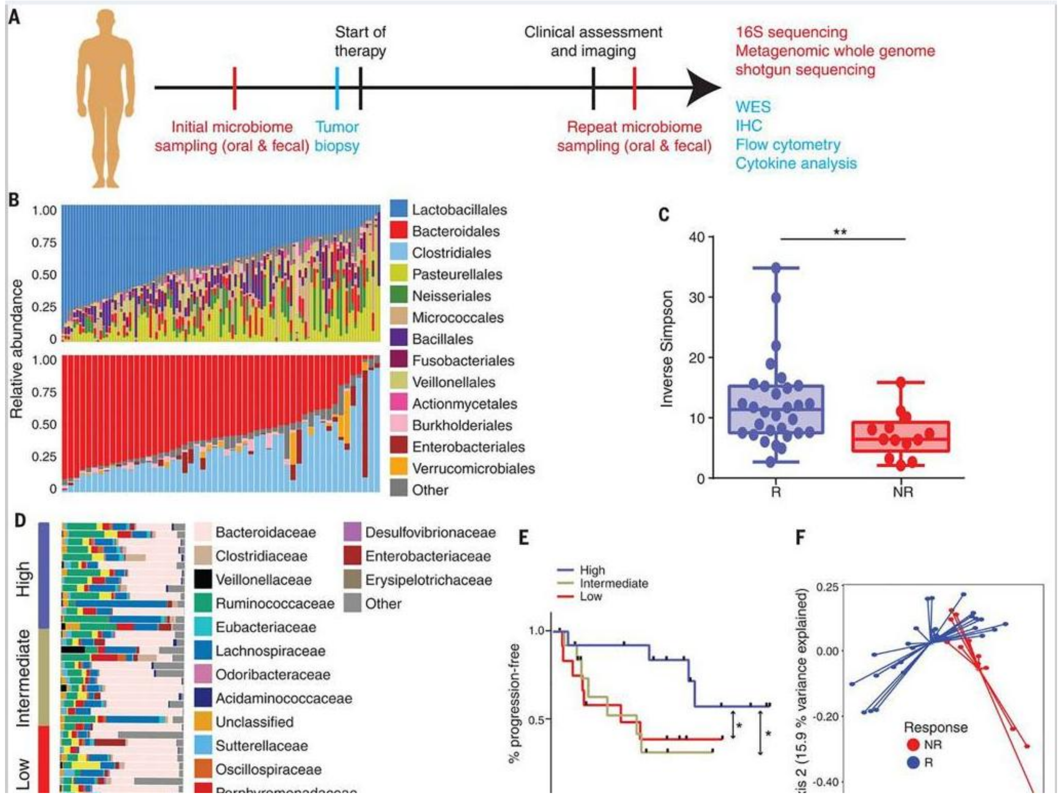




GenAI to optimize radiation oncology treatments

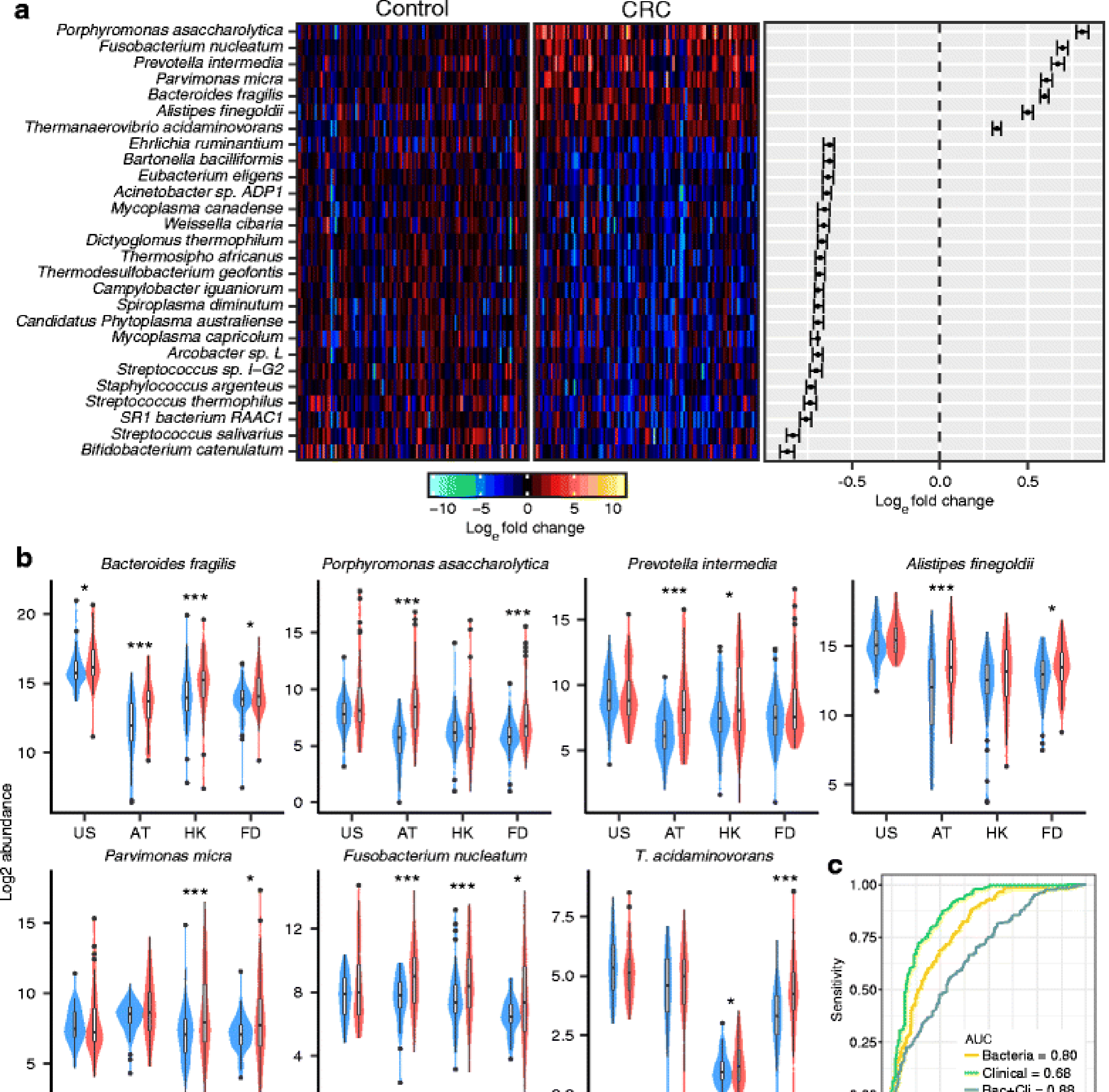


- Generative Adversarial Network (GAN)
- An AI tool designed by a team at the University of Toronto has shown promise for reducing the time to tailor radiation treatment plans to individual patients.
- This particular AI used historical radiation data to recommend treatment strategies with comparable success to radiation oncology specialists.
- In 20 minutes, the Toronto team's AI was able to replicate the complex treatment plans that top specialists arrived at after several days of work, optimizing radiation therapy treatment planning.
- Autocontouring: **LimbusAI** - Expert level deep learning autocontouring within 1-3 minutes



Gopalakrishnan V, et al. Gut microbiome modulates response to anti-PD-1 immunotherapy in melanoma patients. Science. 2018 Jan 5;359(6371):97-103. doi: 10.1126/science.aan4236.

Machine Learning and the Microbiome
Gut Microbiome Impacts Response to Immunotherapy
Significantly higher alpha diversity (p<0.01) in responding patients



[Multi-cohort analysis of colorectal cancer metagenome identified altered bacteria across populations and universal bacterial markers]

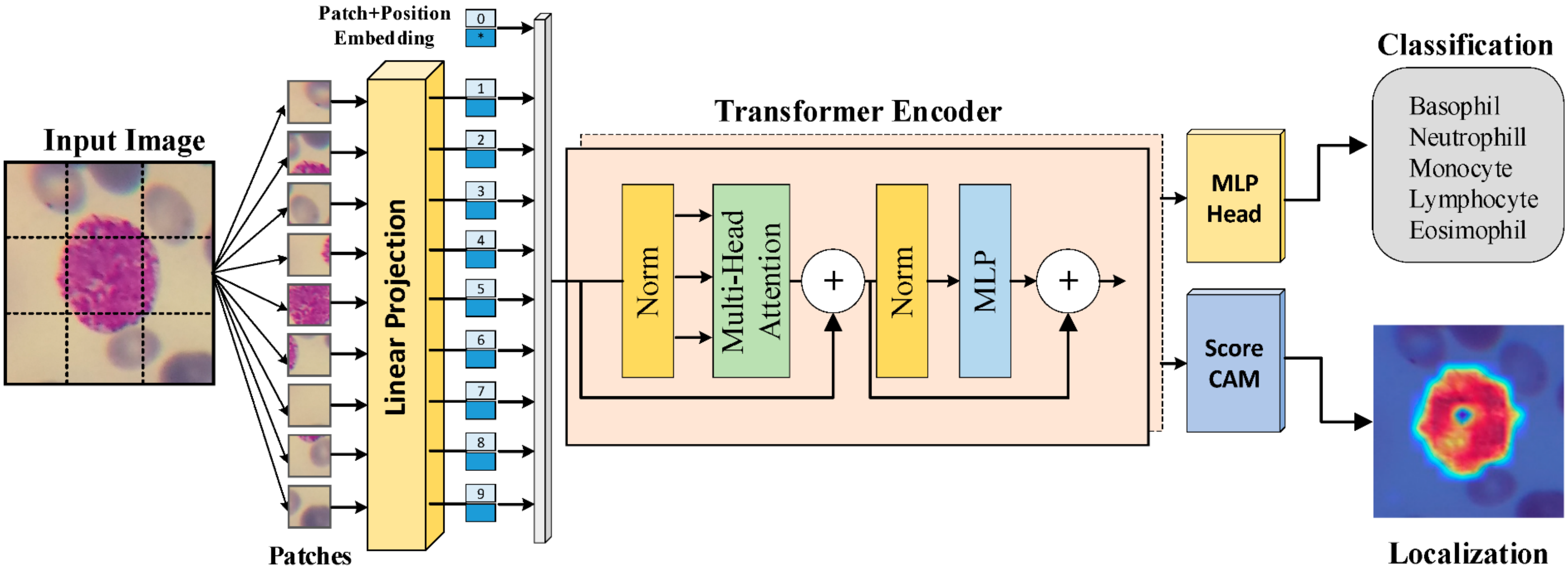
Based on the combined analysis of 526 metagenomic samples from Chinese, Austrian, American, and German and French cohorts, seven CRC-enriched bacteria have been identified across populations:

- Bacteroides fragilis,
- Fusobacterium nucleatum,
- Porphyromonas asaccharolytica,
- Parvimonas micra,
- Prevotella intermedia,
- Alistipes finegoldii,
- Thermanaerovibrio acidaminovorans

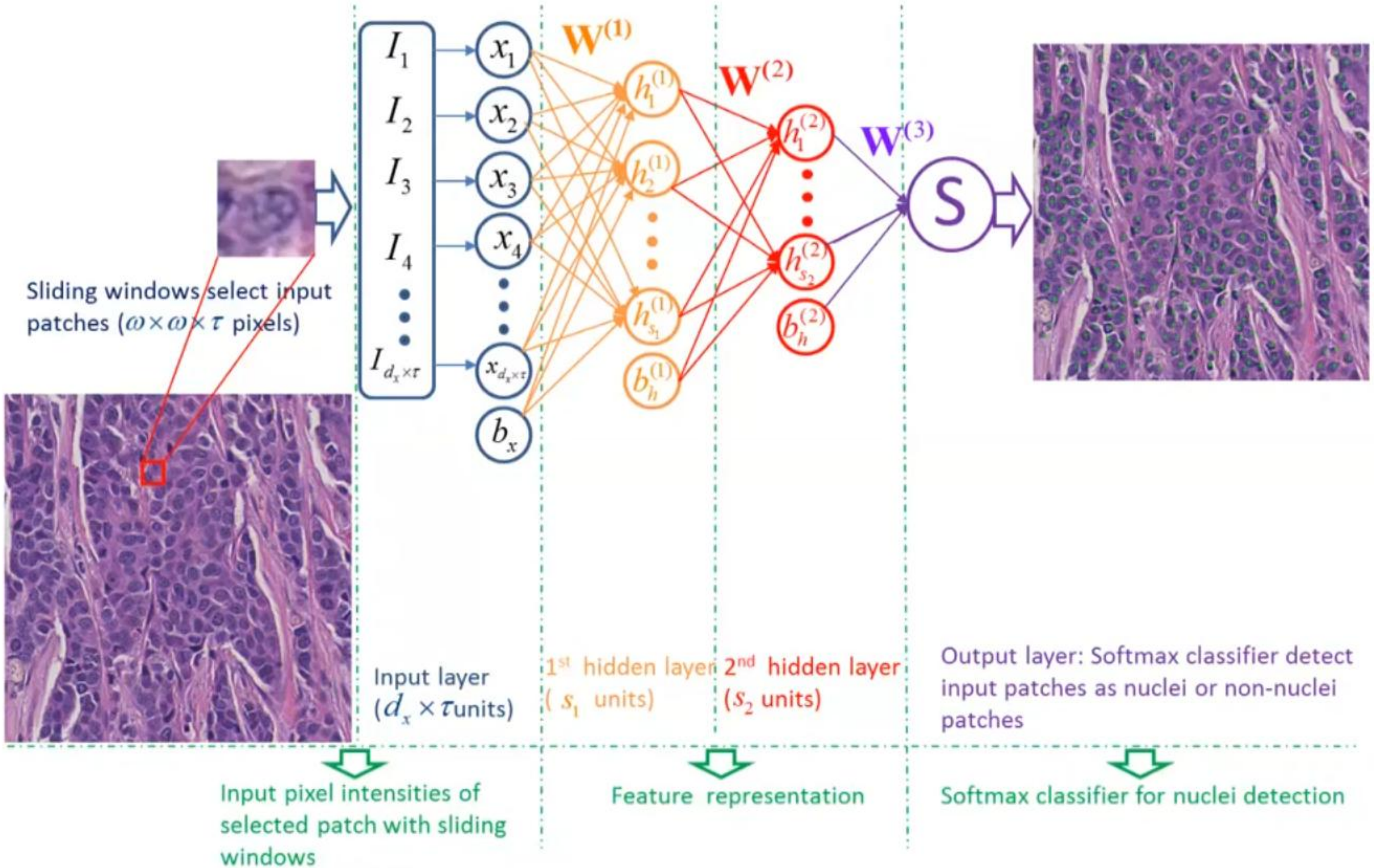
Dai, Z., Coker, O.O., Nakatsu, G. et al. Multi-cohort analysis of colorectal cancer metagenome identified altered bacteria across populations and universal bacterial markers. Microbiome 6, 70 (2018). https://doi.org/10.1186/s40168-018-0451-2

Transformers for Computer Vision

Katar et al. Diagnostics 2023, 13(14), 2459



Stacked Sparse Auto-encoder for Nuclei Detection



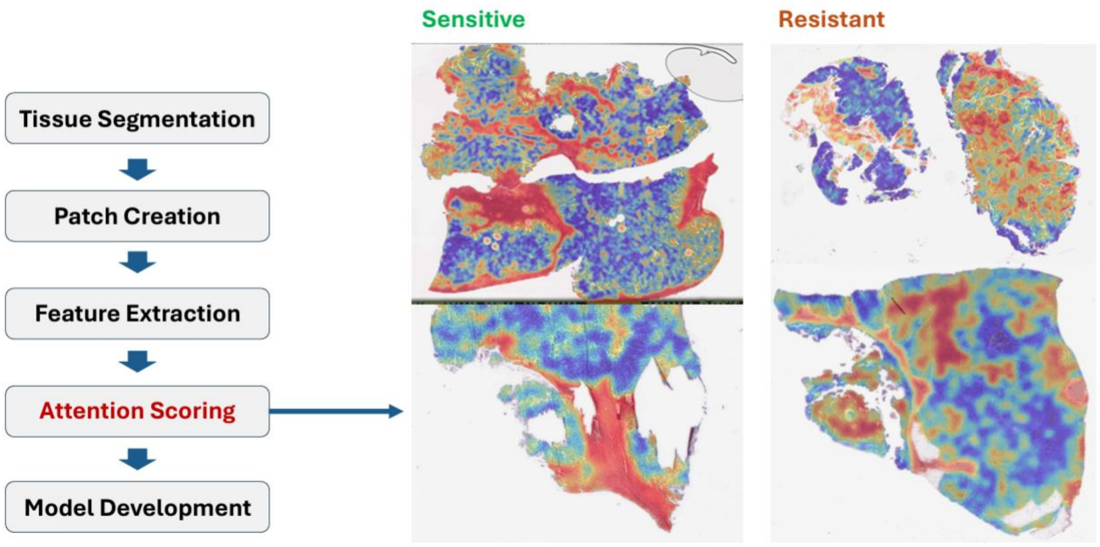
***Xu J**, et al.* "Stacked Sparse Autoencoder (SSAE) based Framework for Nuclei Patch Classification on Breast Cancer Histopathology", ISBI2014.

