Publications

communications medicine

Article

https://doi.org/10.1038/s43856-024-00471-5

A systematic pan-cancer study on deep learning-based prediction of multi-omic biomarkers from routine pathology images

Check for updates

Salim Arslan[1] ✉, Julian Schmidt[1], Cher Bass[1], Debapriya Mehrotra[1,2], Andre Geraldes[1], Shikha Singhal[1,3], Julius Hense[1], Xiusi Li[1], Pandu Raharja-Liu[1], Oscar Maiques[4,5], Jakob Nikolas Kather[6,7] & Pahini Pandya[1]

Table 1 | Average performanc

Biomarker type/omic	Mean AUC ± std.
Standard clinical biomarkers	0.742 ± 0.120 (n = 135)
Clinical outcomes and treatment responses	0.671 ± 0.120 (n = 480)
Under-/over-expression of proteins	0.666 ± 0.108 (n = 1728)
Gene signatures and molecular subtypes	0.653 ± 0.097 (n = 810)
Under-/over-expression of transcriptomes	0.637 ± 0.108 (n = 3090)
Presence of single nucleotide variants (SNVs)	0.636 ± 0.117 (n = 5850)

The table is sorted by the average performanc .

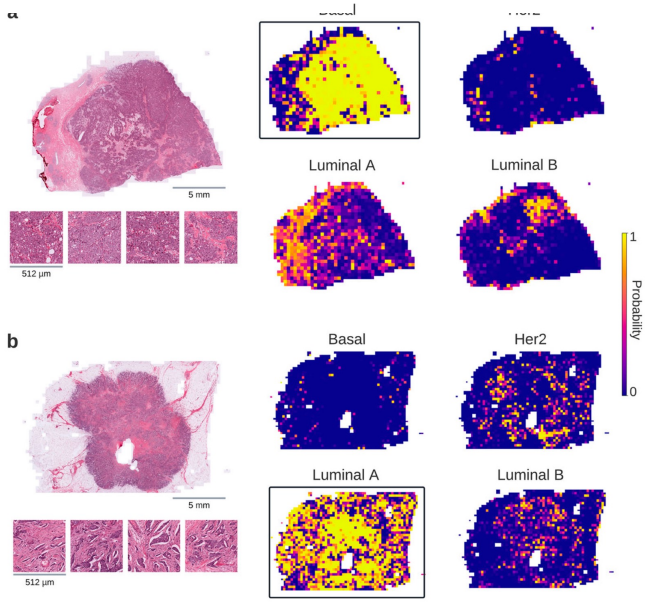

Fig. 6 | Visualization of predictability with deep learning from histopathological images. Deep learning (DL)-based predictions for the molecular subtypes of breast cancer (i.e., Basal, HER2, Luminal A, and Luminal B) are visualized for two selected patients using heatmaps. The correctly-predicted subtype in each case is enclosed with a rectangle and the highest-ranking tiles from that class are given alongside the original whole slide image (WSI). The Basal type (**a**) shows sheets of tumor cells without any discernible gland formation, while the Luminal A patient's tumor (**b**) is composed of well-formed glands. Considering the heatmaps in both cases, one can notice that DL models can identify spatial regions that are relevant to the target class. Scale bar for WSIs: 5 mm. Scale bar for tiles: 512 µm.

Topff *et al. European Radiology*
https://doi.org/10.1007/s00330-024-10676-w

EUROPEAN SOCIETY OF RADIOLOGY
European Radiology

IMAGING INFORMATICS AND ARTIFICIAL INTELLIGENCE

Artificial intelligence-assisted double reading of chest radiographs to detect clinically relevant missed findings: a two-centre evaluation

Laurens Topff[1,2*], Sanne Steltenpool[3,4], Erik R. Ranschaert[5,6], Naglis Ramanauskas[7,8], Renee Menezes[9], Jacob J. Visser[3], Regina G. H. Beets-Tan[1,2†] and Nolan S. Hartkamp[4†]

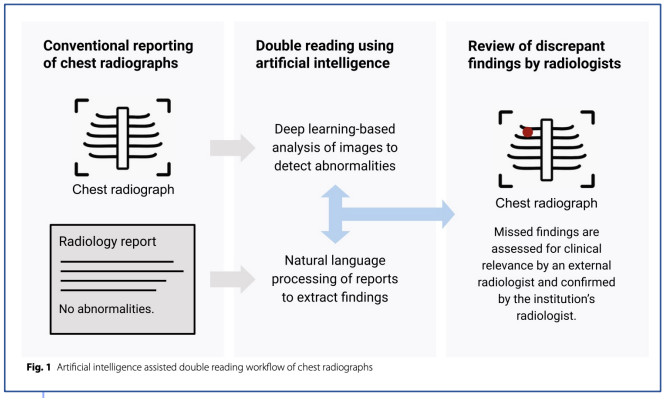

Fig. 1 Artificial intelligence assisted double reading workflow of chest radiographs

findings consisted of lung nodules (71.4%, 25 of 35), pneumothoraces (17.1%, 6 of 35) and consolidations (11.4%, 4 of 35).

Conclusion The AI-assisted double reading system was able to identify missed findings on chest radiographs after report authorisation. The approach required an external radiologist to review the AI-detected discrepancies. The number of clinically relevant missed findings by radiologists was very low.

Clinical relevance statement The AI-assisted double reader workflow was shown to detect diagnostic errors and could be applied as a quality assurance tool. Although clinically relevant missed findings were rare, there is potential impact given the common use of chest radiography.

Contents lists available at ScienceDirect

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journal homepage: www.elsevier.com/locate/jpi

Utility of artificial intelligence in a binary classification of soft tissue tumors

Jing Di [a], Caylin Hickey [a], Cody Bumgardner [a], Mustafa Yousif [b], Mauricio Zapata [c], Therese Bocklage [a], Bonnie Balzer [d], Marilyn M. Bui [e], Jerad M. Gardner [f], Liron Pantanowitz [g], Shadi A. Qasem [a,h,*]

[a] University of Kentucky College of Medicine, Lexington, KY, United States

Table 3
Representative AI models metrics, classifying benign and malignant soft tissue tumors (Study arm 3).

