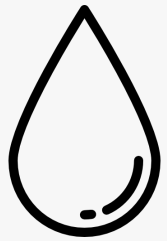
Monthly Steering Committee Meetings

June 29 2022 3-4PM ET

Pathology Innovation Collaborative Community

FDA Guidance



Circulating tumor DNA (ctDNA)

Cybersecurity in medical devices

Quantitative imaging in radiological devices

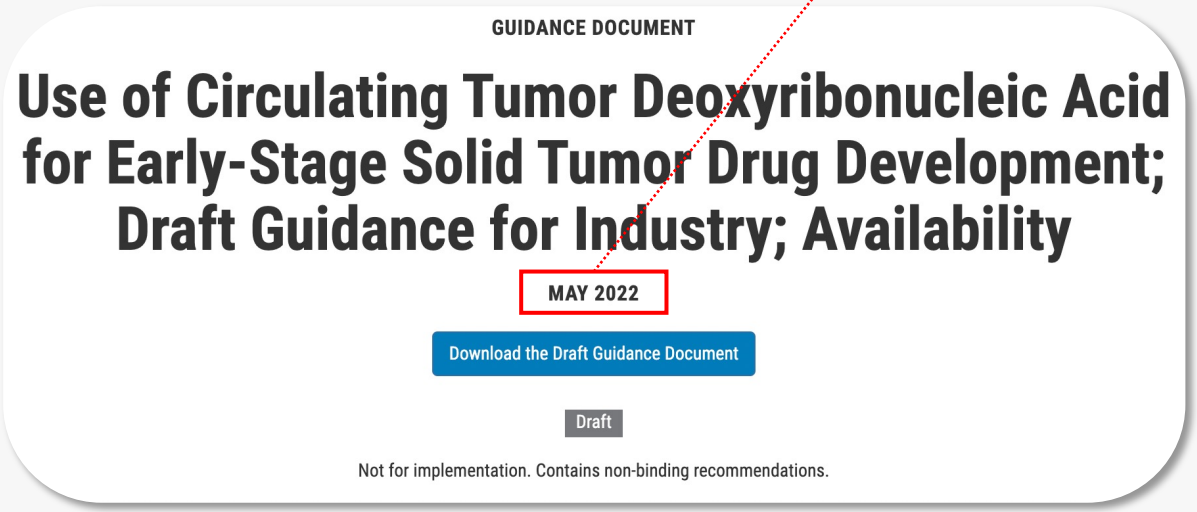
ctDNA – Out of the Dark
Guidance Review Session

PIcc project aims to provide:

- A brief summary of the document
- relevant references
- And consider providing comment on the draft guidance

Join on Thursday, July 21 at 11AM ET

Comments due July 2


GUIDANCE DOCUMENT

Use of Circulating Tumor Deoxyribonucleic Acid for Early-Stage Solid Tumor Drug Development; Draft Guidance for Industry; Availability

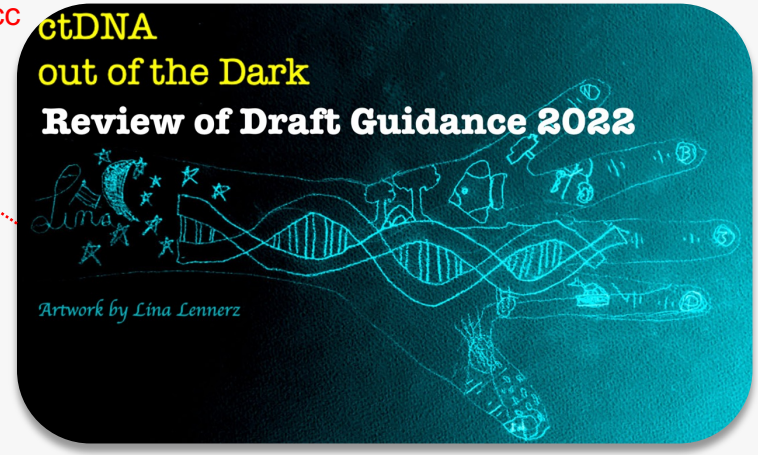
MAY 2022

Download the Draft Guidance Document

Draft

Not for implementation. Contains non-binding recommendations.