***Xu J**, et al.* "Stacked Sparse Autoencoder (SSAE) for Nuclei Detection on Breast Cancer Histopathology". *IEEE Trans. on Medical Imaging,* 2015

*Zhang X, Dou H, **Xu J,** Zhang S,* "Fusing Heterogeneous Features for the Image-Guided Diagnosis of Intraductal Breast Lesions", *IEEE Journal of Biomedical and Health Informatics,* 2015

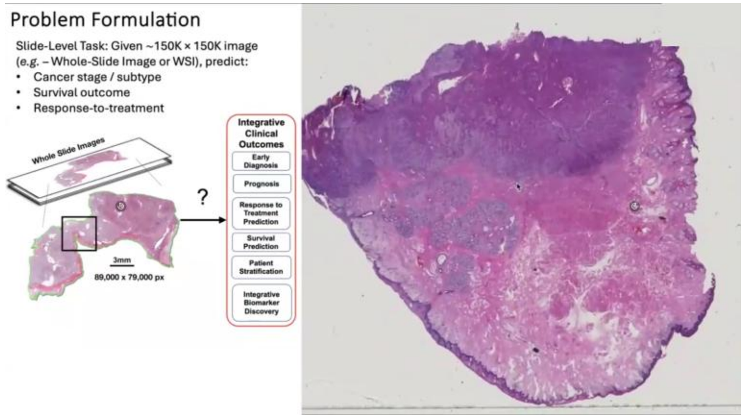
Lu C, Xu H, ***Xu J***, Mandal M, and Madabhushi A, "Multiple Passes Adaptive Voting for Nuclei Detection in Histopathlogical Images", *IEEE Journal of Biomedical and Health*

Example of Attention Heatmap of Ovarian Cancer WSIs



=> Higher attention area is used more importantly for training

Dr. Daoud Meerzaman Computational Genomics and Bioinformatics Branch (CGBB) NCI Center for Biomedical Informatics and IT



Adapted from Dr. Faisal Mahmood.
https://faisal.ai/

Mahmood Lab
AI for Pathology

NIH NATIONAL CANCER INSTITUTE

Intensifying an existing workforce shortage

↓17.5%

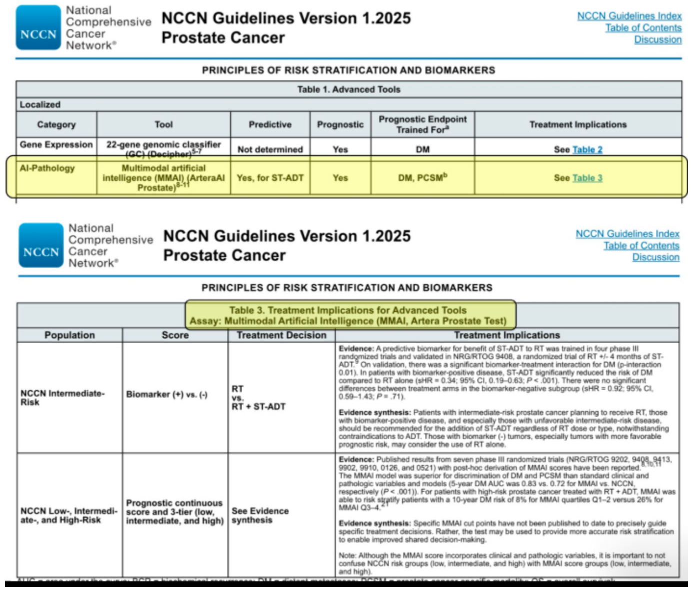
In the US, the pathologist population declined by **17.5%** between 2007 and 2017.[3]

Already impacting pathologists and patients

35%

of pathologists are burnt out.[4]

Patients can wait **60+ days** to begin treatment.[5]



NCCN National Comprehensive Cancer Network®

NCCN Guidelines Version 1.2025
Prostate Cancer

NCCN Guidelines Index
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Discussion

PRINCIPLES OF RISK STRATIFICATION AND BIOMARKERS

Table 1. Advanced Tools

Localized					
Category	Tool	Predictive	Prognostic	Prognostic Endpoint Trained For[a]	Treatment Implications
Gene Expression	22-gene genomic classifier (GC) (Decipher)[5-7]	Not determined	Yes	DM	See Table 2
AI-Pathology	Multimodal artificial intelligence (MMAI) (ArteraAI Prostate)[8-11]	Yes, for ST-ADT	Yes	DM, PCSM[b]	See Table 3

NCCN National Comprehensive Cancer Network®

NCCN Guidelines Version 1.2025
Prostate Cancer

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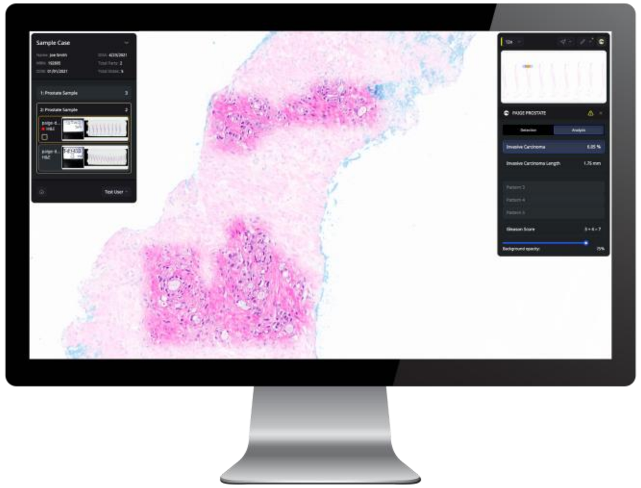
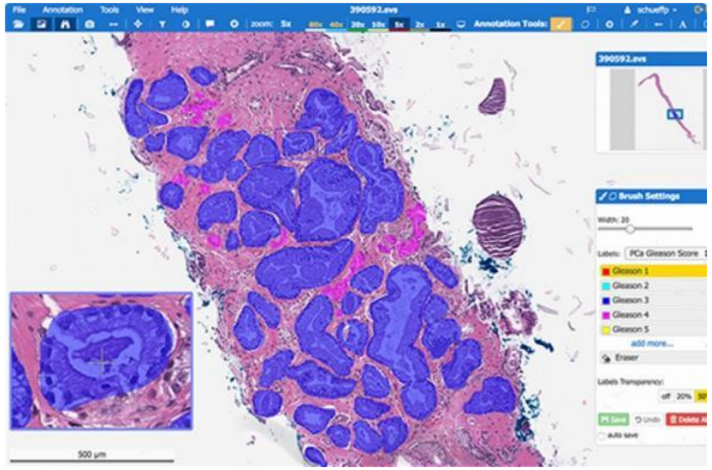
PRINCIPLES OF RISK STRATIFICATION AND BIOMARKERS

Table 3. Treatment Implications for Advanced Tools
Assay: Multimodal Artificial Intelligence (MMAI, Artera Prostate Test)

Population	Score	Treatment Decision	Treatment Implications
NCCN Intermediate-Risk	Biomarker (+) vs. (-)	RT vs. RT + ST-ADT	**Evidence:** A predictive biomarker for benefit of ST-ADT to RT was trained in four phase III randomized trials and validated in NRG/RTOG 9408, a randomized trial of RT +/- 4 months of ST-ADT.[9] On validation, there was a significant biomarker-treatment interaction for DM (p-interaction 0.01). In patients with biomarker-positive disease, ST-ADT significantly reduced the risk of DM compared to RT alone (sHR = 0.34; 95% CI, 0.19–0.63; *P* < .001). There were no significant differences between treatment arms in the biomarker-negative subgroup (sHR = 0.92; 95% CI, 0.59–1.43; *P* = .71). **Evidence synthesis:** Patients with intermediate-risk prostate cancer planning to receive RT, those with biomarker-positive disease, and especially those with unfavorable intermediate-risk disease, should be recommended for the addition of ST-ADT regardless of RT dose or type, notwithstanding contraindications to ADT. Those with biomarker (-) tumors, especially tumors with more favorable prognostic risk, may consider the use of RT alone.
NCCN Low-, Intermediate-, and High-Risk	Prognostic continuous score and 3-tier (low, intermediate, and high)	See Evidence synthesis	**Evidence:** Published results from seven phase III randomized trials (NRG/RTOG 9202, 9408, 9413, 9902, 9910, 0126, and 0521) with post-hoc derivation of MMAI scores have been reported.[8,10,11] The MMAI model was superior for discrimination of DM and PCSM than standard clinical and pathologic variables and models (5-year DM AUC was 0.83 vs. 0.72 for MMAI vs. NCCN, respectively (*P* < .001)). For patients with high-risk prostate cancer treated with RT + ADT, MMAI was able to risk stratify patients with a 10-year DM risk of 8% for MMAI quartiles Q1–2 versus 26% for MMAI Q3–4.[21] **Evidence synthesis:** Specific MMAI cut points have not been published to date to precisely guide specific treatment decisions. Rather, the test may be used to provide more accurate risk stratification to enable improved shared decision-making. Note: Although the MMAI score incorporates clinical and pathologic variables, it is important to not confuse NCCN risk groups (low, intermediate, and high) with MMAI score groups (low, intermediate, and high).





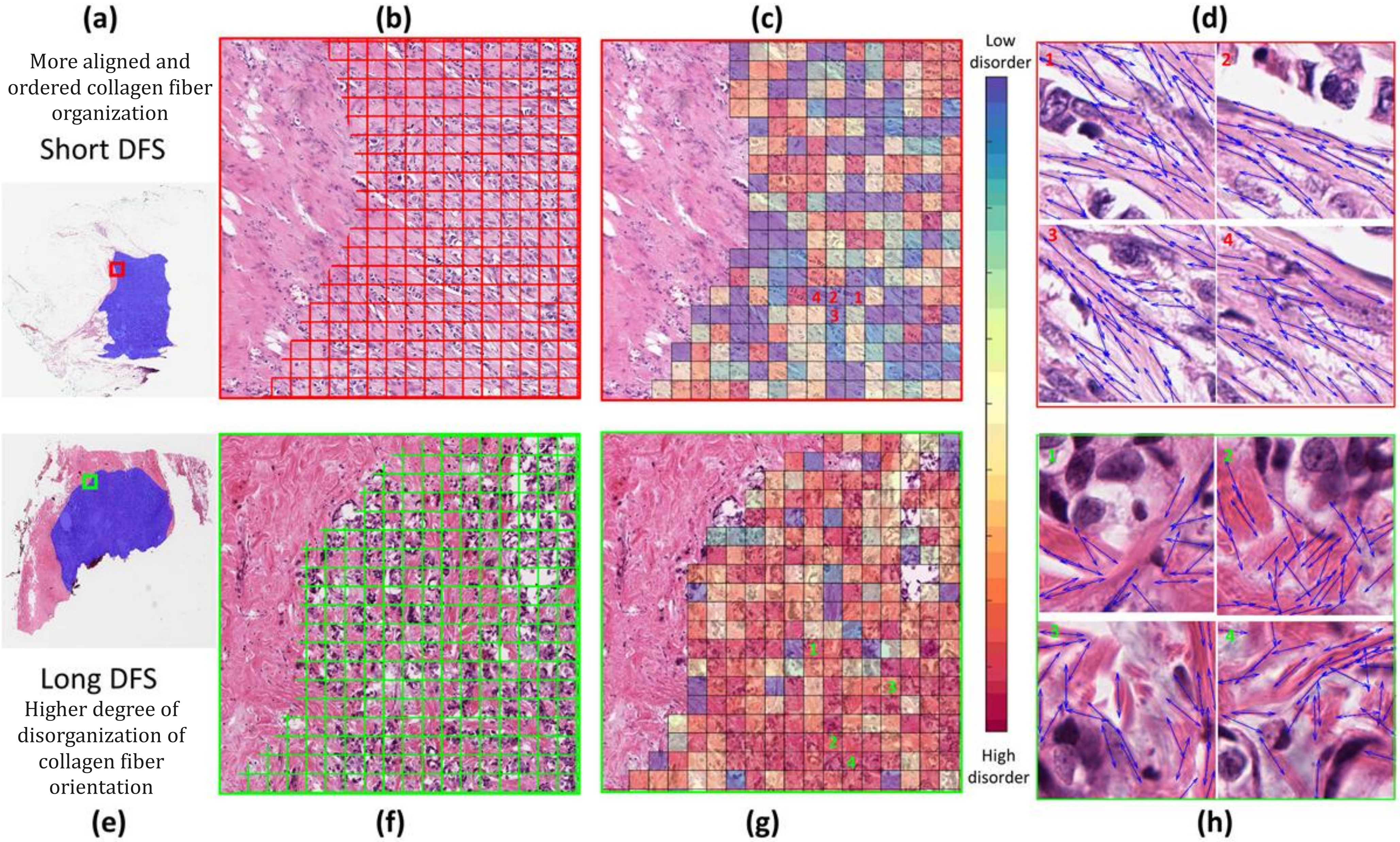
Digital Pathology and AI

On September 21, 2021, **the FDA authorized the commercialization of software** to assist pathologists in detecting suspicious areas of cancer as an adjunct to reviewing digitally scanned plate images or histology slides from prostate biopsies.

The software, called **Paige Prostate**, is the first AI-based software designed to identify in the prostate biopsy image an area of interest with the highest likelihood of harboring cancer, so that it can be further reviewed by the pathologist if such an area had not initially been identified.

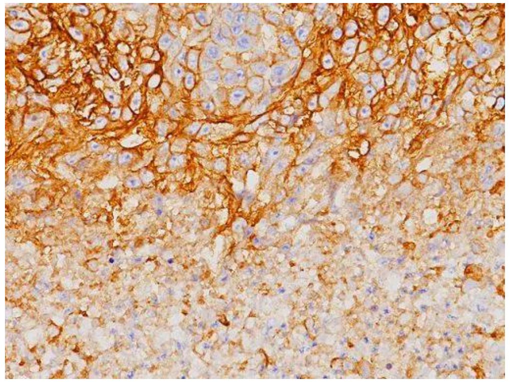
- The FDA evaluated data from a clinical trial in which 16 pathologists examined 527 slide images of prostate biopsies (171 cancer and 356 benign) that were digitized using a scanner.
- For each slide image, each pathologist completed two evaluations, one without the assistance of Paige Prostate (unassisted reading) and one with the assistance of Paige Prostate (assisted reading).
- The study found that **Paige Prostate improved cancer detection on individual slide images by 7.3% on average** compared to pathologists' unhelped readings for full slide images of individual biopsies, with no impact on reading benign slide images.
- Potential risks include false-negative and false-positive results, which are mitigated by the use of the device as an adjunct and by professional evaluation by a qualified pathologist who takes into account the patient's history among other relevant clinical information, and who may perform additional laboratory studies on the samples before making a final diagnosis.
- **ArteraAI** got FDA approval in August 2025, included in NCCN guidelines

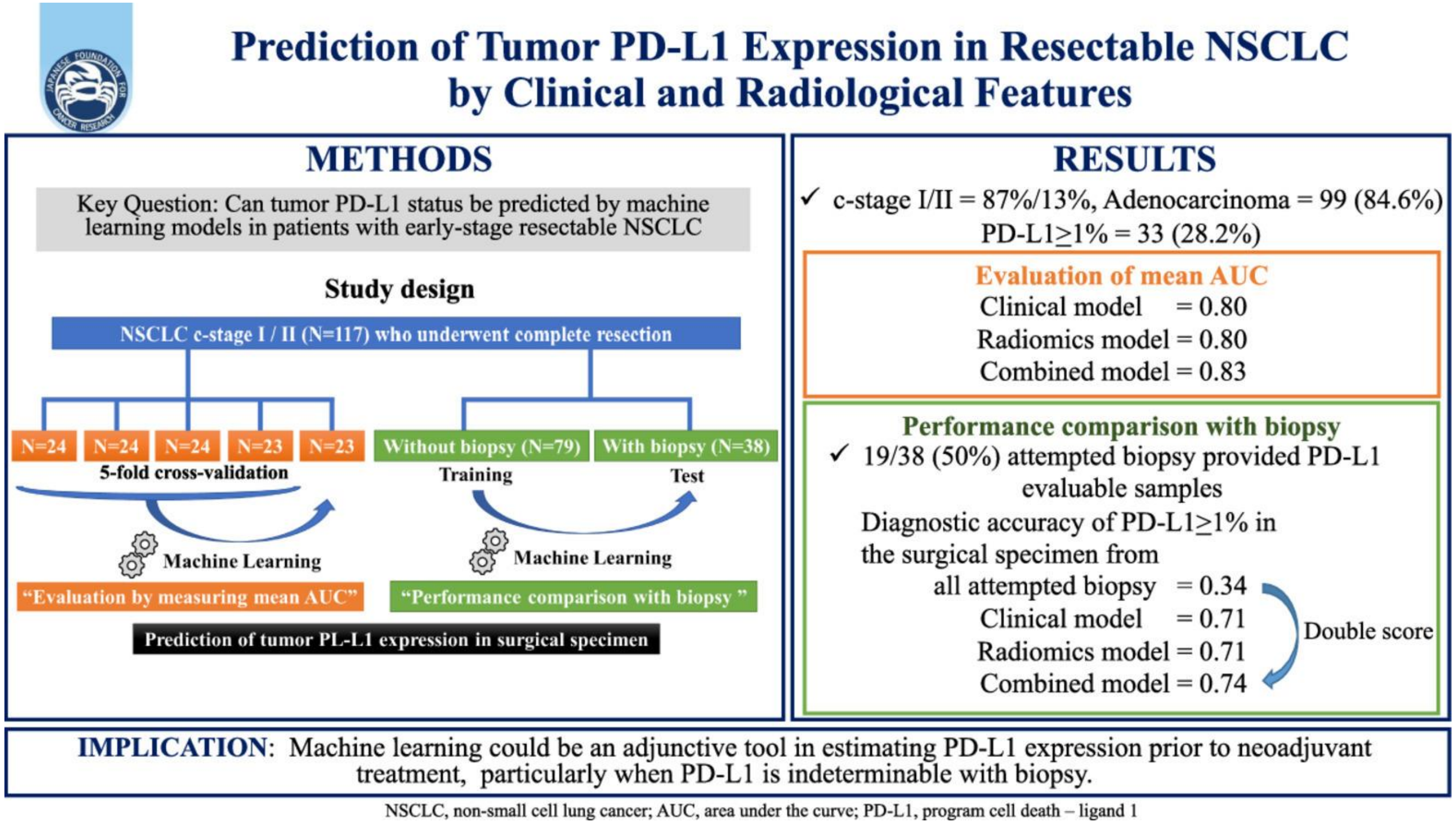
Entropy theory to calculate CFOD-TS: Degree of disorder of collagen fiber orientations at the tumor leading edge and across the entire tumor region