Metric	AUC	Accuracy	Sensitivity	Specificity
Gradientboosting	0.664	0.667	0.579	0.75
Neuralnetwork	0.638	0.641	0.526	0.75
Xgboost	0.639	0.641	0.579	0.7
Randomforest	0.717	0.718	0.684	0.75
Bagging	0.666	0.667	0.632	0.7
Tabpfn	0.743	0.744	0.737	0.75
Histgradientboosting	0.664	0.667	0.579	0.75
Sgdclassifier	0.584	0.59	0.368	0.8
Logisticregression	0.768	0.769	0.737	0.8

Next-Generation Sequencing Trends among Adult Patients with Select Advanced Tumor Types

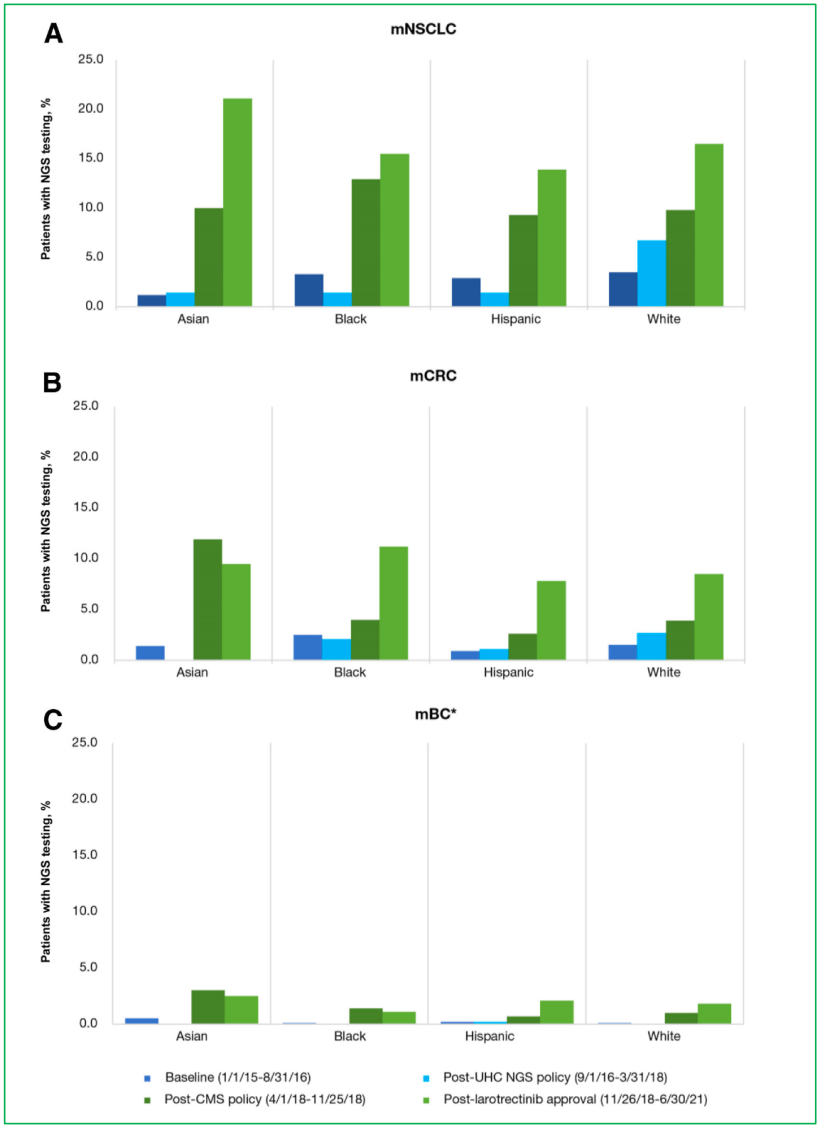
A Real-World Evidence Evaluation

Andrea Ferreira-Gonzalez,* Brian Hocum,† Gilbert Ko,† Sohul Shuvo,† Sreevalsa Appukkuttan,† and Svetlana Babajanyan†

From the Department of Pathology, Virginia Commonwealth University, Richmond, Virginia; and Bayer HealthCare Pharmaceuticals, Inc.,† Whippany, New Jersey*

Despite improving payer policies to expand coverage of NGS and molecular biomarker based therapy approvals, **NGS rates remained low across tumor types**.

Given the potential for improved patient outcomes with molecular biomarker based therapy, further efforts to improve NGS rates are warranted.



Policy and Practice

Strategies to Address the Clinical Practice Gaps Affecting the Implementation of Personalized Medicine in Cancer Care

Apostolia M. Tsimberidou, MD, PhD, FASCO, FAAAS[1]; Anthony Sireci, MD, MSc[2]; Robert Dumanois[3]; and Daryl Pritchard, PhD[4]

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View Online Article

INTRODUCTION

Biomarker testing–based personalized medicine strategies can improve outcomes for patients with cancer at the individual and population levels.[1,2] The identification of actionable molecular biomarkers and treatment with matched targeted therapies have been associated with favorable outcomes for individual patients. However, many patients with cancer do not undergo biomarker testing and do not receive targeted therapies.[3-5] Ensuring that all patients with cancer have access to and receive biomarker-driven care remains a challenge.

SCIENCE ADVANCES | REVIEW

GENETICS

The molecular basis of cell memory in mammals: The epigenetic cycle

Mencía Espinosa-Martínez[1,2,3]†, María Alcázar-Fabra[1,2,3]†, David Landeira[1,2,3]*

Cell memory refers to the capacity of cells to maintain their gene expression program once the initiating environmental signal has ceased. This exceptional feature is key during the formation of mammalian organisms and it is believed to be in part mediated by epigenetic factors that can endorse cells with the landmarks re to maintain transcriptional programs upon cell duplication. Here, we review current literature analyzi molecular basis of epigenetic memory in mammals, with a focus on the mechanisms by which transcript repressive chromatin modifications such as methylation of DNA and histone H3 are propagated through r cell divisions. The emerging picture suggests that cellular memory is supported by an epigenetic cycle in reversible activities carried out by epigenetic regulators in coordination with cell cycle transition create a phasic system that can accommodate both maintenance of cell identity and cell differentiation in prolife stem cell populations.