More info on PIcc project page



FRIENDS of CANCER RESEARCH

ctMoniTR Project

- FOCR Virtual Meeting - Expediting Drug Development: Use of ctDNA as an Early Endpoint

  Wednesday, July 20 at 11:30AM ET

Cybersecurity in medical devices

March 23, 2022

Bill: Healthcare Cybersecurity Act of 2022

April 7, 2022

FDA Document Details Cyber Expectations for Device Makers

May 26, 2022

Bill: Strengthening Cybersecurity for Medical Devices Act

Comment period open through July 7, 2022

Cybersecurity Guidance Details

- The FDA's 49-page draft guidance covers a wide range of cybersecurity considerations and actions that medical device makers are recommended to address and document for premarket submissions, including:
- **Threat modeling:** This means identifying the security objectives, risks and vulnerabilities of a device system and then defining countermeasures to prevent, or mitigate the effects of, threats to the system throughout its life cycle.
- **Third-party software components:** This includes providing to the FDA - and to customers as part of product "labeling" - a software bill of materials, or SBOMs, containing information about device maker-developed components, as well as third-party purchased, licensed and open-source software.
- **Security risk management:** This includes providing a report summarizing the manufacturer's risk evaluation methods and processes and including details of the security risk assessment and risk mitigation activities undertaken, controls and the testing to ensure a device is reasonably secure.
- **Implementation of security controls:** This includes authentication; authorization; cryptography; code, data and execution integrity; confidentiality; event detection and logging; resiliency and recovery; updatability and patching.
- **Cybersecurity testing:** This includes security requirements, threat mitigation, vulnerability testing and penetration testing.
- **Cybersecurity transparency:** This includes transparency in labeling relevant security information for users, such as device instructions and product specifications related to cybersecurity controls, a list of network ports and other interfaces that are expected to receive and/or send data, and SBOMs that are available on a continuous basis and are machine-format readable.
- **Vulnerability management plans:** This means submitting plans for vulnerability communication so that the FDA can assess whether the manufacturer has sufficiently addressed how to maintain the safety and effectiveness of the device after marketing authorization is achieved.

Quantitative imaging in radiological devices

- FDA Issues Final Guidance For Radiological Devices Using Quantitative Imaging
- This document is an update to FDA 2019 guidance

European Artificial Intelligence Act (AIA)

EUROPEAN COMMISSION

Brussels, 21.4.2021

COM(2021) 206 final

2021/0106(COD)

Proposal for a

REGULATION OF THE EUROPEAN PARLIAMENT AND OF THE COUNCIL

LAYING DOWN HARMONISED RULES ON ARTIFICIAL INTELLIGENCE (ARTIFICIAL INTELLIGENCE ACT) AND AMENDING CERTAIN UNION LEGISLATIVE ACTS

{SEC(2021) 167 final} - {SWD(2021) 84 final} - {SWD(2021) 85 final}

- April 2021
- First law on AI by major regulator

HHS withdrawing the SUNSET final rule

Withdrawing Rule on Securing Updated and Necessary Statutory Evaluations Timely

AGENCY: Department of Health and Human Services.

ACTION: Final rule; withdrawal.

SUMMARY: The Department of Health and Human Services (HHS or Department) is issuing a final rule withdrawing a rule entitled "Securing Updated and Necessary Statutory Evaluations Timely" (SUNSET final rule), which published in the Federal Register of January 19, 2021. The SUNSET final rule was originally scheduled to take effect on March 22, 2021. However, after a lawsuit was filed on March 9, 2021, seeking to overturn the SUNSET final rule, HHS extended

"Had this withdrawal of the SUNSET rule not gone through, the FDA, according to HHS, would have faced the massive task of reviewing over 7,000 sections of the CFR that were promulgated by the agency and which are more than 10 years old or would become more than 10 years old during the first five years the rule would be in effect, representing over 95% of the FDA's current regulations." –*Endpoints News*