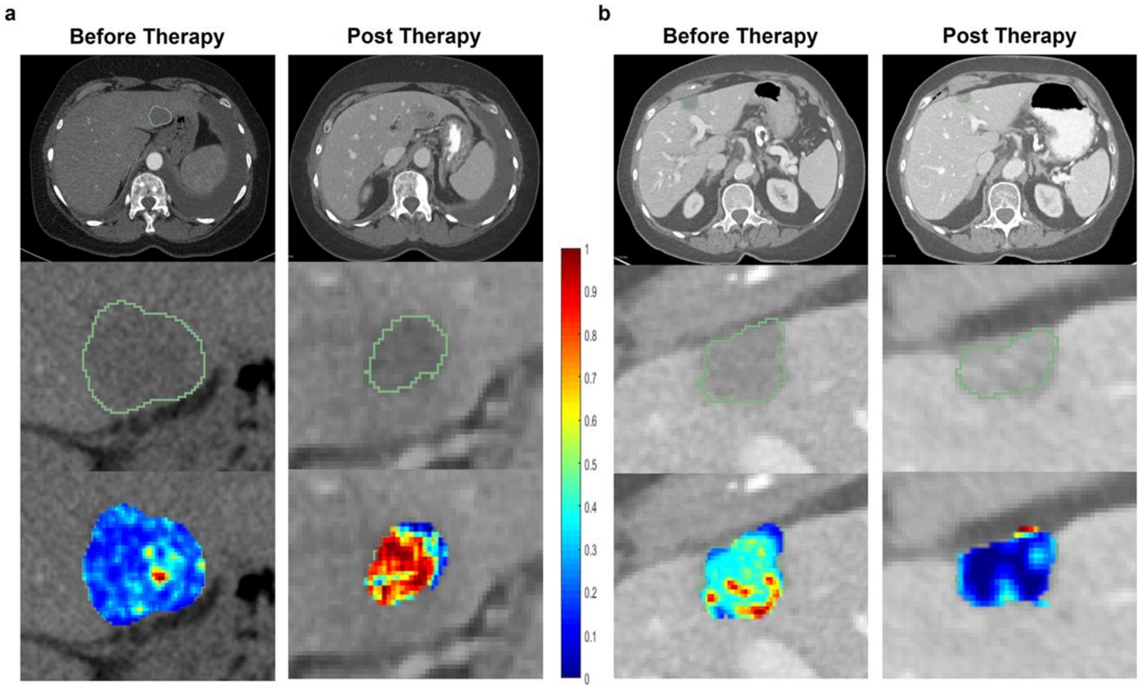
Li, H., Bera, K., Toro, P. et al. Collagen fiber orientation disorder from H&E images is prognostic for early stage breast cancer: clinical trial validation. npj Breast Cancer 7, 104 (2021). https://doi.org/10.1038/s41523-021-00310-z

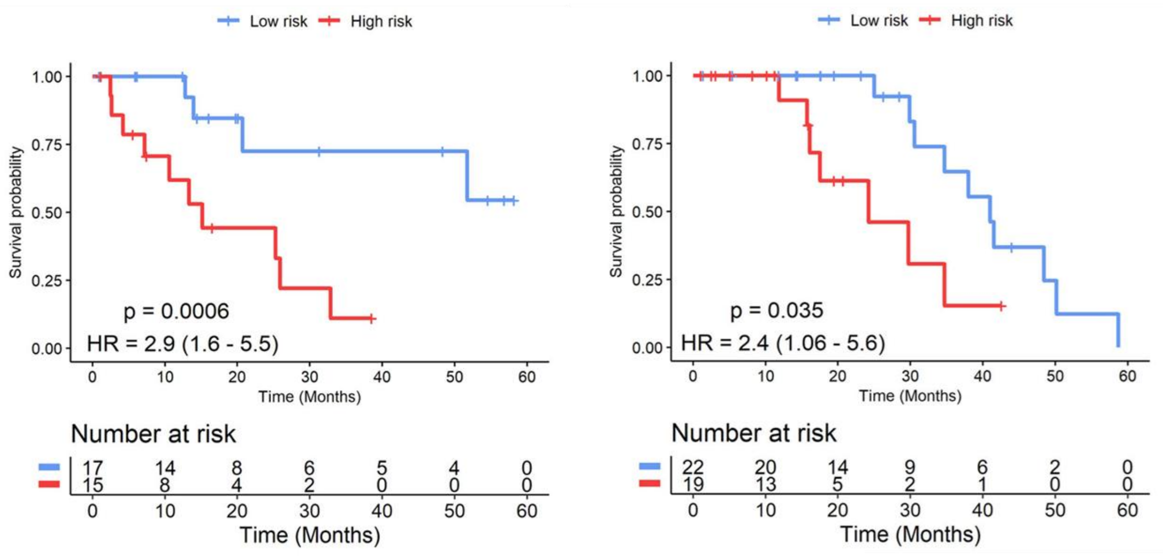
- According to results of a performance comparison, a machine learning tool based on clinical and radiological features can accurately predict PD-L1 expression prior to neoadjuvant treatment in c-stage 1/2 non-small cell lung cancer (NSCLC) when PD-L1 expression is indeterminable by biopsy.
- Clinical/radiomics features predicted PD-L1 in NSCLC with AUC0.83.





Clin Lung Cancer. Published online: August 10, 2023.
doi: 10.1016/j.cllc.2023.08.010



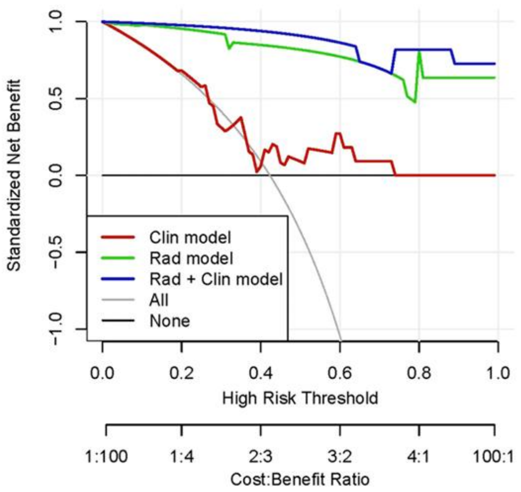


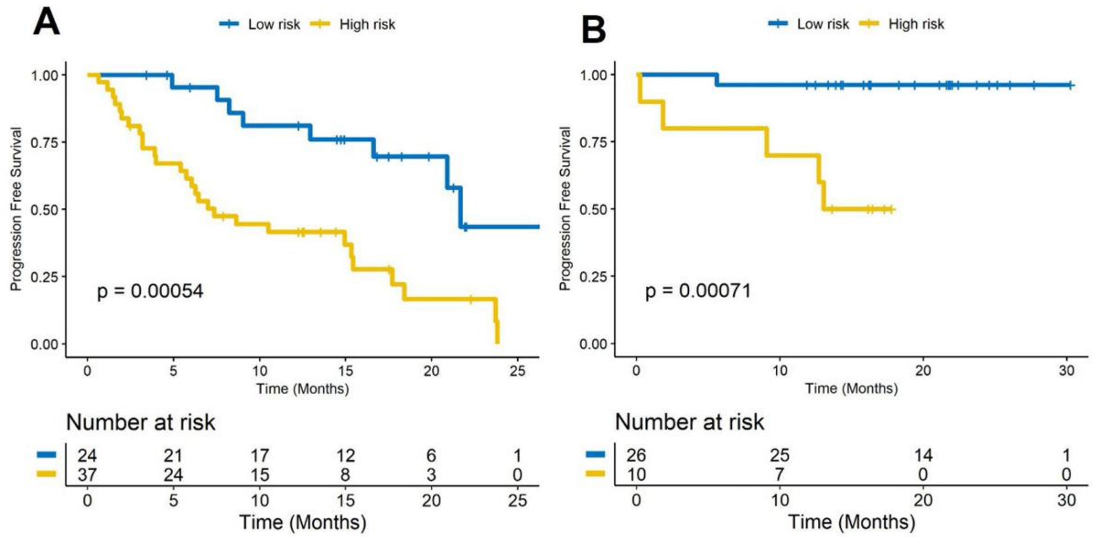
Training Set

Validation Set

Radiomic predicts early response to CDK4/6 inhibitors in hormone receptor positive metastatic breast cancer

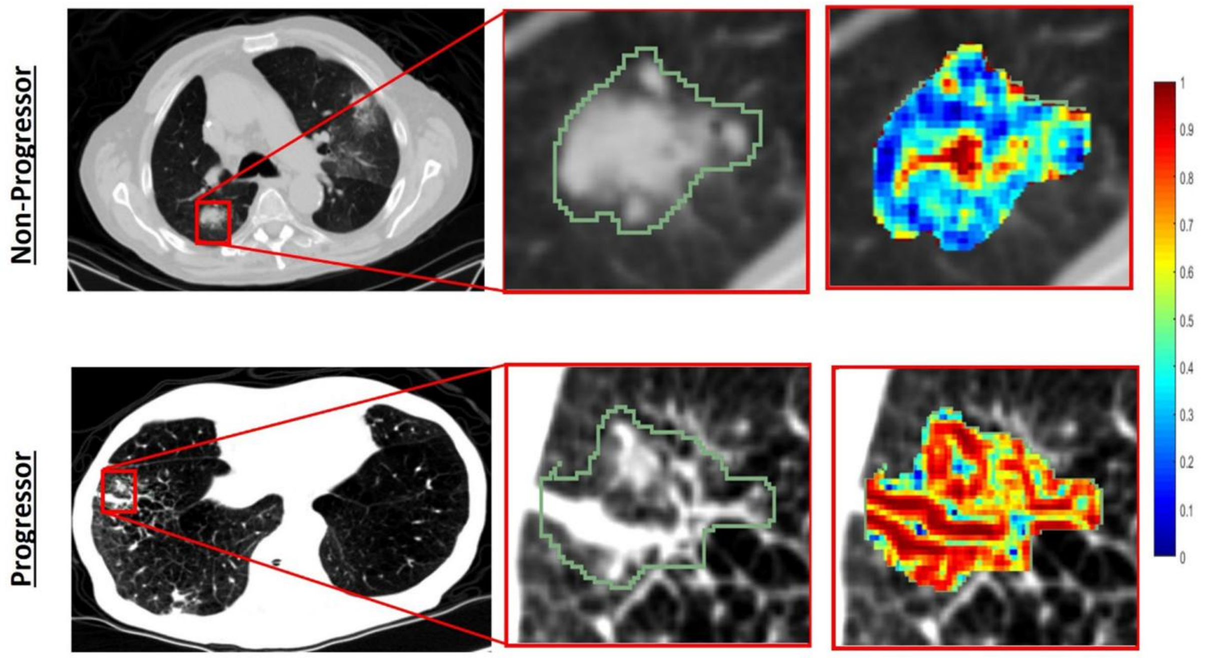
Khorrami M, et al. NPJ Breast Cancer. 2023 Aug 11;9(1):67. doi: 10.1038/s41523-023-00574-7.

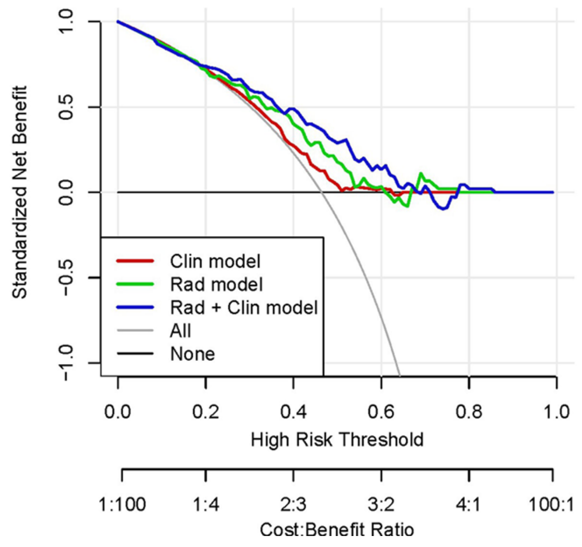




High PD-L1 >50%

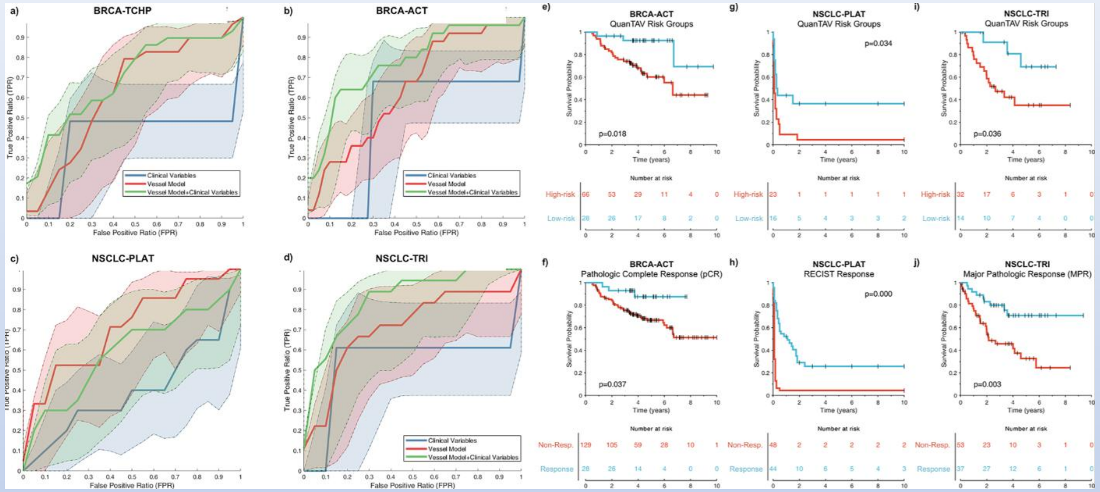
Low PD-L1 <50%

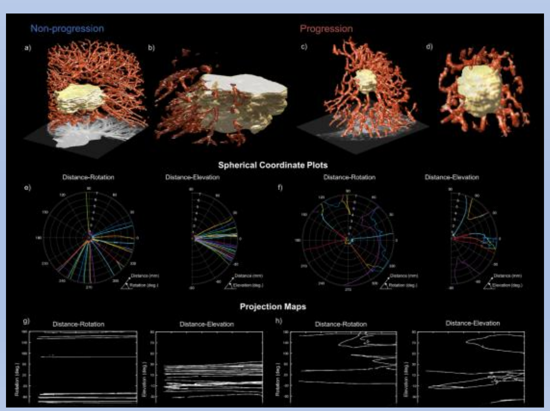




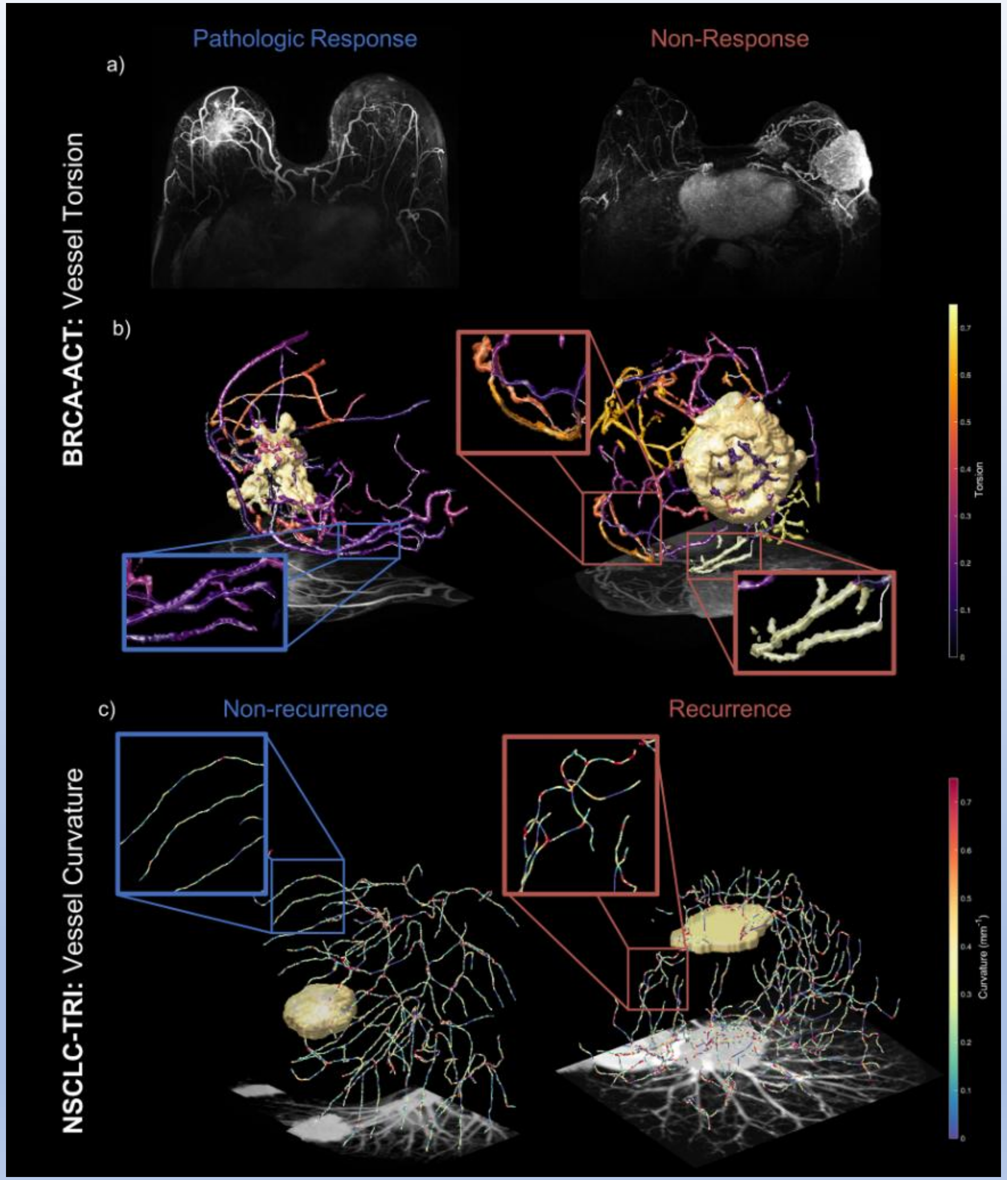
Novel imaging biomarkers predict outcomes in stage III unresectable non-small cell lung cancer treated with chemoradiation and durvalumab

Jazieh K, et al. J Immunother Cancer. 2022 Mar;10(3):e003778. doi: 10.1136/jitc-2021-003778





QuanTAV: Quantitative tumor-associated vasculature response and risk scores as potential prognostic and predictive biomarkers



Braman N, et al. Clin Cancer Res. 2022 Oct 14;28(20):4410-4424. doi: 10.1158/1078-0432.CCR-21-4148.