SCIENCE ADVANCES | REVIEW

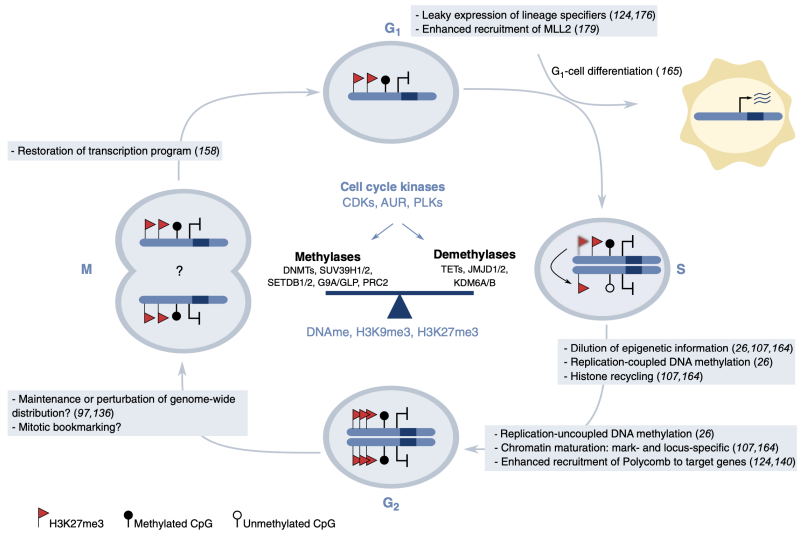
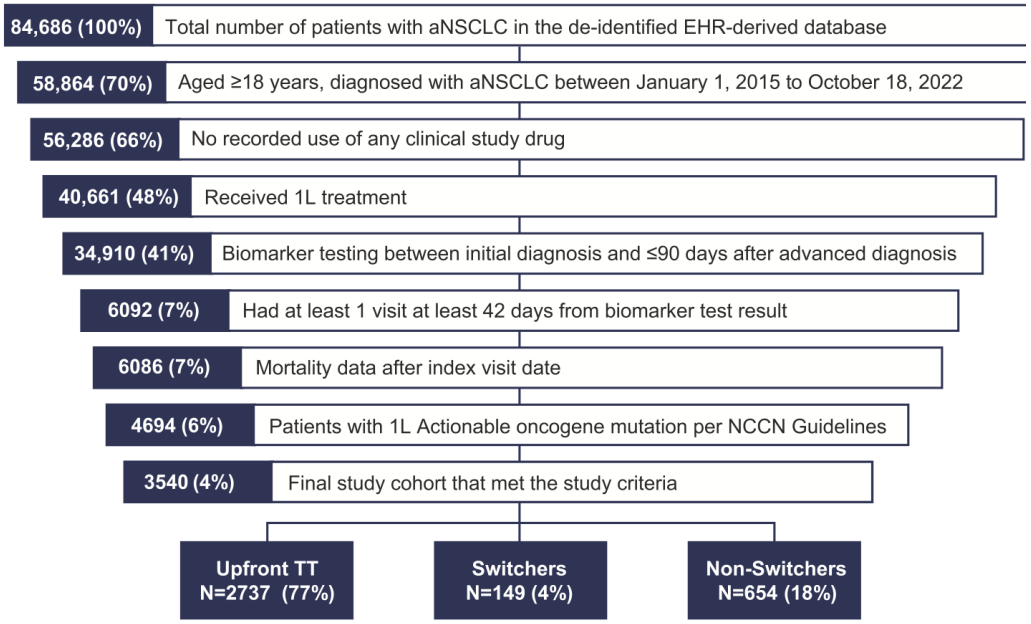


Fig. 3. Model of transmission of epigenetic memory in pluripotent cells: The epigenetic cycle. Undifferentiated cell nuclei during cell cycle transition (G_1, S, G_2, and M phases) are represented as light blue circles, while differentiated cells are depicted in yellow. Blue bars inside the nuclei represent a chromatid in which a gene encoding for a lineage-specifier protein is highlighted in dark blue. Promoters are indicated by black lines. Methylated and unmethylated CpGs are represented as filled or empty lollipops, respectively. Red flags indicate H3K27me3.

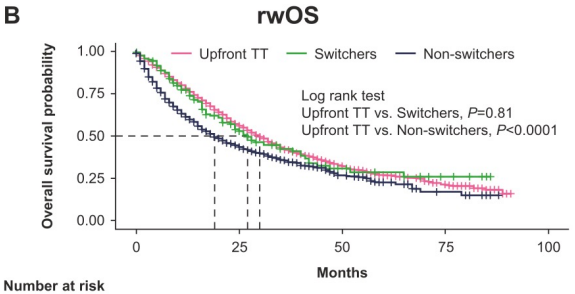
The Oncologist, 2024, **XX**, 1–9
https://doi.org/10.1093/oncolo/oyae022
Advance access publication 28 February 2024
Original Article

Clinical Value of Timely Targeted Therapy for Patients With Advanced Non–Small Cell Lung Cancer With Actionable Driver Oncogenes

Thomas Stricker[*,1,2], Neha Jain[2], Esprit Ma[3], Elaine Yu[3], Rongrong Wang[3], Robert Schuldt[3], Richard Price[3], Tania Szado[3], Jesse Sussell[3], Sarika Ogale[3], Victor Lin[2,4], Edward Arrowsmith[1,2], Dennis Slater[2,5], Daniel Vaena[2,6], Harry Staszewski[2,7], Bruno Fang[2,8], Lasika Seneviratne[2,9], Davey Daniel[1,2]



B

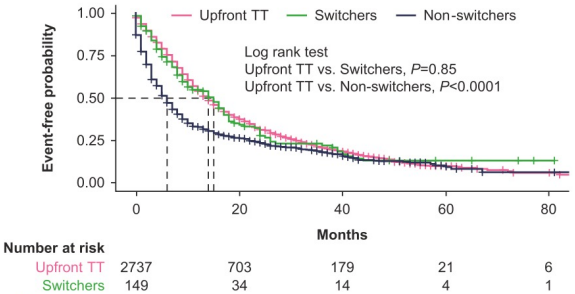


Number at risk

Upfront TT	2737	967	267	58	0
Switchers	149	51	16	5	0
Non-switchers	654	183	51	8	0

	Duration of follow-up, median (IQR) months	rwOS, median (95% CI), months	Adjusted HRs
Upfront TT, n=2737	17 (8-32)	30 (28-32)	Reference group
Switchers, n=149	16 (8-33)	27 (21-40)	0.9697, *P*=0.8002
Non-switchers, n=654	11 (4-26.75)	19 (16-23)	1.3673, *P*=0.0000

C



Number at risk

Upfront TT	2737	703	179	21	6
Switchers	149	34	14	4	1
Non-switchers	654	122	44	10	2

	Duration of follow-up, median (IQR) months	rwTTNTD, median (95% CI), months	Adjusted HRs
Upfront TT, n=2737	10 (5-20)	14 (13-15)	Reference group
Switchers, n=149	10 (4-18)	15 (10-17)	0.9869, *P*=0.9008
Non-switchers, n=654	5 (1-13)	6 (5-7)	1.3308, *P*=0.0000

GENOME DIAGNOSTICS IN THE FAST LANE

Streamlined workflows for DNA and RNA sequencing are helping clinicians to deliver prompt, targeted care to people in days – or even hours. **By Michael Eisenstein**

Sometimes good news arrives too late. About a decade ago, clinical geneticist Zornitza Stark and her colleagues at the Murdoch Children's Research Institute in Melbourne, Australia, set out to learn how genome sequencing might improve the care of young children with suspected hereditary disorders. The researchers sequenced the protein-coding regions in the genomes of 80 infants, looking for genetic changes to explain their conditions. For one nine-month-old boy with severe neurological symptoms, Stark's team homed in on a mutation that resulted in a crucial vitamin B1 deficiency, which could be readily treated with supplements for just under Aus$150 per year (US$136 at the time).