Economic Impact Analyses of FDA Regulations

Share | Tweet | Linkedin | Email | Print

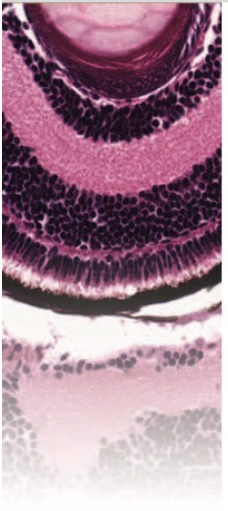
The Food and Drug Administration conducts economic analyses of all important proposed and final regulations. Each economic analysis includes an assessment of the costs, benefits, and cost-effectiveness of the action, as well as assessments of the costs, benefits and cost-effectiveness of the most promising alternative actions. The full economic impact analyses of significant FDA regulations are no longer (as of April 2012) published in the Federal Register but are available on this site.

AMA CPT Announces New Digital Pathology Codes

AMA AMERICAN MEDICAL ASSOCIATION

CPT® Editorial Summary of Panel Actions
May 2022

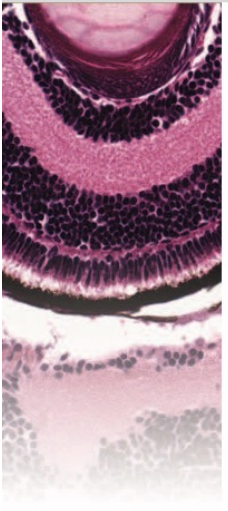
Tab #	Name	Codes	Request-Description	Effective Date
37	Post Operative Low Level Laser Therapy	●9X022	**Accepted addition** of code 9X022 code to report low-level laser therapy for post operative pain reduction	January 2024
38	Electroencephalogram Monitoring	---------- ----------	**WITHDRAWN**	
39	Human Milk Donation Services	---------- ----------	**REJECTED**	
40	Therapeutic Monitoring Services	---------- ----------	**WITHDRAWN**	
41	Vaccine Counseling	---------- ----------	**WITHDRAWN**	
42	Respiratory Syncytial Virus (RSV) Vaccine	●9X018	**Accepted addition** of code 9X018 to report RSV vaccine product and administration	January 2023
43	Cat II - Medication Adherence for Opioid Use Disorder	---------- ----------	**WITHDRAWN**	
44	Cat III - Digital Pathology	✚●X018T ✚●X025T ✚●X019T ✚●X026T ✚●X020T ✚●X027T ✚●X021T ✚●X028T ✚●X022T ✚●X029T ✚●X023T ✚●X030T ✚●X024T	**Accepted addition** of add-on codes X018T-X030T to report additional clinical staff work and service requirements associated with digitizing glass microscope slides for primary diagnosis; and **addition** of a new heading in the Category III section and guidelines to define digital pathology digitization procedures	January 2023
45	Cat III - AI Analysis for Cardiac Function Services	✚●X044T ●X045T	**Accepted addition** of add-on codes X044T and child code X045T to report assistive algorithmic electrocardiogram risk assessment for cardiac dysfunction	January 2023



CPT codes per January 2022

- Accepted addition of add-on codes X018T X030T to report additional **clinical staff** work and **service requirements** associated with **digitizing glass** microscope slides for primary diagnosis; and addition of a new heading in the **Category III** section and guidelines to define digital pathology digitization procedures

DIGITAL PATHOLOGY DPA ASSOCIATION



What is DPA working on

- Allow labs to record activity and **begin tracking the value** of DP
- Categorization, cross walk, PC and/or TC
- Work with organizations like the **AMA and CAP** to determine the best approach to value DP solutions (including AI) and more
- DPA-F is seeking funding to focus on **outcome studies**

DIGITAL PATHOLOGY DPA ASSOCIATION

CURE ID

- collaboration between FDA and the National Center for Advancing Translational Sciences (NCATS), part of the National Institutes of Health (NIH)