Pan-cancer integrative histology-genomic analysis via multimodal deep learning

Richard J. Chen, Ming Y. Lu, Drew F.K. Williamson, Tiffany Y. Chen, Jana Lipkova, Zahra Noor, Muhammad Shaban, Maha Shady, Mane Williams, Bumjin Joo, Faisal Mahmood

Cancer Cell
Volume 40 Issue 8 Pages 865-878.e6
(August 2022)
DOI: 10.1016/j.ccell.2022.07.004

Deep-learning-based multimodal fusion (MMF) algorithm that uses both H&E whole-slide images (WSIs) and molecular profile features (mutation status, copy-number variation, RNA sequencing [RNA-seq] expression) to measure and explain relative risk of cancer death

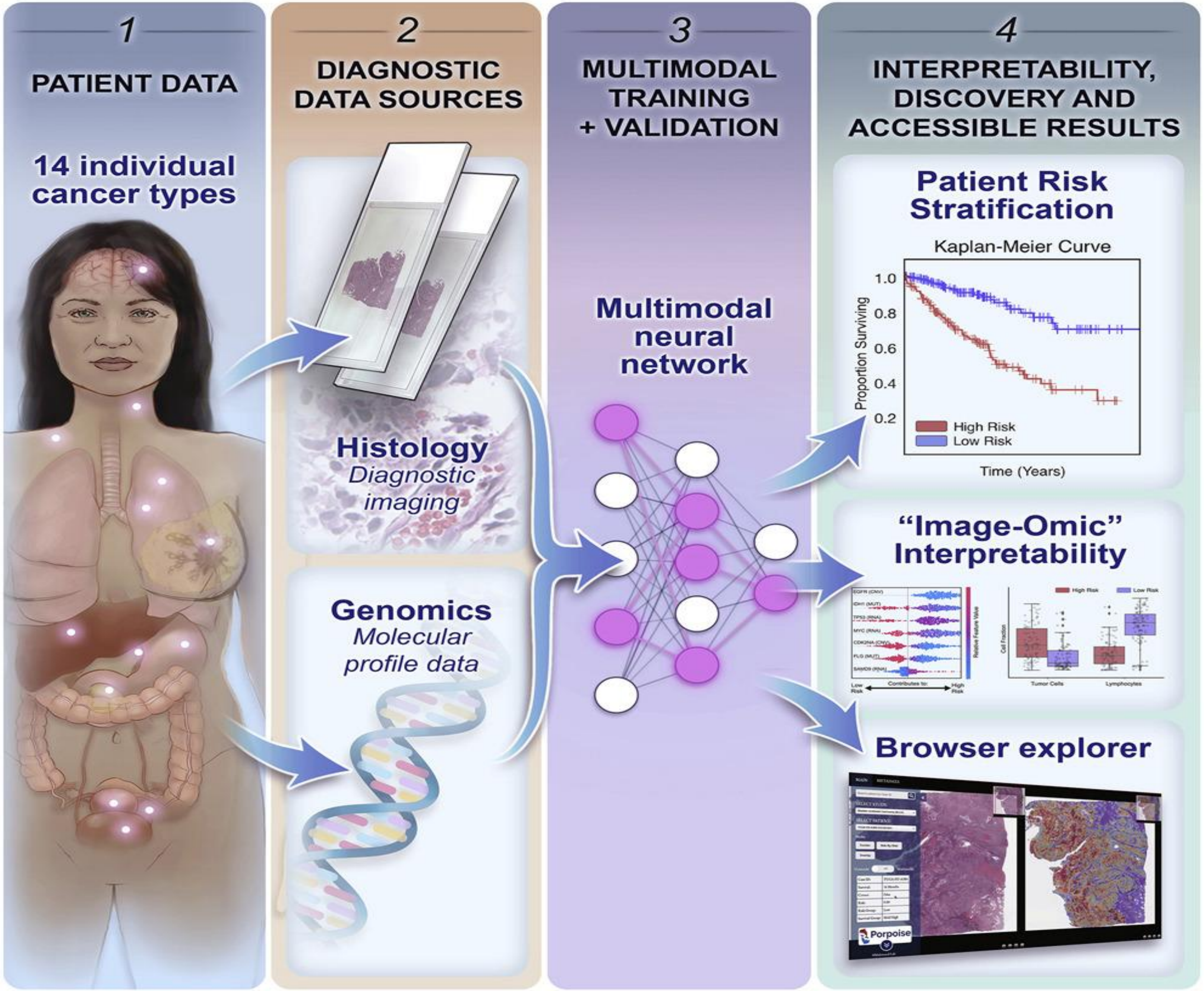
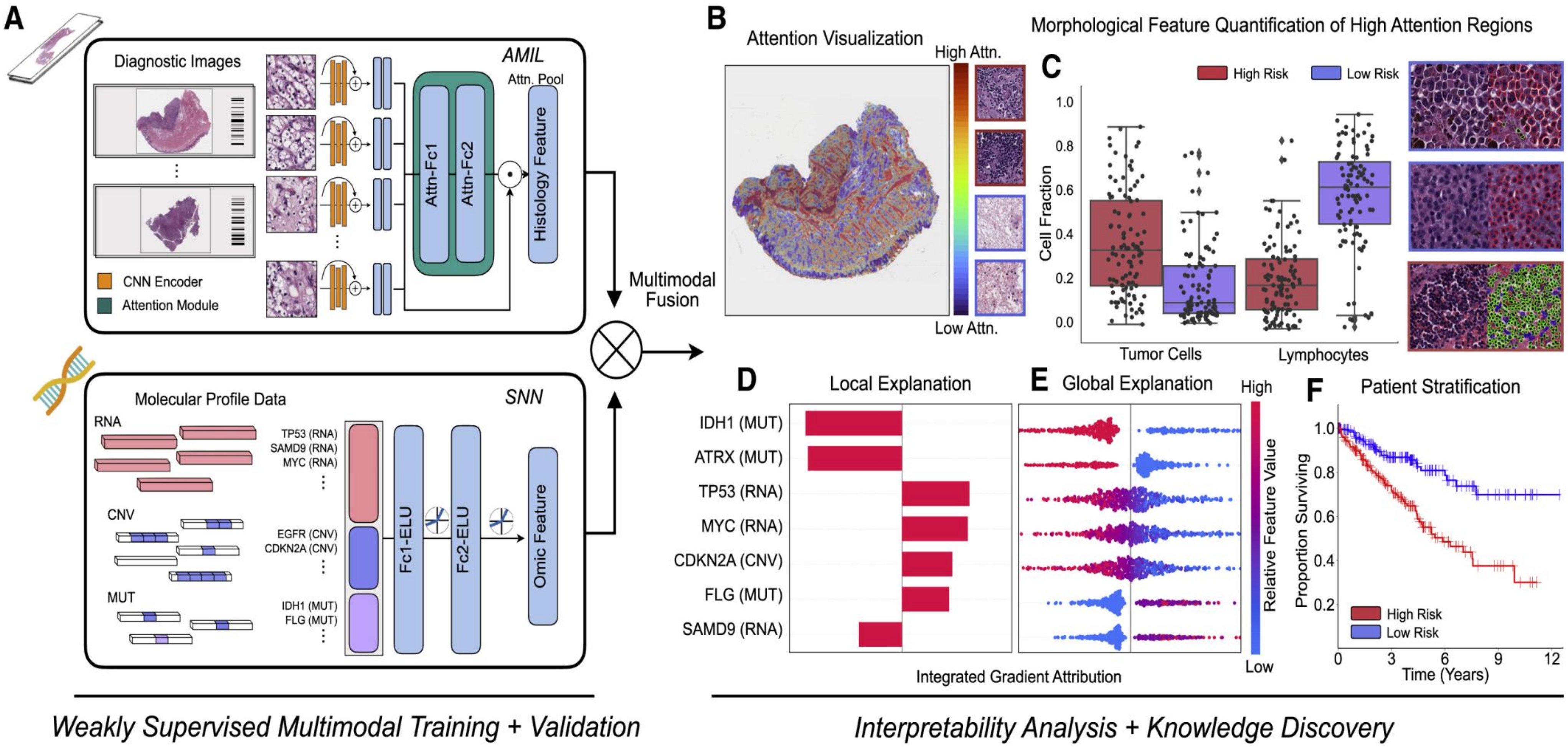


Figure 1

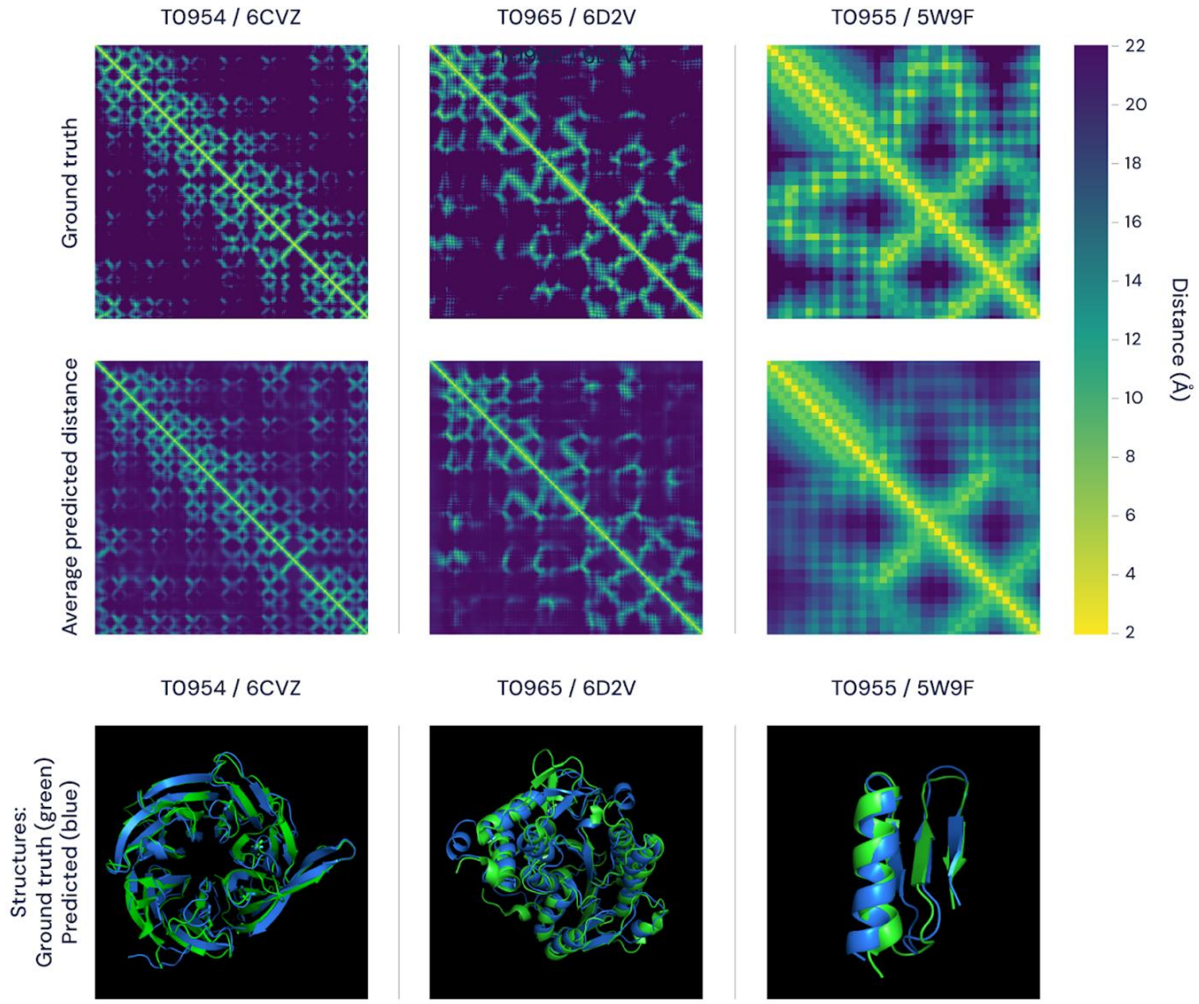


http://pancancer.mahmoodlab.org/

Cancer Cell 2022 40865-878.e6DOI: (10.1016/j.ccell.2022.07.004)

Artificial general intelligence (AGI) and Research

- An artificial general intelligence (AGI) is a hypothetical type of intelligent agent. If realized, an AGI could learn to accomplish any intellectual task that human beings or animals can perform.
- Alternatively, AGI has been defined as an autonomous system that surpasses human capabilities in the majority of economically valuable tasks



Two ways of visualising the accuracy of AlphaFold's predictions. The top figure features the distance matrices for three proteins. The brightness of each pixel represents the distance between the amino acids in the sequence comprising the protein–the brighter the pixel, the closer the pair. Shown in the top row are the real, experimentally determined distances and, in the bottom row, the average of AlphaFold's predicted distance distributions. Importantly, these match well on both global and local scales. The bottom panels represent the same comparison using 3D models, featuring AlphaFold's predictions (blue) versus ground-truth data (green) for the same three proteins.

Google DeepMind's AlphaFold: AI for therapeutic discovery

- AI research can drive and accelerate new developments in the fields of structural biology, physics, and machine learning by predicting the 3D structure of a protein based solely on its genetic sequence. and the 3D models of proteins generated by AlphaFold are much more accurate.
- As demonstrated by Levinthal's paradox, it would take longer than the age of the known universe to randomly enumerate all possible configurations of a typical protein before reaching the true 3D structure - yet proteins themselves fold spontaneously, within milliseconds.
- Proteins can vary in their function based on their unique 3D structure and their genetic sequence does not translate into knowledge of their shape.
- The larger the protein, the more difficult it is to model it, given interactions between amino acids.
- This "protein folding problem" has inspired countless developments, from stimulating IBM's efforts in supercomputing (BlueGene), to new initiatives (Folding@Home and FoldIt) and engineering fields, such as rational protein design.
- These methods based on deep neural networks can contribute to drug discovery and reduce experimentation costs.

The Nobel Prize in Chemistry 2024

David Baker

"for computational protein design"

David Baker. Ill. Niklas Elmehed © Nobel Prize Outreach

Demis Hassabis

"for protein structure prediction"

Demis Hassabis. Ill. Niklas Elmehed © Nobel Prize Outreach

John Jumper

"for protein structure prediction"

John Jumper. Ill. Niklas Elmehed © Nobel Prize Outreach

CLINICAL IMPLICATIONS OF BASIC RESEARCH FREE PREVIEW

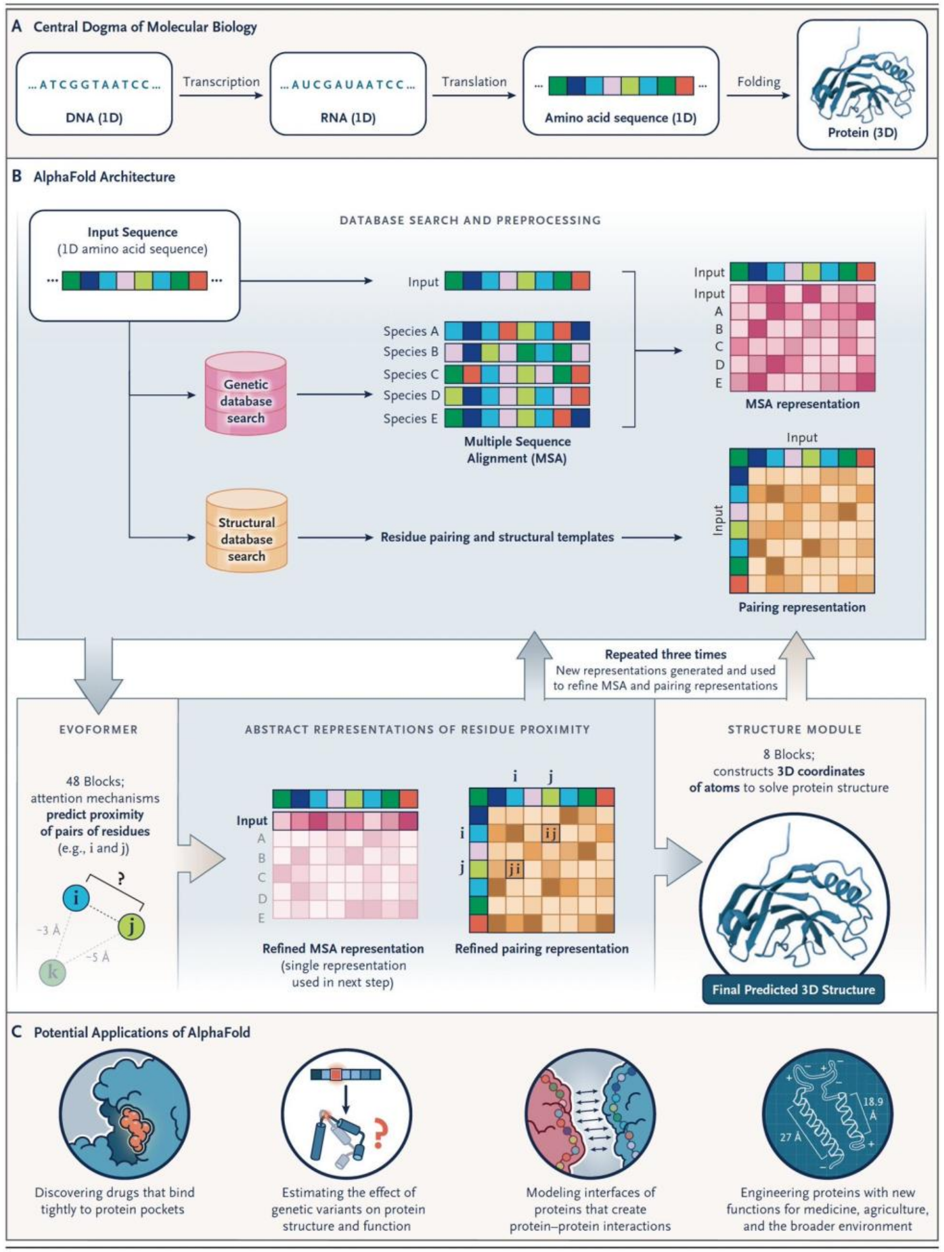
A Holy Grail — The Prediction of Protein Structure

Russ B. Altman, M.D., Ph.D.