Unfortunately, it took six months from when the sample was taken to get that answer. Treatment with vitamin B1 safeguarded the boy's

ETTY

Original Reports | Artificial Intelligence

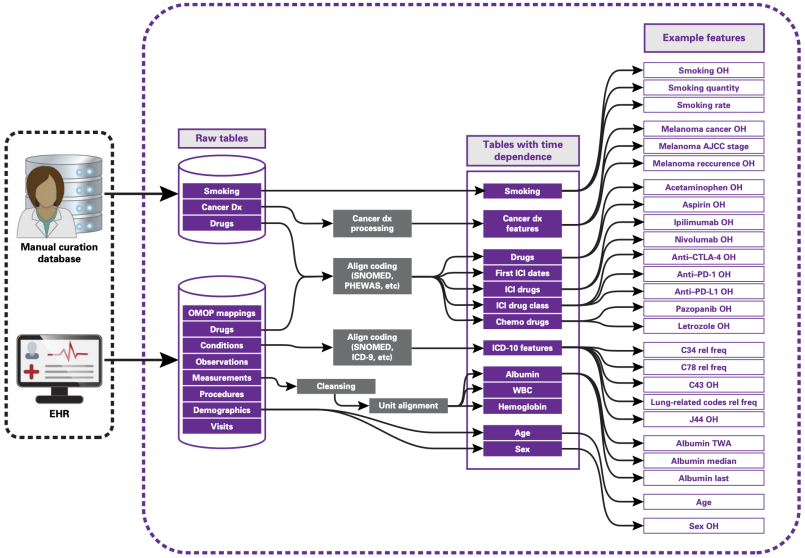
Prediction of Effectiveness and Toxicities of Immune Checkpoint Inhibitors Using Real-World Patient Data

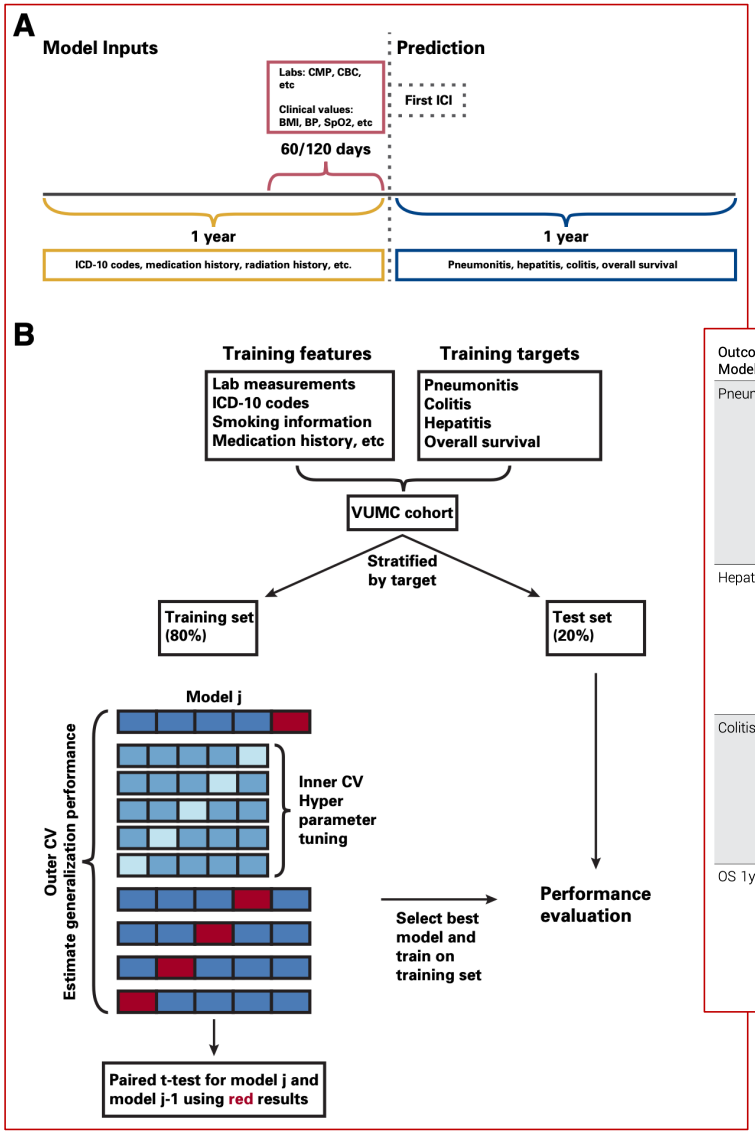
Levente Lippenszky, MS[1]; Kathleen F. Mittendorf, PhD[2]; Zoltán Kiss, MS[1]; Michele L. LeNoue-Newton, PhD[2,3]; Pablo Napan-Molina, MS[1]; Protiva Rahman, PhD[4,5]; Cheng Ye, PhD[4]; Balázs Laczi, MS[1]; Eszter Csernai, MS[1]; Neha M. Jain, PhD[2,6]; Marilyn E. Holt, PhD[2,7]; Christina N. Maxwell, MS[2]; Madeleine Ball, BA[2,8]; Yufang Ma, PhD, PharmD[2,9]; Margaret B. Mitchell, MD, MHPE[2,10]; Douglas B. Johnson, MD, MSCI[2,11]; David S. Smith, PhD[12]; Ben H. Park, MD, PhD[2,11]; Christine M. Micheel, PhD[2,11]; Daniel Fabbri, PhD[4]; Jan Wolber, PhD, MBA[13]; and Travis J. Osterman, DO, MS[2,4,11]

DOI https://doi.org/10.1200/CCI.23.00207

colitis, and 1-year overall survival models, respectively. Each model relies on an outcome-specific feature set, though some features are shared among models.

CONCLUSION To our knowledge, this is the first ML solution that assesses individual ICI risk-benefit profiles based predominantly on routine structured EHR data. As such, use of our ML solution will not require additional data collection or documentation in the clinic.