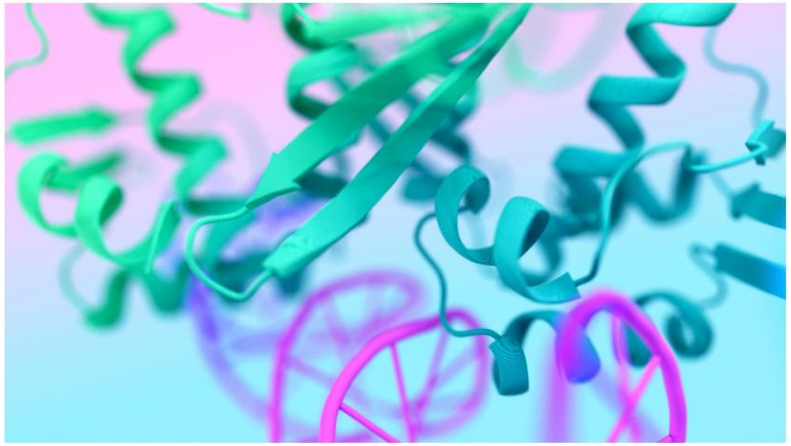
The 2023 Lasker Award for Basic Medical Research underscores the value of an AI system that predicts the three-dimensional structure of proteins from the one-dimensional sequence of their amino acids.

September 21, 2023
DOI: 10.1056/NEJMcibr2307735

Editors



README License



AlphaFold 3

This package provides an implementation of the inference pipeline of AlphaFold 3. See below for how to access the model parameters. You may only use AlphaFold 3 model parameters if received directly from Google. Use is subject to these terms of use.

Any publication that discloses findings arising from using this source code, the model parameters or outputs produced by those should cite the Accurate structure prediction of biomolecular interactions with AlphaFold 3 paper.

Please also refer to the Supplementary Information for a detailed description of the method.

AlphaFold 3 is also available at alphafoldserver.com for non-commercial use, though with a more limited set of ligands and covalent modifications.

If you have any questions, please contact the AlphaFold team at alphafold@google.com.

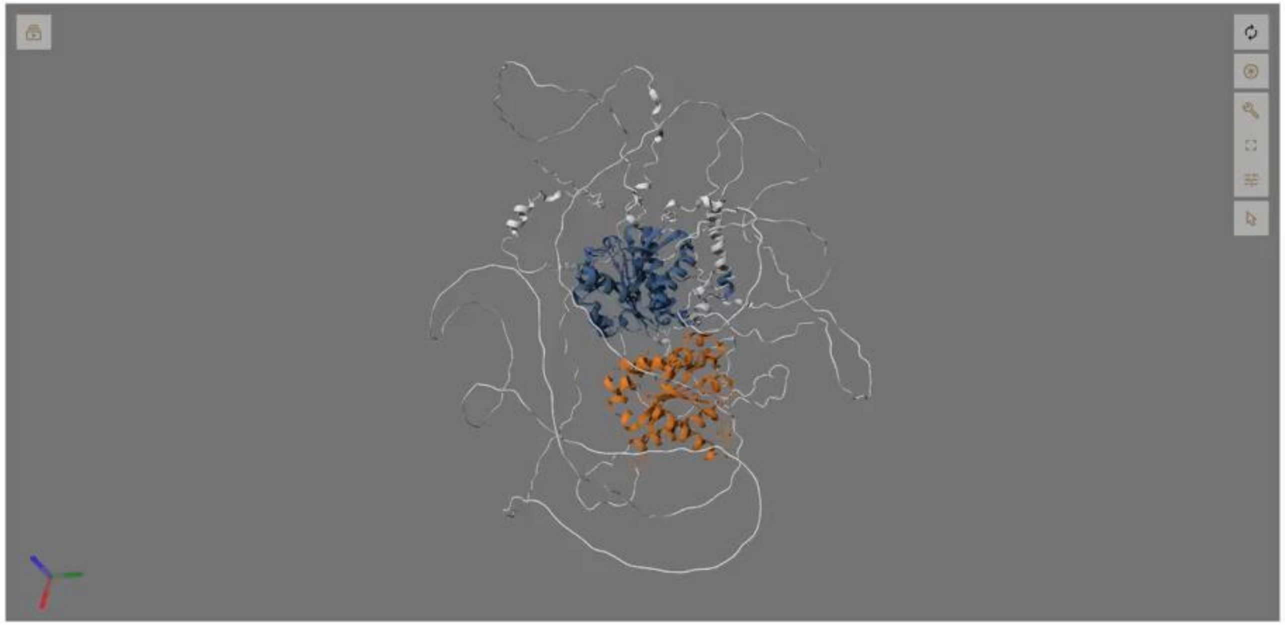
Obtaining Model Parameters

This repository contains all necessary code for AlphaFold 3 inference. To request access to the AlphaFold 3 model parameters, please complete this form. Access will be granted at Google DeepMind's sole discretion. We will aim to respond to requests within 2–3 business days. You may only use AlphaFold 3 model parameters if received directly from Google. Use is subject to these terms of use.

Installation and Running Your First Prediction

See the installation documentation.

Once you have installed AlphaFold 3, you can test your setup using e.g. the following input JSON file named `alphafold_input.json`:



TED Consensus Domains 2

	DOMAIN	BOUNDARIES	CATH	RESIDUES	AV PLDDT	PACKING	GLOBULARITY	INTERACTIONS	P
	TED01	88-141_252-302_379-423_811-913	3.40.50.300	253	68.6	11.4	0.311	TED02 15.0	
	TED02	919-932_951-973_995-1118_1138-1172	3.40.50.300	196	75.0	12.1	0.287	TED01 15.0	

https://github.com/google-deepmind/alphafold3

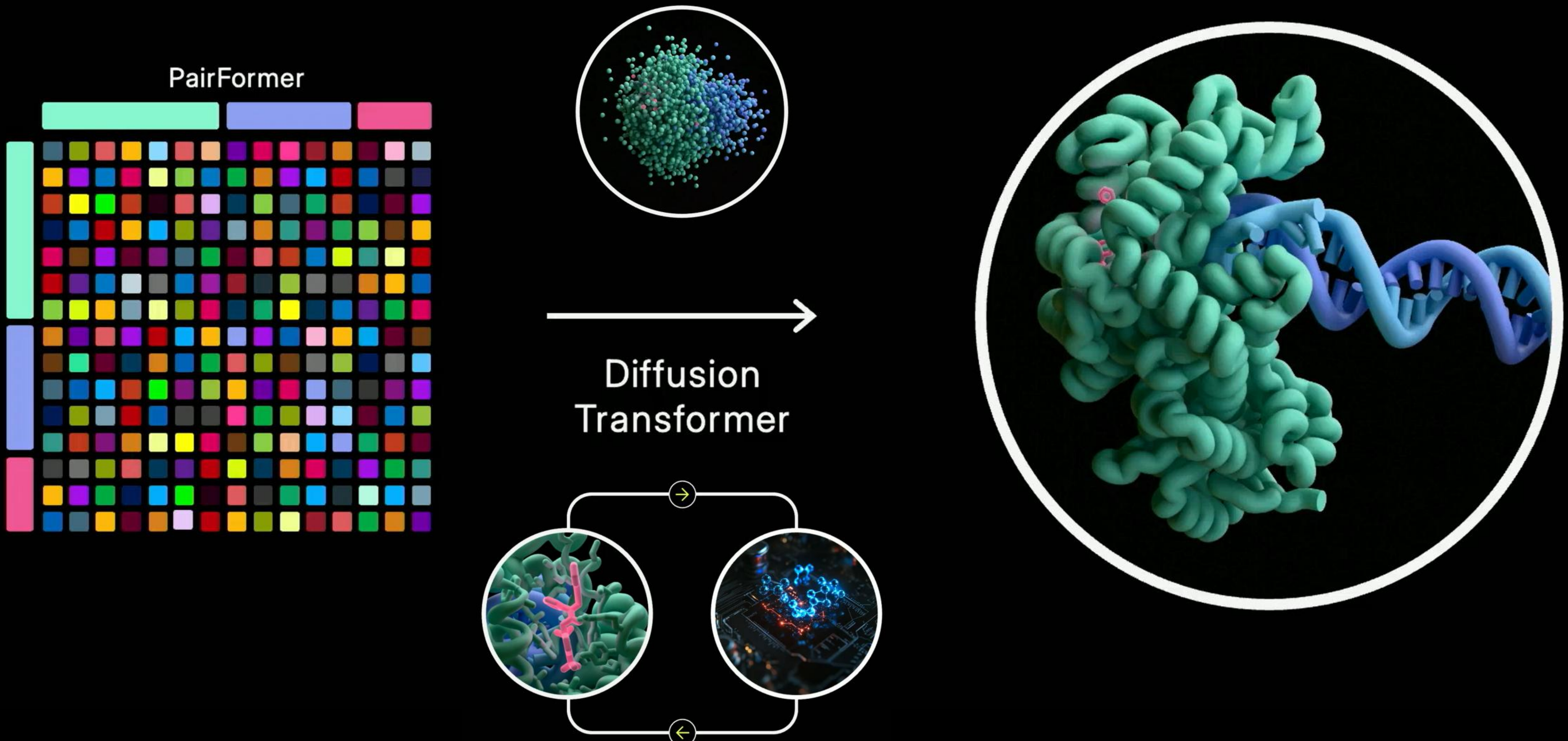
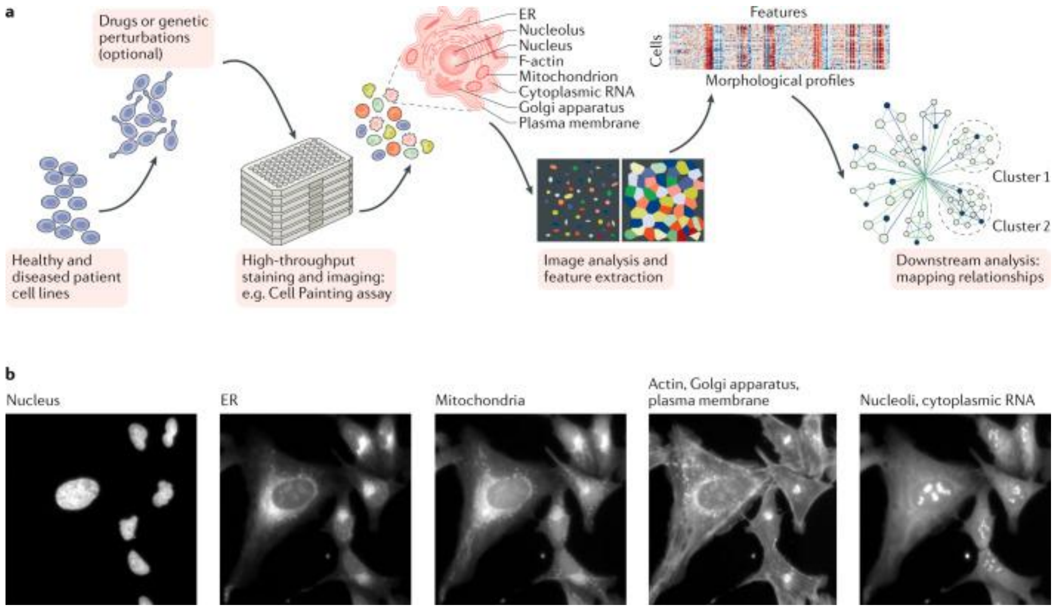
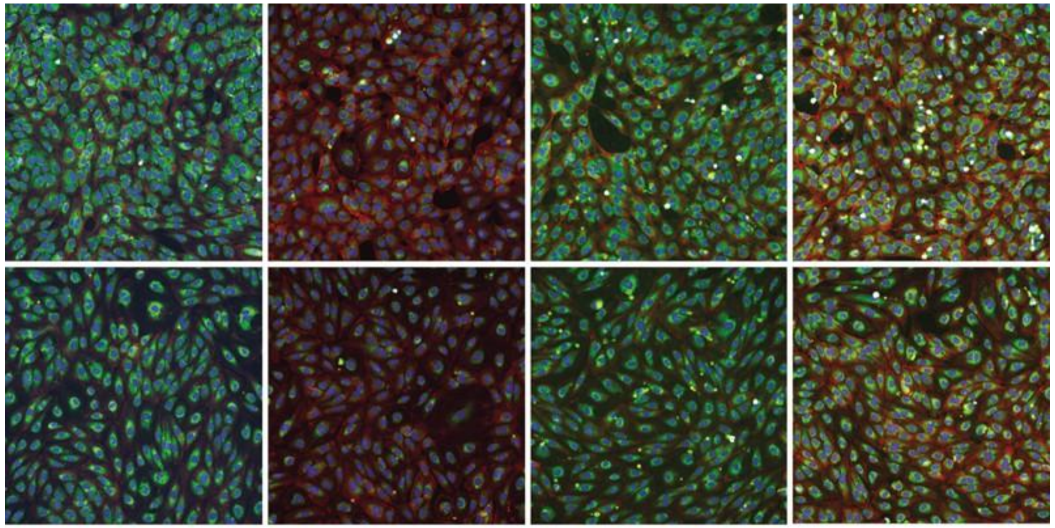

PairFormer
Diffusion
Transformer

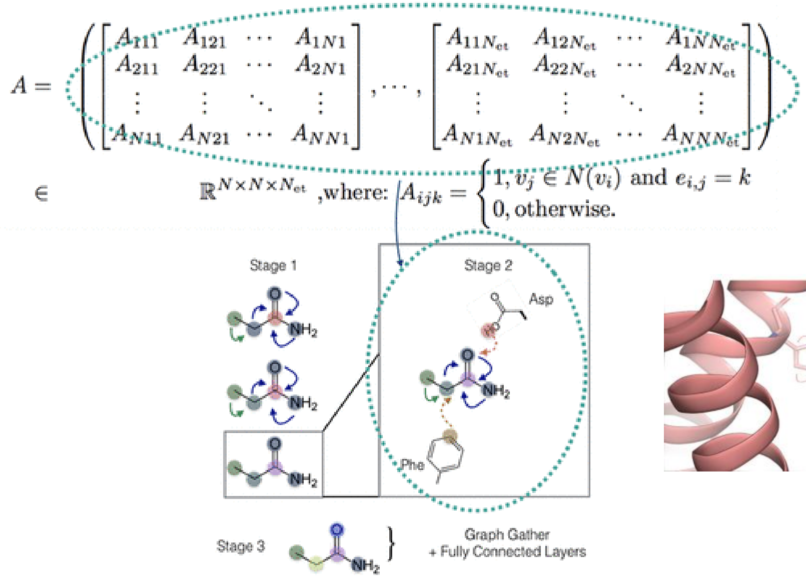
Image-based Profiling and Machine Learning for Drug Discovery

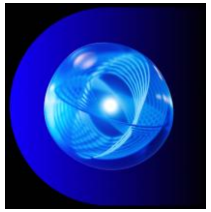
- Array of robots treat millions of cell samples with drugs and genetic perturbations, stain them, and image them.
- It then applies machine learning algorithms to search for informative relationships between the perturbations and the morphological features of the cells.
- The creation of well-curated image data could also be useful across a wide array of problems in drug discovery, including target identification, target deconvolution, library enrichment, lead optimization and toxicity testing.

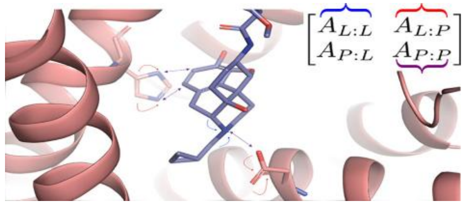


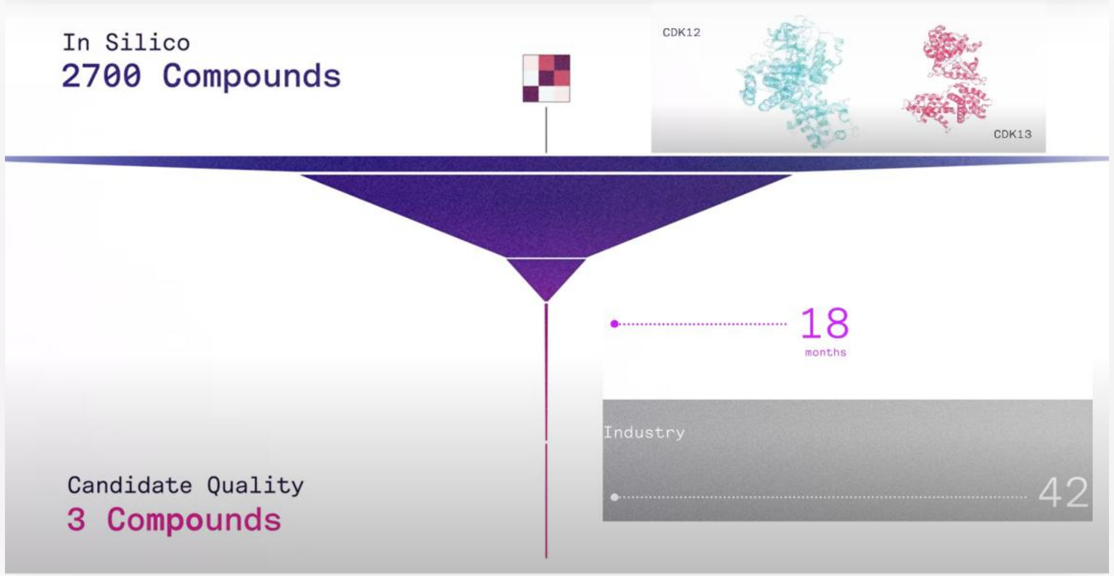


https://www.nature.com/articles/d41573-019-00144-2









- On October 02, 2024, FDA cleared an investigational new drug (IND) application for a Phase 1/2 clinical trial of REC-1245, a new chemical entity for the treatment of biomarker-enriched solid tumors and lymphoma.
- RMB39 was identified in biology maps as a novel target that looks functionally similar to the well-known but hard to drug target CDK12.
- Also identified and optimized small molecules that target RBM39 without directly impacting CDK12 or CDK13 using these same AI-enabled maps.