Outcome Modeled	Diagnosis (N)	AUC (95% bootstrap CI)
Pneumonitis 1y	All cancer types (n = 416)	0.739 (0.638 to 0.823)
	Melanoma (n = 166)	0.590 (0.353 to 0.841)
	Lung cancer (n = 111)	0.723 (0.600 to 0.840)
	GU cancer (n = 67)	0.845 (0.686 to 0.960)
Hepatitis 1y	All (n = 392)	0.729 (0.655 to 0.804)
	Melanoma (n = 136)	0.567 (0.373 to 0.777)
	Lung cancer (n = 107)	0.884 (0.792 to 0.965)
	GU cancer (n = 53)	0.639 (0.376 to 0.863)
Colitis 1y	All (n = 427)	0.755 (0.638 to 0.856)
	Melanoma (n = 161)	0.747 (0.631 to 0.850)
	Lung cancer (n = 112)	0.853 (0.717 to 0.964)
	GU cancer (n = 68)	0.560 (0.447 to 0.672)
OS 1y	All (n = 403)	0.752 (0.706 to 0.796)
	Melanoma (n = 158)	0.794 (0.716 to 0.861)
	Lung cancer (n = 115)	0.681 (0.580 to 0.781)
	GU cancer (n = 63)	0.741 (0.600 to 0.858)

npj | digital medicine

Comment

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The lucent yet opaque challenge of regulating artificial intelligence in radiology

James M. Hillis, Jacob J. Visser, Edward R. Scheffer Cliff, Kelly van der Geest – Aspers, Bernardo C. Bizzo, Keith J. Dreyer, Jeremias Adams-Prassl & Katherine P. Andriole

Table 1 | Summary of radiology AI/ML device

Regulatory agency	United States Food and
Organizational structure for regulatory clearance	Centralized process thro Health
Typical risk classification for radiology AI/ML device	Class II
Predicate pathway	510(k) pathway (for subs I/II device.
Product types / codes	Regulation numbers defi associated 'special cont multiple product codes v have been used for radic
Minimal device metrics	Defined for some produc assisted prioritization so >0.95). Many product codes do
Model change process	Draft guidance to define Control Plan. Separate g software change to an e
Accelerated / conditional pathway	No; the Breakthrough De still requires the applicat
Consideration of cost-effectiveness in clearance	No
Post-market surveillance	Yes
Database of approved devices	FDA website[2]

nature medicine

Comment | Published: 18 March 2024

New AI regulation in the EU seeks to reduce risk without assessing public benefit

Barbara Prainsack & Nikolaus Forgó

Nature Medicine (2024) | Cite this article

The European Union's new AI Act focuses on risk without considering benefits, which could hinder the development of new technology while failing to protect the public.

healthcare

MDPI

Article

Economics of Artificial Intelligence in Healthcare: Diagnosis vs. Treatment

Narendra N. Khanna [1], Mahesh A. Maindarkar [2,3], Vijay Viswanathan [4], Jose Fernande, Sudip Paul [3], Mrinalini Bhagawati [3], Puneet Ahluwalia [6], Zoltan Ruzsa [7], Aditya, Inder M. Singh [2], John R. Laird [10], Mostafa Fatemi [11], Azra Alizad [12], Luca Saba [13], V, Aman Sharma [14], Jagjit S. Teji [15], Mustafa Al-Maini [16], Vijay Rathore [17], Subbaram Nai, Amer M. Johri [19], Monika Turk [20], Lopamudra Mohanty [21], David W. Sobel [22], Marti, Klaudija Viskovic [24], George Tsoulfas [25], Athanasios D. Protogerou [26], George D. K, Mostafa M. Fouda [29], Seemant Chaturvedi [30], Mannudeep K. Kalra [31] and Jasjit S. Su

Figure 5. Applications of AI in healthcare diagnosis. AI: artificial intelligence, ML: machine learning, DL: deep learning, TL: transfer learning, CVD: cardiovascular diseases.

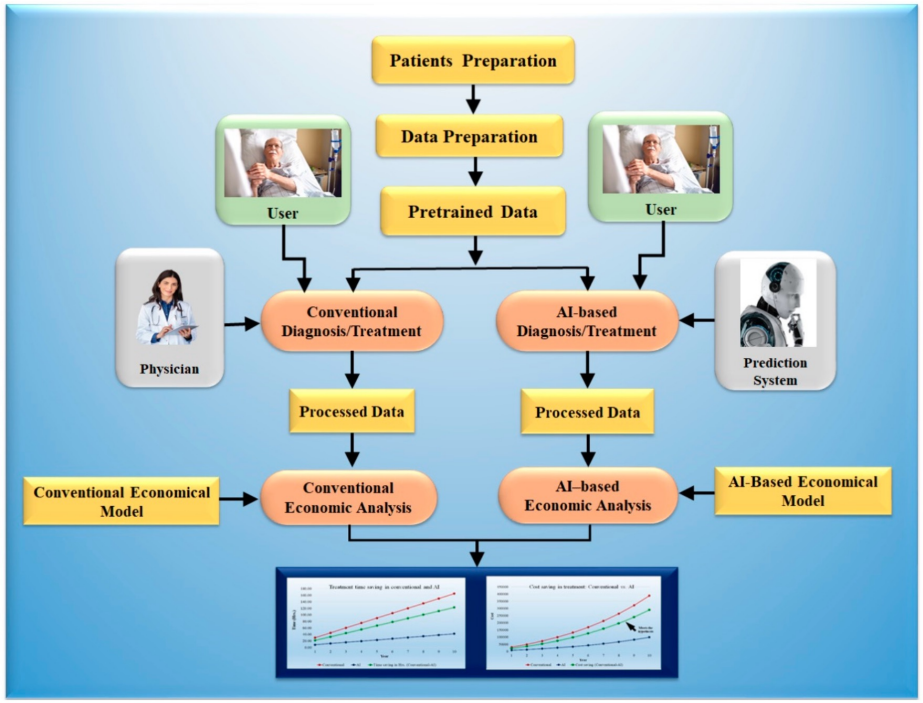

Figure 9. The AI economical model for the diagnosis and treatment against the conventional model.