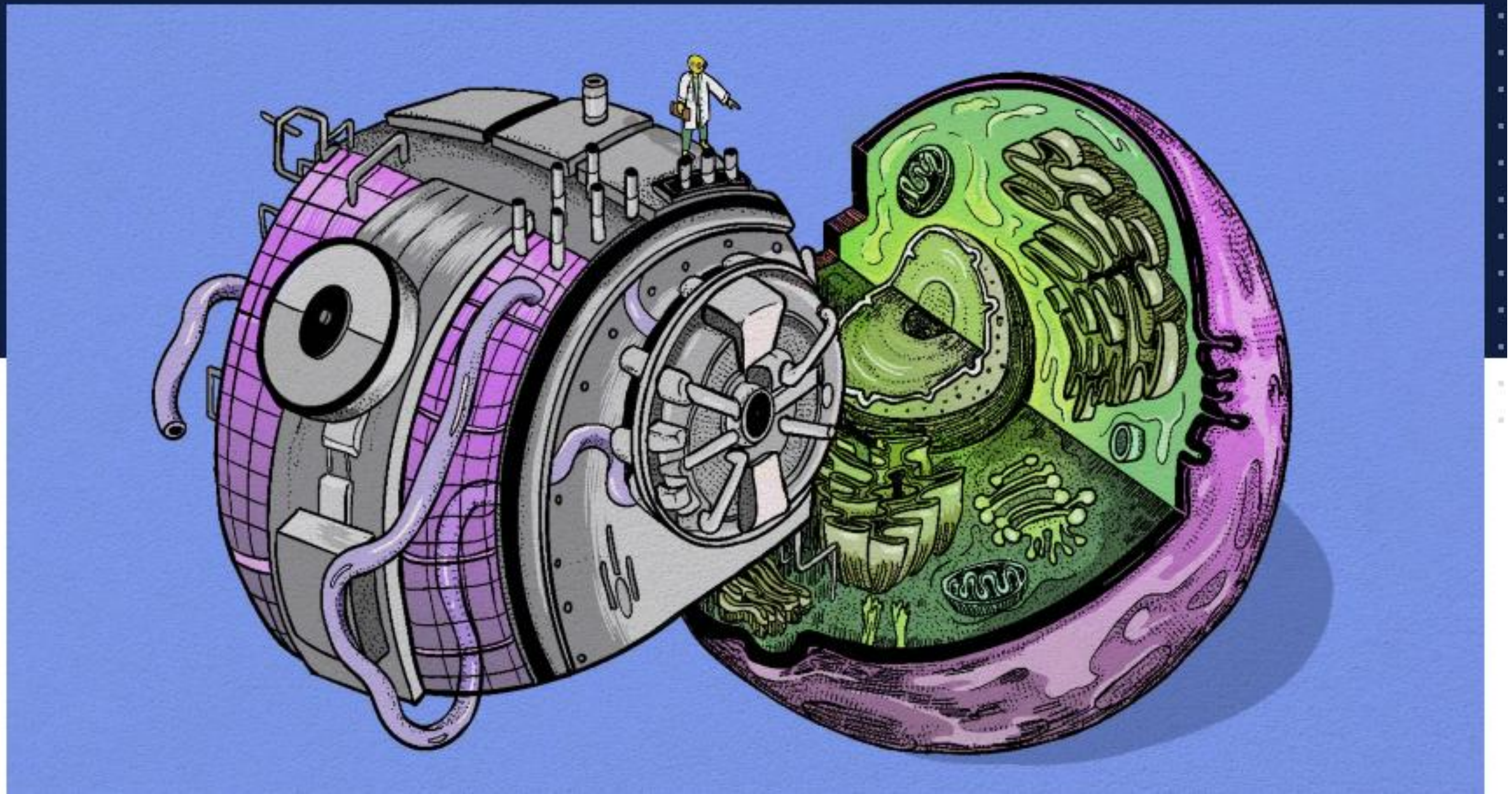
BIOTECHNOLOGY AND HEALTH

How AI can help us understand how cells work—and help cure diseases

A virtual cell modeling system, powered by AI, will lead to breakthroughs in our understanding of diseases, argue the cofounders of the Chan Zuckerberg Initiative.

By Priscilla Chan & Mark Zuckerberg

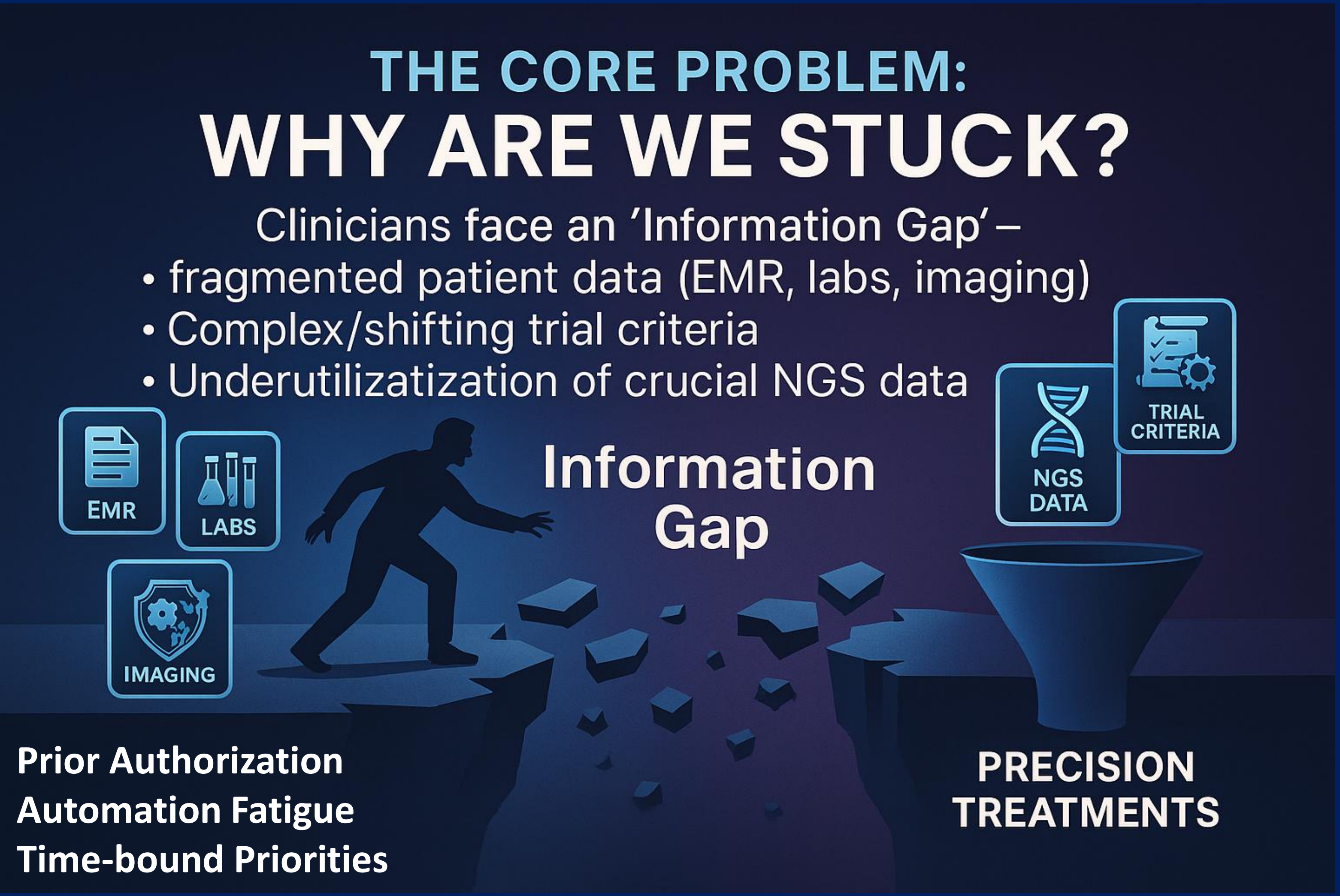
September 19, 2023

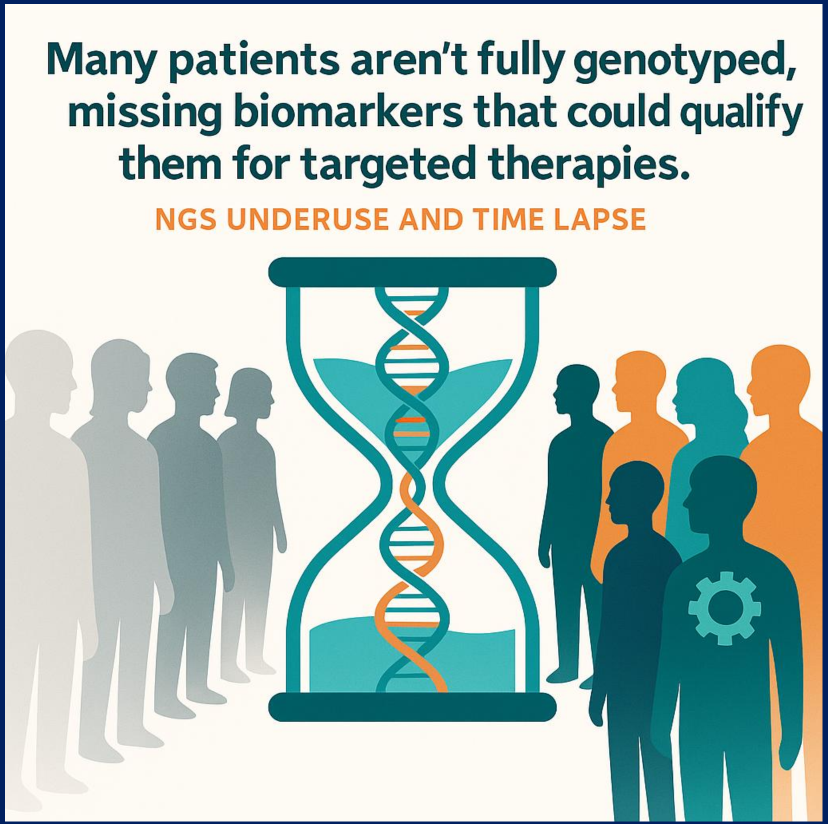


- Researchers from across the world, including [MIT’s San Francisco Biohub](), are using AI to create an open-source Human Cell Atlas. Mark Zuckerberg’s foundation will deploy one of the world's largest AI clusters for nonprofit scientific research to create “virtual cells” that simulate different conditions.

Addressing Challenges in AI-driven Healthcare

- Interpretability and Transparency: The need for clearer understanding of AI decisions.
- Data Requirements: Tackling the need for large, diverse datasets.
- Ethics: Discussing privacy, security, and potential biases in AI applications.
- Essential to address risks like data security, bias, and regulatory compliance.
- Human-in-the-loop involvement and rigorous risk and compliance review are crucial.





This bottleneck directly hinders the translation of biomarker innovation into clinical practice, delaying or denying precision treatments.

The Clinical Trial Enrollment Paradox

Based on an analysis of more than 12 million patients and their initial course of treatment for 46 cancers from 2004 to 2015: Of 12,097,681 patients in the NCDB, 11,576 (0.1%) were enrolled in clinical trials (National Cancer Database)

Zaorsky NG, et al. J Natl Compr Canc Netw. 2019 Nov 1;17(11):1309-1316.

About 55% of clinical trials are shut down prematurely because of enrollment issues lack of enough patients to participate. Across all trials, ~80% fail to meet their original enrollment deadline.

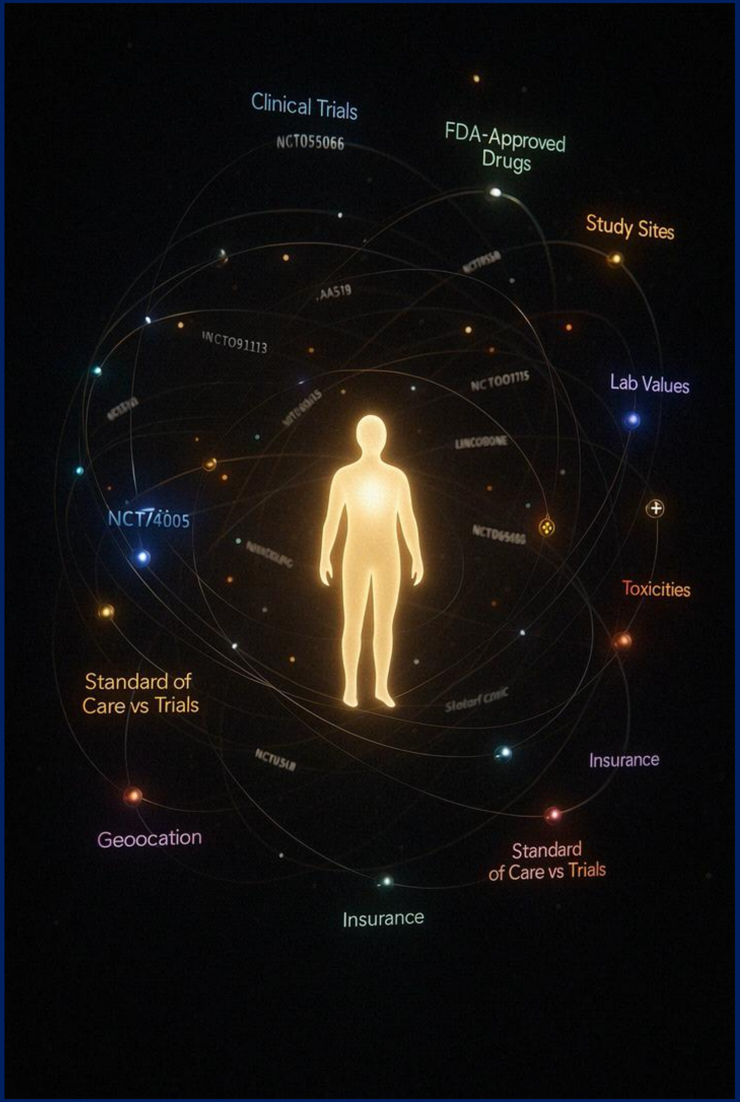
GlobalData Healthcare – 2018 | Desai M. Perspect Clin Res. 2020 Apr-Jun;11(2):51-53.

Currently, there are more than 14,900 active cancer clinical trials globally, with more than 18 million new patients being diagnosed with cancer every year (2M US alone).

Siegel RL, et al. CA Cancer J Clin. 2025 Jan-Feb;75(1):10-45.
Bray F, et al. CA Cancer J Clin. 2024 May-Jun;74(3):229-263

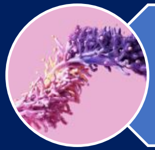
The solution to these problems is to find a technological way to bring together patients and developers of new cancer treatments, in near-real time, collaboratively at-scale and patient-centric approach.

Beyond Static Checks: Handling Real-Time "Data Drift"

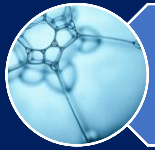


The Reality: Trial matching isn't static. It's a dynamic environment with constant "data drift":

Trial Changes: Amendments, site openings/closures, competitive enrollment, regulatory holds.

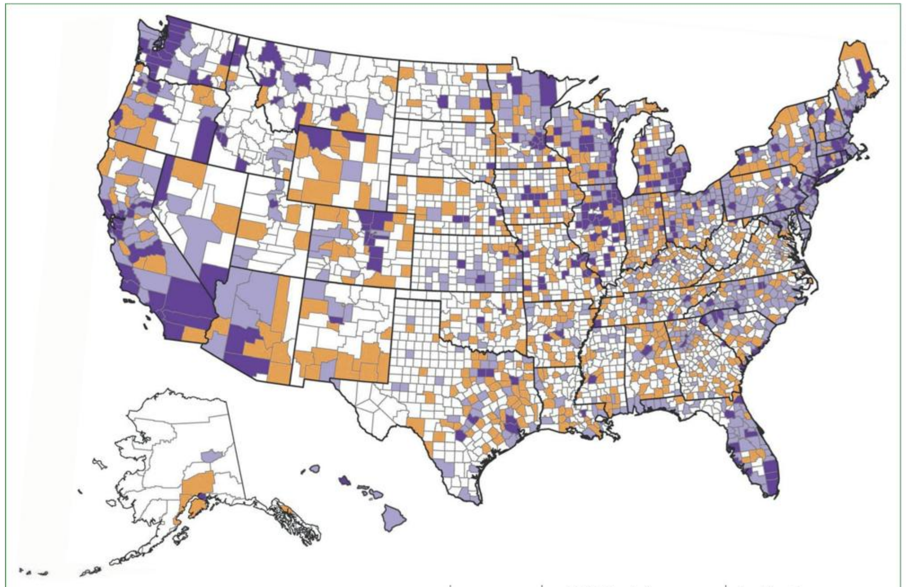


Patient Evolution: Disease progression, new biomarkers, changing performance status, completion of prior therapies.



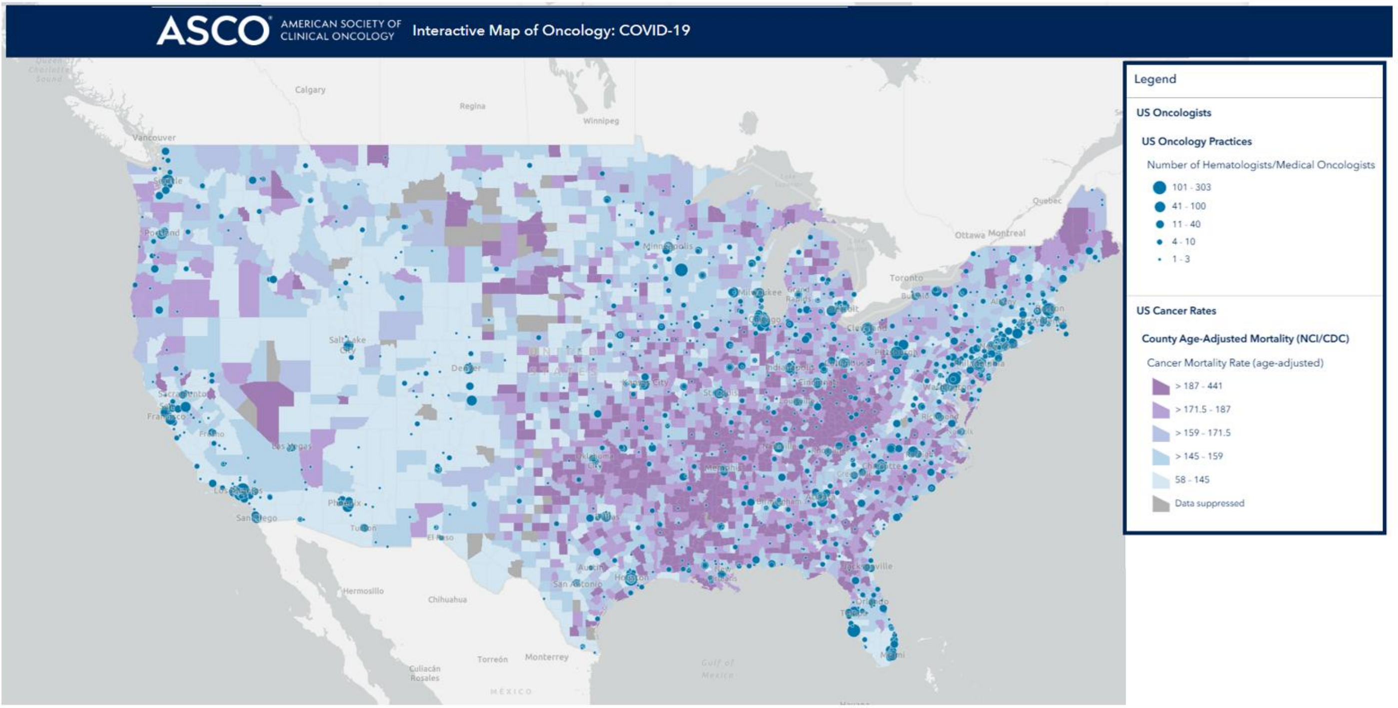
Standard of Care Shifts: New approvals impacting eligibility or treatment landscape.

Analogy: Think "Logistics for Trials" – like Uber or Instacart, needing real-time awareness of availability, need, and location. Manual tracking simply cannot keep pace.



Legend	Counties	(%)	100,000 People Age ≥55 years	(%)	Land Area (square miles)	(%)
No trials-no oncologists	1,593	(51)	87	(9)	1,958,451	(55)
No trials-oncologists	618	(20)	92	(10)	653,822	(19)
1-99 trials	656	(21)	316	(33)	600,336	(17)
100+ trials	276	(9)	450	(48)	320,431	(9)
Total	3,143	(100)	945	(100)	3,533,041	(100)

JCO Oncology Practice
https://ascopubs.org/doi/10.1200/OP.24.00261



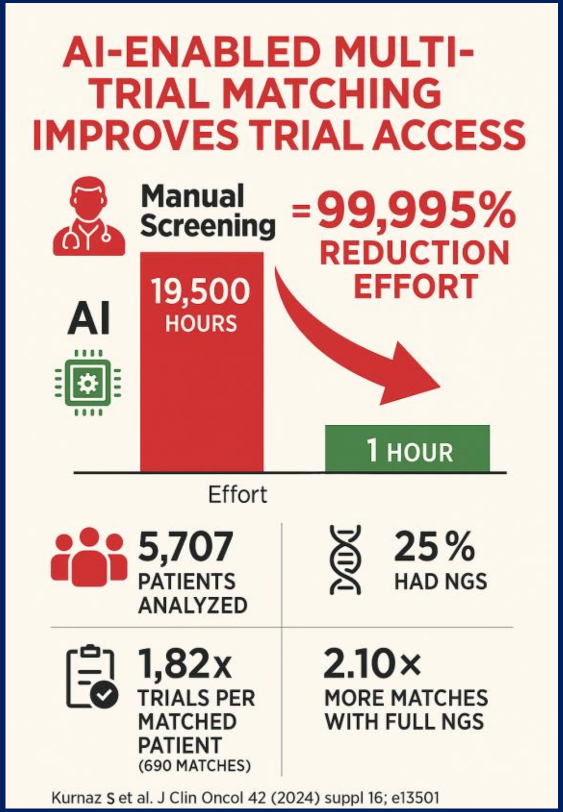
ARPA-H

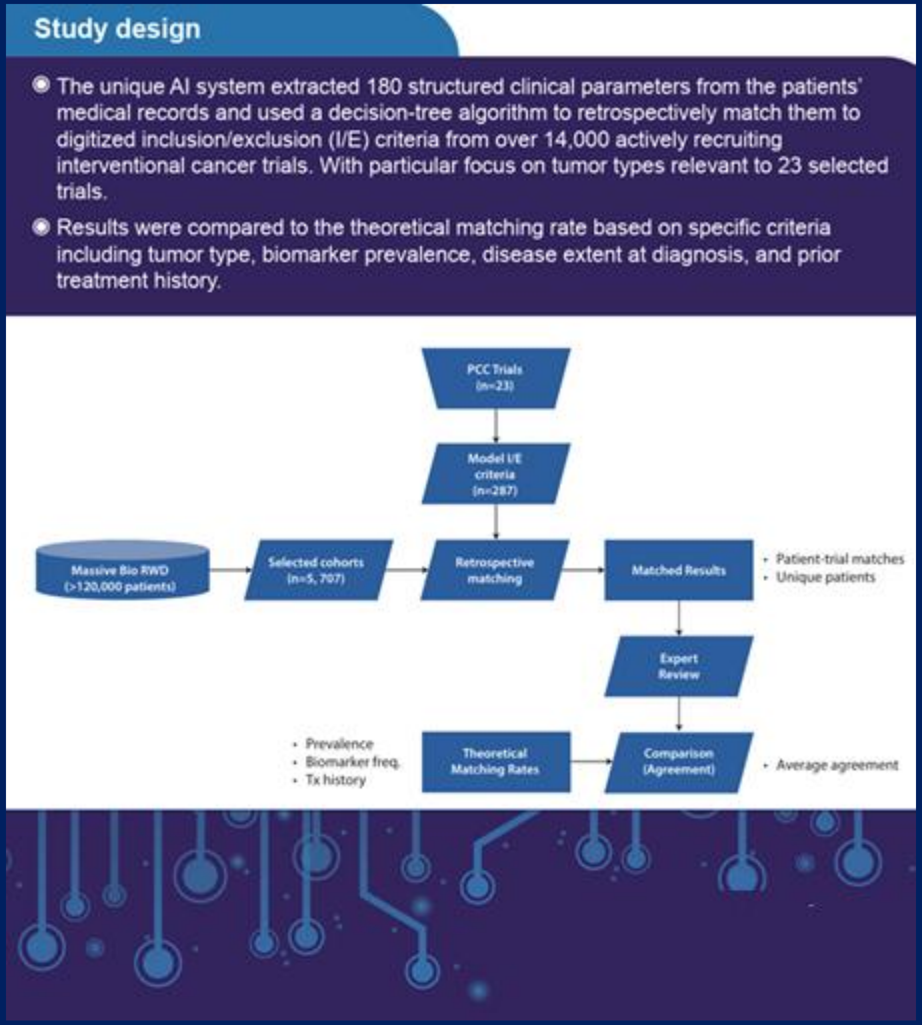
BARDA

- Trial and Cancer Care Deserts: Financial challenges are closely related to the geographic hurdle of trial access
- 85% of the 1,700,000 Americans diagnosed with cancer in 2021 receive care at community-based practices
- Gen-AI can help us analyze SDoH and solve barriers

An AI-Driven Approach – Evidence of Impact

Digital Enablement and Artificial intelligence offer a powerful way to cut through this complexity.





Kurnaz S, et al. J Clin Oncol 42, 2024 (suppl 16; abstr e13501). 2024 ASCO Annual Meeting.

This is enabled by interoperability standards like FHIR, allowing secure, seamless data flow from EHRs and other sources.

The Result: we move from hours per potential match to seconds.

Defining Patient-Centric Pre-Screening Hubs

Uber, Amazon, or Instacart but for clinical trials

- Manual methods fail to capture eligibility windows opened by **time passage, complex sequences, or dynamic clinical changes**.
- Opportunities for patients and trials are lost due to information latency
- **Hybrid "Click-and-Mortar" Model**

Only an **AI-powered, real-time pre-screening hub** can effectively manage this data drift, ensuring patients are matched to the right trials precisely when they become eligible.

Flips the paradigm from "trials waiting for patients" to "patients discovered for trials," echoing Cancer Moonshot's mandate to "bring trials to patients."

ACS ACTS: Finding the right clinical trial for you.

We understand the challenges of finding the right clinical trial, navigating your treatment options, and accessing the support you need. The American Cancer Society is here to guide you every step of the way.

American Cancer Society

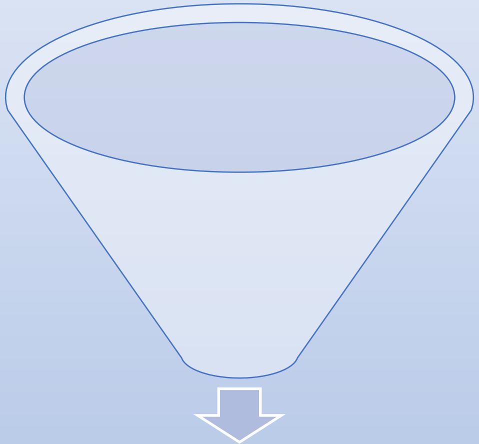
ACTS

ACS ACTS is empowering you, through a personalized clinical trial matching service, to navigate clinical trials and find the best treatment options available.

Fill out the form to get started

Clinical Trials Education	Health-related Social Needs Screening	Trial Eligibility & Enrollment Navigation	AI-powered Clinical Trials Matching	Transportation Assistance to Trials	Lodging Support Near Trial Sites

Source: American Cancer Society - https://acts.cancer.org/



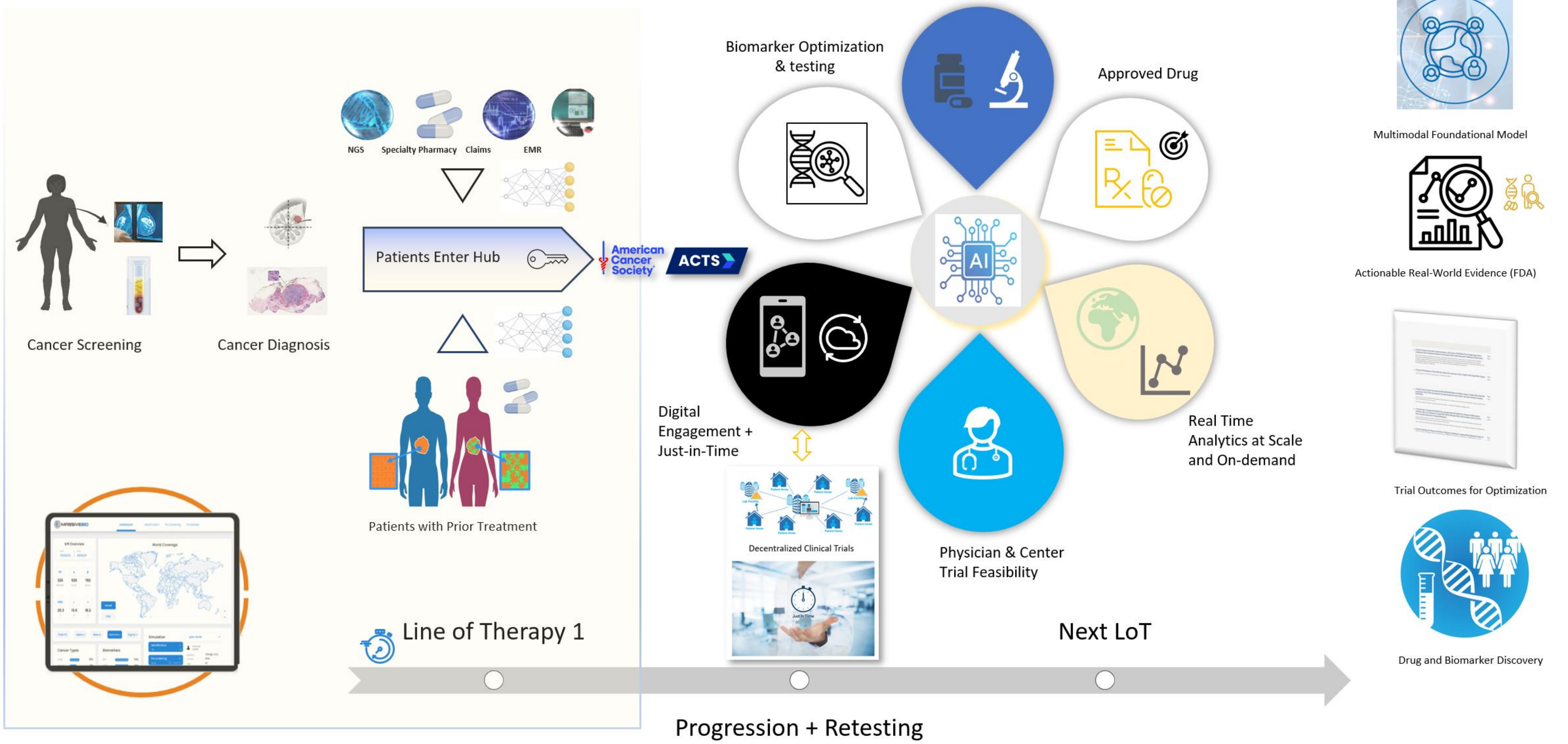
AI as Multiplier Force for Trials: ACS ACTS

SCAN ME

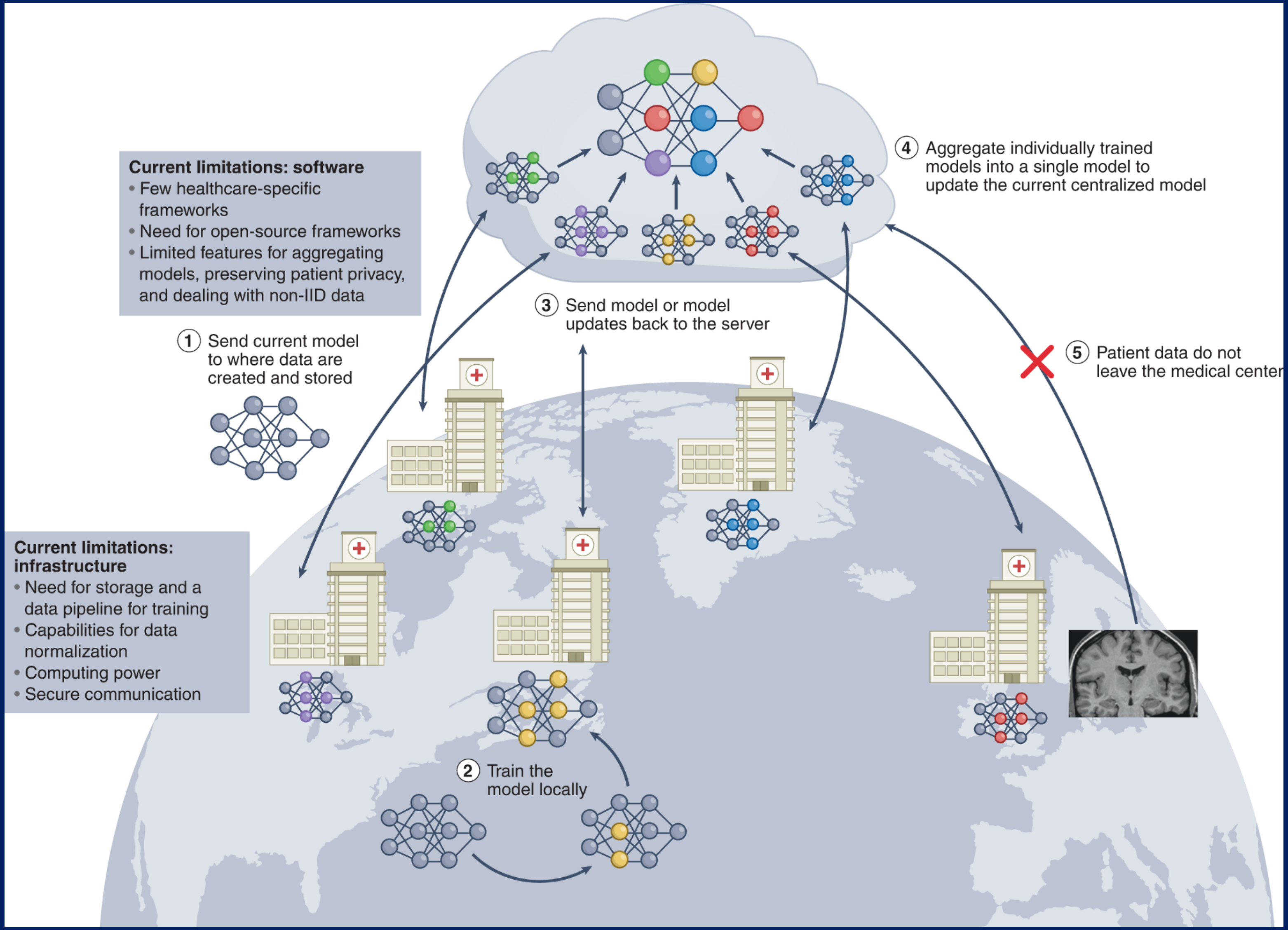
Pre-screening hub-and-spoke population wide approach