IEEE Access
Multidisciplinary | Rapid Review | Open Access Journal

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Smart Healthcare in the Age of AI: Recent Advances, Challenges, and Future Prospects

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[2]Mohamed Bin Zayed University of Artificial Intelligence, Abu Dhabi, United Arab Emirates
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Corresponding authors: Mahmoud Nasr (mmmnasrm@uwaterloo.ca) and Md. Milon Islam (milonislam@uwaterloo.ca)

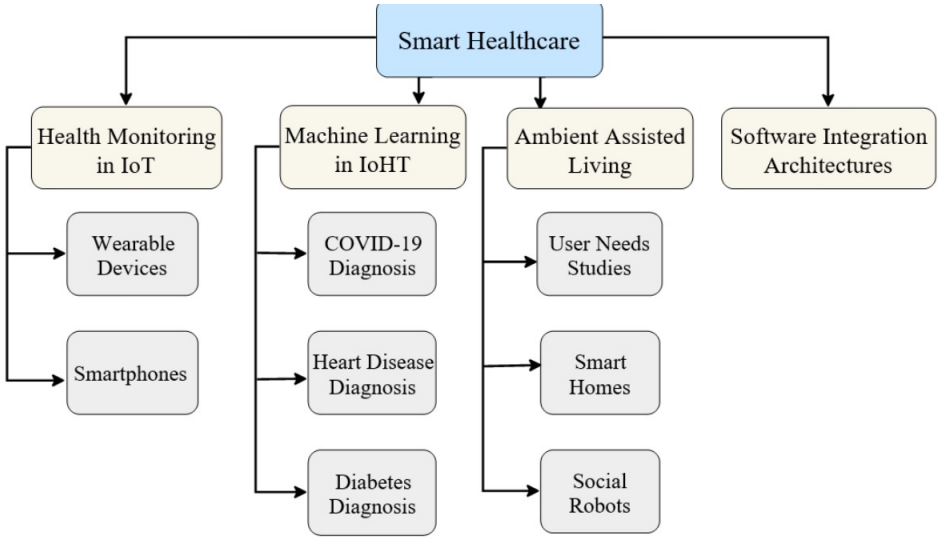

FIGURE 1. The overall workflow of the reviewed systems of smart healthcare.

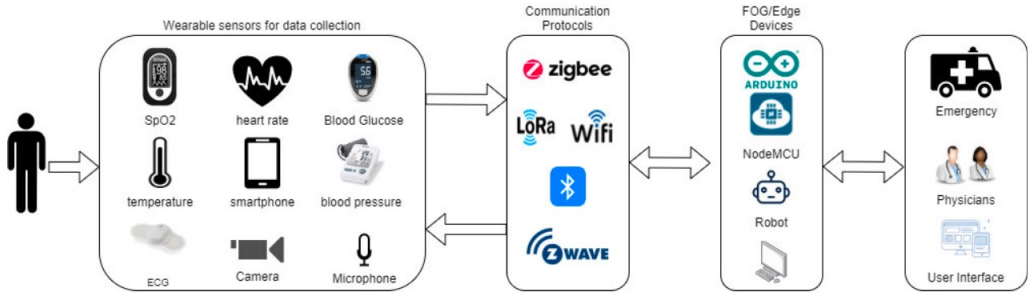

FIGURE 2. A general pipeline of a health monitoring system based on wearable devices.

nature medicine

Article

https://doi.org/10.1038/s41591-024-02850-w

Heterogeneity and predictors of the effects of AI assistance on radiologists

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Accepted: 1 February 2024

Feiyang Yu[1,2,5], Alex Moehring[3,5], Oishi Banerjee[1], Tobias Salz[4,6], Nikhil Agarwal[4,6] & Pranav Rajpurkar[1,6]

experience-based factors, such as years of experience, subspecialty and familiarity with AI tools, fail to reliably predict the impact of AI assistance. Additionally, lower-performing radiologists do not consistently benefit more from AI assistance, challenging prevailing assumptions. Instead, we found that the occurrence of AI errors strongly influences treatment outcomes, with inaccurate AI predictions adversely affecting radiologist performance on the aggregate of all pathologies and on half of the individual pathologies investigated. Our findings highlight the importance of personalized approaches to clinician–AI collaboration and the importance of accurate AI models. By understanding the factors that shape the effectiveness of AI assistance, this study provides valuable insights for targeted implementation of AI, enabling maximum benefits for individual clinicians in clinical practice.

nature immunology

Resource

https://doi.org/10.1038/s41590-024-01782-4

An immunophenotype-coupled transcriptomic atlas of human hematopoietic progenitors

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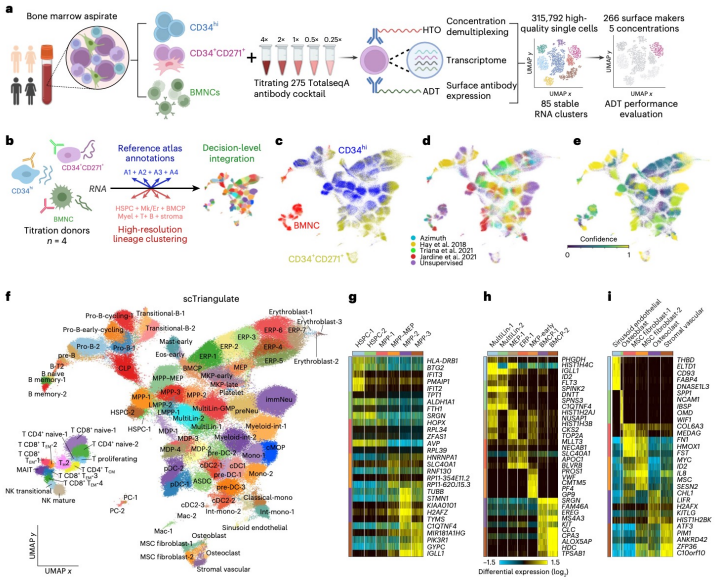
Check for updates

Xuan Zhang[1,14], Baobao Song[1,2,14], Maximillian J. Carlino[3,4], Guangyuan Li[5], Kyle Ferchen[1], Mi Chen[3,4], Evrett N. Thompson[3,4,6], Bailee N. Kain[1], Dan Schnell[5], Kairavee Thakkar[5], Michal Kouril[5], Kang Jin[5], Stuart B. Hay[5], Sidharth Sen[5], David Bernardicius[1], Siyuan Ma[1], Sierra N. Bennett[1], Josh Croteau[7], Ornella Salvatori[7], Melvin H. Lye[8], Austin E. Gillen[9,10], Craig T. Jordan[9], Harinder Singh[11], Diane S. Krause[3,4,6], Nathan Salomonis[5,12] ✉ & H. Leighton Grimes[1,12,13] ✉