Patient centric just-in-time, decentralized/hybrid trials

Transforming every patient's journey into a catalyst for discovery



Arturo Loaiza-Bonilla, MD MEd FACP

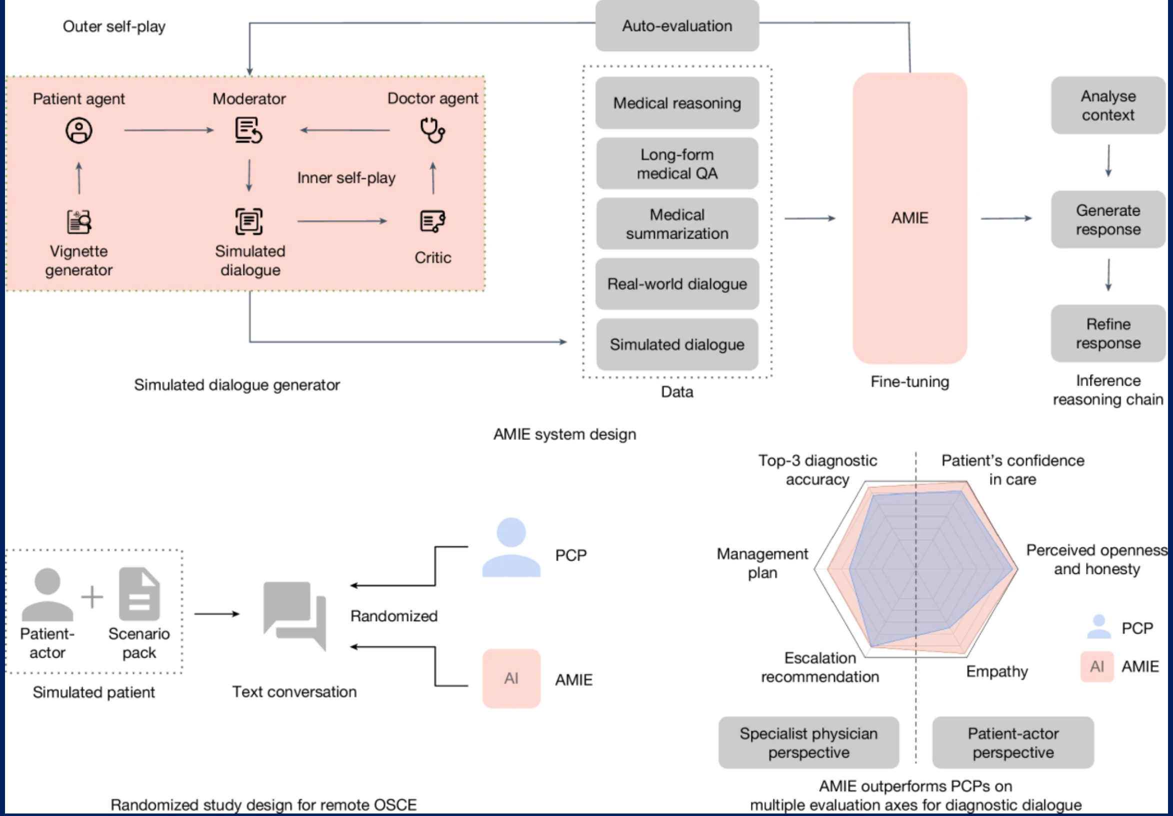


Nat. Biomed. Eng **6**, 1330–1345 (2022)

Aspect	Federated Learning in Healthcare
Data Location	Remains at local institutions
Data Sharing	No raw data exchanged; only model updates shared
Privacy	Strongly enhanced; supports compliance with healthcare regulations
Collaboration	Multi-institutional, often international
Model Performance	Comparable to centralized models; improved generalizability
Applications	Imaging, EHR analysis, drug discovery, rare disease research

Federated learning is a transformative approach in healthcare, enabling large-scale, privacy-preserving, and collaborative AI development across institutions, while addressing the critical challenges of data privacy, security, and governance

AMIE (Articulate Medical Intelligence Explorer), a large language model (LLM)-based AI system optimized for diagnostic dialogue



Tu, T., Schaekermann, M., Palepu, A. *et al. Nature* (2025)

"Nope—I'm the 3 a.m. consult note, not the attending with the pager."

Arturo Loaiza-Bonilla, MD MEd FACP

Keeping It Human – AI as Augmentation, Not Replacement

NEJM AI

NEJM AI 2025;2(5)
DOI: 10.1056/AIp2500005

PERSPECTIVE

Harnessing Moravec's Paradox in Health Care: A New Era of Collaborative Intelligence

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Abstract

Artificial intelligence excels at complex data analytics, yet struggles with nuanced, sensorimotor tasks that humans perform almost effortlessly — a dichotomy encapsulated by Moravec's paradox. By strategically harnessing these complementary strengths, health care can usher in an era of collaborative intelligence, optimizing data-intensive workflows, such as clinical trial enrollment, and creating more patient-centric models of care.

Introduction

Moravec's paradox highlights a counterintuitive truth: advanced mathematical or data-driven tasks are often easier for computers than the everyday sensorimotor and social tasks humans perform and take for granted.[1] Nowhere is this more evident than in health care. A seasoned clinician can, within seconds, detect a patient's anxiety or discomfort by reading subtle body language — yet manually sifting through thousands of laboratory results or complex clinical trial protocols can be laborious and time-consuming. Meanwhile, artificial intelligence (AI) systems can handle those data-heavy tasks at superhuman speed, but remain clumsy with seemingly easy tasks like empathetic bedside manner or dexterous physical procedures.

This tension need not be a limitation. By aligning each domain — human and machine — with the tasks to which it is best suited, we can create a collaborative model of care that increases efficiency and, more importantly, preserves a deeply humane approach to medicine.

The Evolutionary Clue

Why is this mismatch so prominent? Evolution devoted vast energy to refining our sensorimotor and social skills — abilities critical for survival and social bonding over millions of years.[1] By comparison, advanced formal reasoning and numerical computation are relatively recent additions to our cognitive repertoire. AI research, conversely, has historically focused on algorithms for large-scale computations and pattern recognition. It is thus unsurprising that algorithms excel at high-dimensional data analysis well before mastering the physical dexterity or empathic presence we expect of a clinician, and concepts of artificial general

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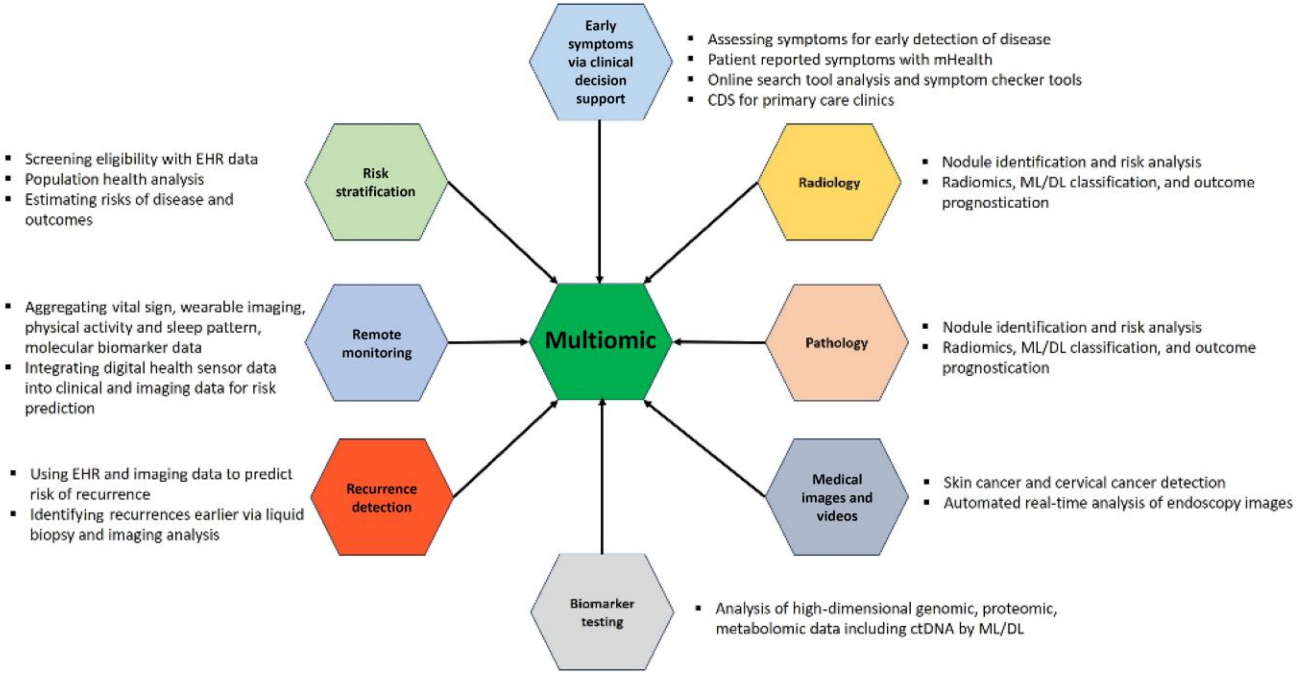
Easy for Humans (Hard for AI)	Easy for AI (Hard for Humans)
Empathy and bedside communication	Large-scale data analysis
Physical dexterity in exams	Rapid trial eligibility scanning
Contextual flexibility	Automated EHR summarization

Moravec's Paradox

The human element – be it patient navigators, physicians, or study staff – remains vital to complement the technology, providing empathy, trust, and final verification in the enrollment process.



Invited Articles | Care Delivery and Quality Care

ASCO Educational Book

Driving Knowledge to Action: Building a Better Future With Artificial Intelligence–Enabled Multidisciplinary Oncology

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Am Soc Clin Oncol Educ Book 45:e100048

OVERVIEW

Artificial intelligence (AI) is transforming multidisciplinary oncology at an unprecedented pace, redefining how clinicians detect, classify, and treat cancer. From earlier and more accurate diagnoses to personalized treatment planning, AI's impact is evident across radiology, pathology, radiation oncology, and medical oncology. By leveraging vast and diverse data—including imaging, genomic, clinical, and real-world evidence—AI algorithms can uncover complex patterns, accelerate drug discovery, and help identify optimal treatment regimens for each patient. However, realizing the full potential of AI also necessitates addressing concerns regarding data quality, algorithmic bias, explainability, privacy, and regulatory oversight—especially in low- and middle-income countries (LMICs), where disparities in cancer care are particularly pronounced. This study provides a comprehensive overview of how AI is reshaping cancer care, reviews its benefits and challenges, and outlines ethical and policy implications in line with ASCO's 2025 theme, *Driving Knowledge to Action*. We offer concrete calls to action for clinicians, researchers, industry stakeholders, and policymakers to ensure that AI-driven, patient-centric oncology is accessible, equitable, and sustainable worldwide.

HHS Public Access
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Artificial Intelligence for Clinical Oncology

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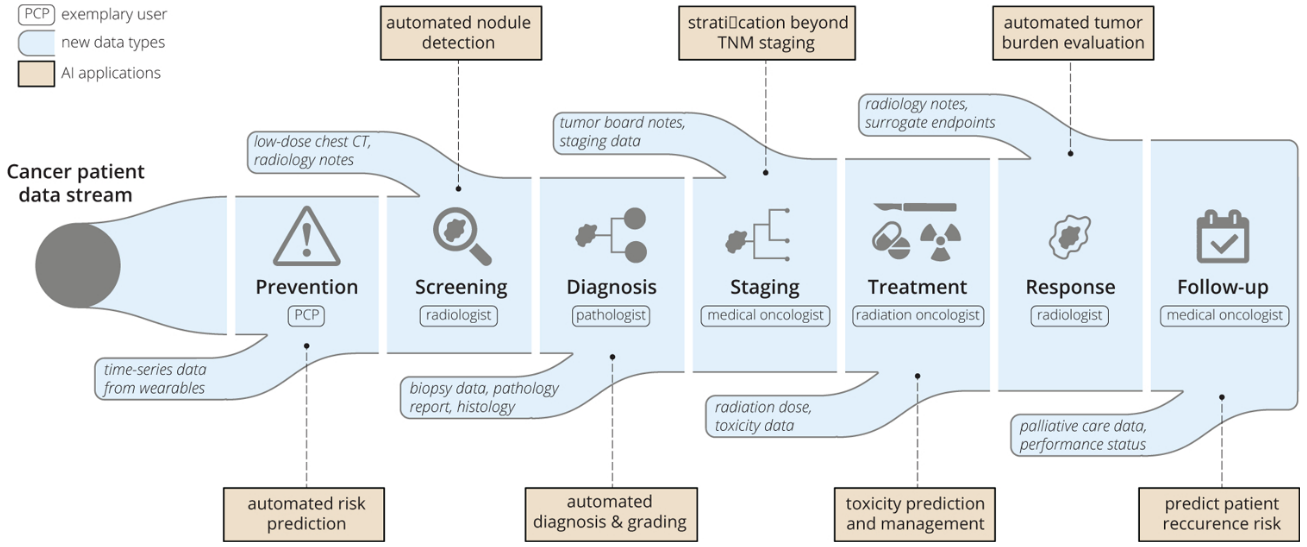
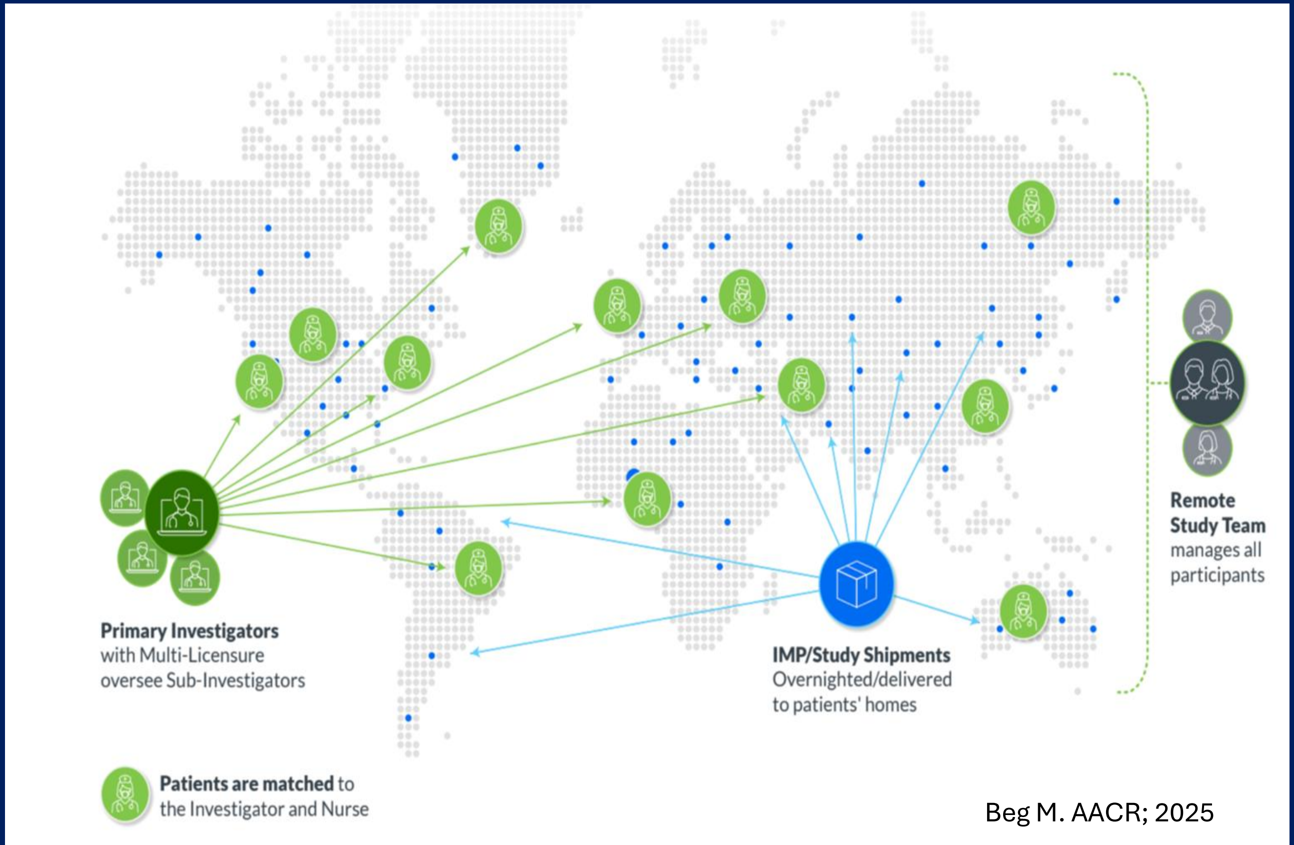
SUMMARY

Clinical oncology is experiencing rapid growth in data that are collected to enhance cancer care. With recent advances in the field of Artificial Intelligence (AI), there is now a computational basis to integrate and synthesize this growing body of multi-dimensional data, deduce patterns, and predict outcomes to improve shared patient and clinician decision-making. While there is high potential, significant challenges remain. In this perspective, we propose a pathway of clinical cancer care touchpoints for narrow-task AI applications and review a selection of applications. We describe the challenges faced in the clinical translation of AI and propose solutions. We also suggest paths forward in weaving AI into individualized patient care, with an emphasis on clinical validity, utility, and usability. By illuminating these issues in the context of current AI applications for clinical oncology, we hope to help advance meaningful investigations that will ultimately translate to real-world clinical use.



Planetary AI + Trials Hubs. Patient-First Network.



Beg M. AACR; 2025

This isn't futuristic; it's actionable now

Théâtre D’opéra Spatial