Article

Evolutionary trajectories of small cell lung cancer under therapy

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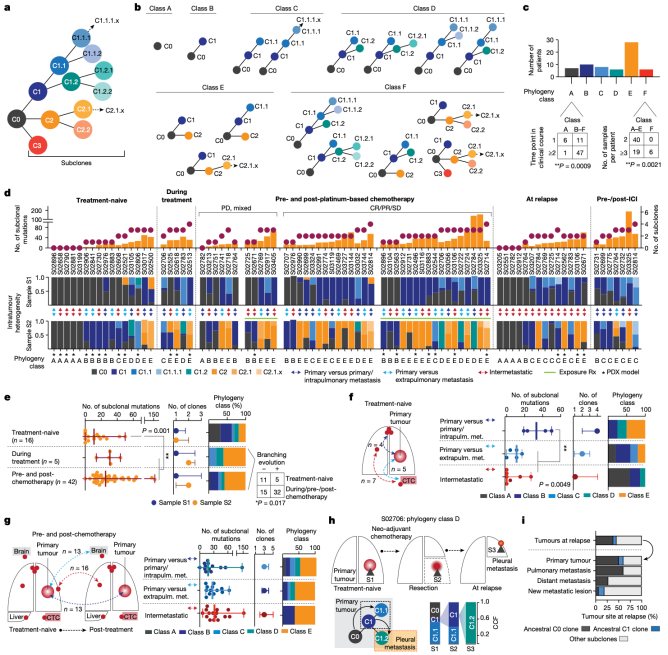
Open access

Check for updates

Julie George[1,2]✉, Lukas Maas[1], Nima Abedpour[1,3,4], Maria Cartolano[1,5], Laura Kaiser[1], Rieke N. Fischer[6], Andreas H. Scheel[7], Jan-Philipp Weber[6], Martin Hellmich[8], Graziella Bosco[1], Caroline Volz[3,5], Christian Mueller[1,2], Ilona Dahmen[1], Felix John[6], Cleidson Padua Alves[1], Lisa Werr[1], Jens Peter Panse[9,10], Martin Kirschner[9,10], Walburga Engel-Riedel[11], Jessica Jürgens[11], Erich Stoelben[12], Michael Brockmann[13], Stefan Grau[14,15], Martin Sebastian[16,17,18], Jan A. Stratmann[16,17], Jens Kern[19], Horst-Dieter Hummel[20], Balazs Hegedüs[21], Martin Schuler[18,22], Till Plönes[22,23], Clemens Aigner[21,24], Thomas Elter[3], Karin Toepelt[3], Yon-Dschun Ko[25], Sylke Kurz[26], Christian Grohé[26], Monika Serke[27], Katja Höpker[28], Lars Hagmeyer[29], Fabian Doerr[21,30], Khosro Hekmath[30], Judith Strapatsas[31], Karl-Otto Kambartel[32], Geothy Chakupurakal[33], Annette Busch[34], Franz-Georg Bauernfeind[34], Frank Griesinger[35], Anne Luers[35], Wiebke Dirks[35], Rainer Wiewrodt[36], Andrea Luecke[36], Ernst Rodermann[37], Andreas Diel[37], Volker Hagen[38], Kai Severin[39], Roland T. Ullrich[3,5], Hans Christian Reinhardt[40,41], Alexander Quaas[7], Magdalena Bogus[42], Cornelius Courts[42], Peter Nürnberg[43], Kerstin Becker[43], Viktor Achter[44], Reinhard Büttner[7], Jürgen Wolf[6], Martin Peifer[1,5]✉ & Roman K. Thomas[1,7,18]✉



genome duplications. Gene-damaging *TP53* alterations and co-alterations of *TP53* missense mutations with *TP73*, *CREBBP*/*EP300* or *FMN2* were significantly associated with shorter disease relapse following chemotherapy. In summary, we uncover key processes of the genomic evolution of SCLC under therapy, identify the common ancestor as the source of clonal diversity at relapse and show central genomic patterns associated with sensitivity and resistance to chemotherapy.

nature communications

Article

https://doi.org/10.1038/s41467-024-46873-w

Tertiary lymphoid structures and B cells determine clinically relevant T cell phenotypes in ovarian cancer

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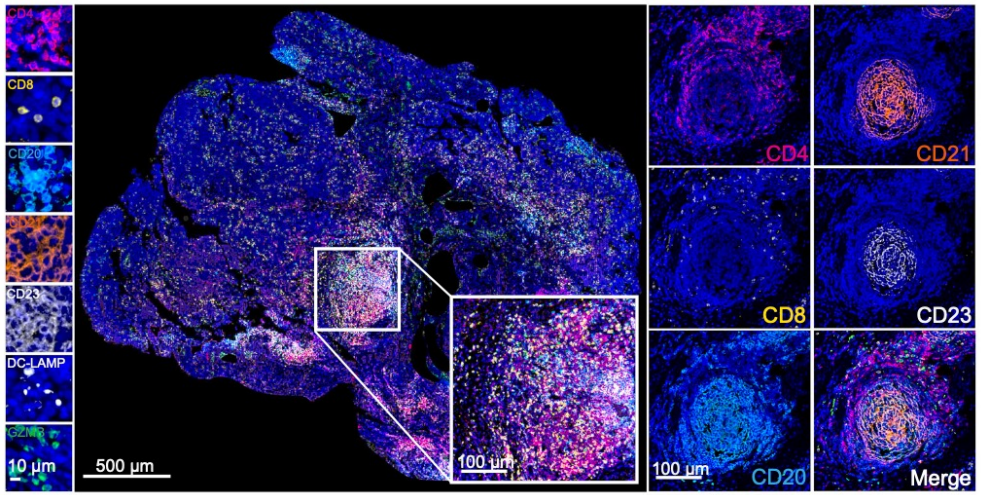
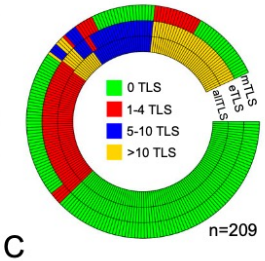
A list of authors and their affiliations appears at the end of the paper

Intratumoral tertiary lymphoid structures (TLSs) have been associated

PD1$^+$ T cells. Spatial B-cell profiling identifies patterns of in situ maturation and differentiation associated with mTLSs. Moreover, B-cell depletion promotes signs of a dysfunctional CD8$^+$ T cell compartment among tumor-infiltrating lymphocytes from freshly isolated HGSOC and NSCLC biopsies. Taken together, our data demonstrate that – at odds with NSCLC – HGSOC is associated with a low density of follicular helper T cells and thus develops a limited number of mTLS that might be insufficient to preserve a ICI-sensitive TCF1$^+$PD1$^+$ CD8$^+$ T cell phenotype. These findings point to key quantitative and qualitative differences between mTLSs in ICI-responsive vs ICI-irresponsive neoplasms that may guide the development of alternative immunotherapies for patients with HGSOC.





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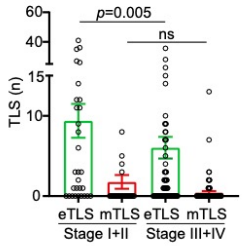

nature communications

Article

https://doi.org/10.1038/s41467-024-46710-0

Allele-specific transcriptional effects of subclonal copy number alterations enable genotype-phenotype mapping in cancer cells

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Accepted: 1 March 2024

Hongyu Shi[1,2], Marc J. Williams[1], Gryte Satas[1], Adam C. Weiner[1,3], Andrew McPherson[1] & Sohrab P. Shah[1]

transcription, and obviates the need to define genotypic clones from a phylogeny a priori, leading to highly granular definitions of clones with distinct expression programs. These improvements enable clone-clone gene expression comparisons with higher resolution and identification of expression programs that are genomically independent. Our approach sets the stage for dissecting the relative contribution of fixed genomic alterations and dynamic epigenetic processes on gene expression programs in cancer.

Oncol Ther
https://doi.org/10.1007/s40487-024-00270-x

ORIGINAL RESEARCH

The Impact of Prior Single-Gene Testing on Comprehensive Genomic Profiling Results for Patients with Non-Small Cell Lung Cancer

Mary K. Nesline · Vivek Subbiah · Rebecca A. Previs · Kyle C. Strickland · Heidi Ko · Paul DePietro · Michael D. Bi Maureen Cooper · Nini Wu · Jeffrey Conroy · Sarabjot Pabla Shengle Zhang · Zachary D. Wallen · Pratheesh Sathyan · Kamal Saini · Marcia Eisenberg · Brian Caveney · Eric A. Sev Shakti Ramkissoon

Received: December 29, 2023 / Accepted: February 29, 2024

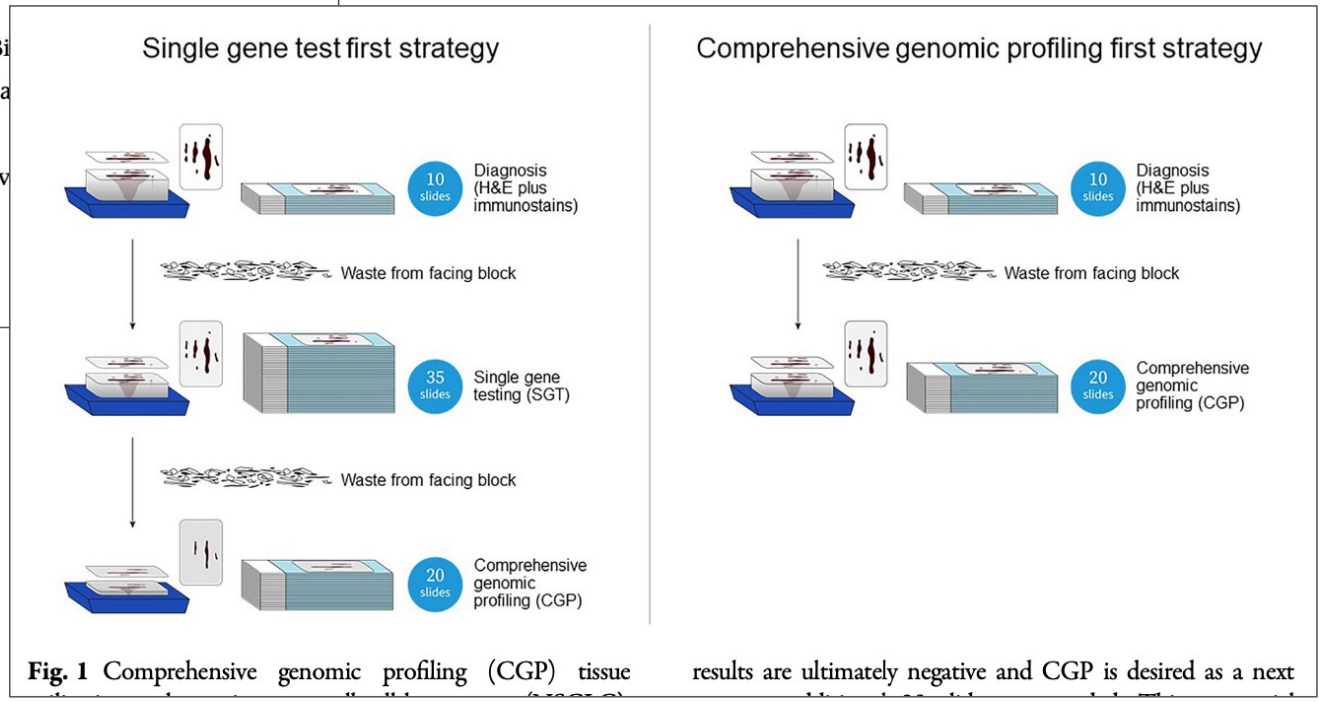

Fig. 1 Comprehensive genomic profiling (CGP) tissue

results are ultimately negative and CGP is desired as a next

nature medicine

NEWS | 12 March 2024

How AI-powered handheld devices are boosting disease diagnostics - from cancer to dermatology

Nature Medicine explores the latest translational and clinical research news, with FDA approval of an AI-assisted optical reader to help in the diagnosis of skin cancer.

Digital and Computational Pathology Are Pathologists' Physician Extenders

Casey P. Schukow, DO; Timothy Craig Allen, MD, JD

"Physician extender" is a long-used term in medicine[1] that denotes a "non-medical healthcare provider who sees patients on behalf of or in conjunction with a lead physician or physician(s)."[2] Increasing physician demand requires continuing assessment of the value of physician extenders, including within pathology.[3,4] During the COVID-19 pandemic, health care institutions and private practice groups across all medical fields felt the unprecedented demand for fast and accurate medical laboratory testing and diagnostics.[5–7] Beyond the COVID-19 pandemic, the urgency for pathologists and medical laboratories across the world to continue to deliver

(often 4–6 years depending on location), and following medical school they complete residency training and fellowship (an additional 4–6 years). Many pathologists who practice in the United States have practiced previously in other countries and go through rigorous financial lengths to obtain US medical licensure, residency training, and legal citizenship to practice in the United States. Although recent pipeline efforts have focused on increasing US medical student and international medical graduate exposure to pathology (because many medical schools lack adequate exposure within their curricula),[19–22] it will be many years

Events

Next steering committee meeting

April 24th 2024

at

3:00PM

(EST)