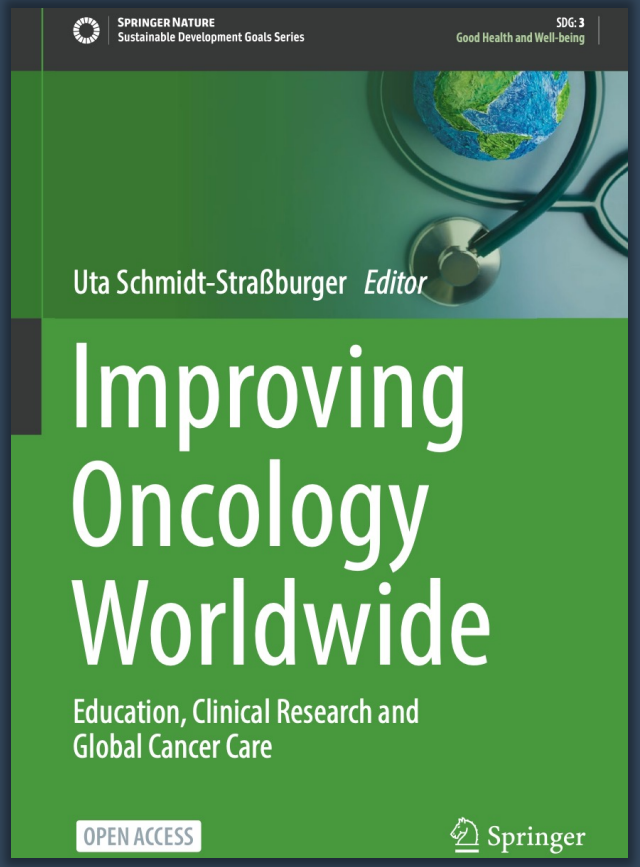
What is the value of CURE ID?

The CURE ID platform will enable collection of real-world treatment experience directly from healthcare providers in a systematic, accurate, and detailed manner. Information from CURE ID can be used to inform ongoing and future clinical trials and potentially drug labeling.

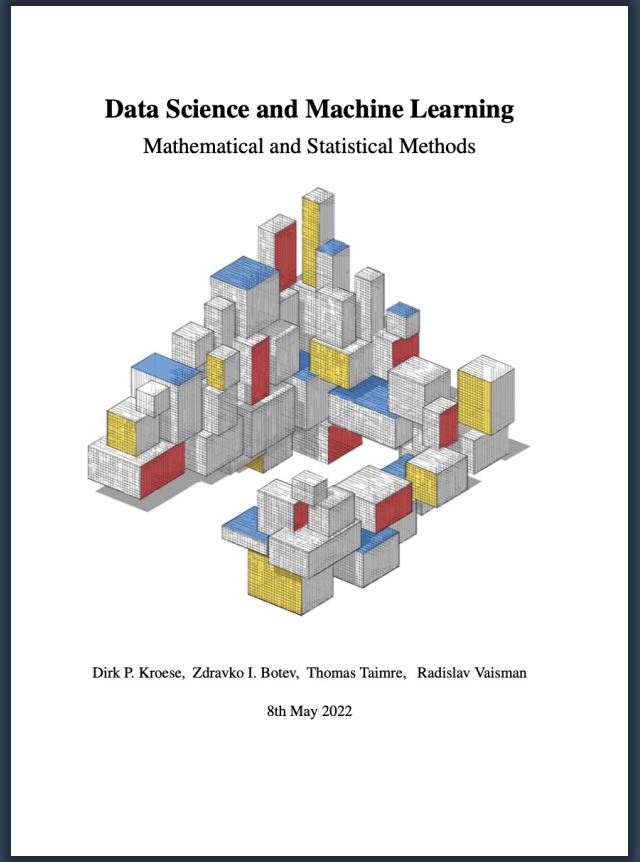
For example, it could:

- Serve as a platform for healthcare providers to exchange their treatment experiences about challenging diseases.
- Spur clinical trial development by collecting better information regarding positive and negative health outcomes about existing products, which may help drug developers narrow potential drug candidates for study. Ultimately, this program could help enrich the armamentarium of drugs available for diseases that are difficult to treat.
- Serve as a resource for healthcare providers to share information where a disease lacks adequate approved treatment options.
- Allow for the rapid identification of promising treatment approaches in urgent situations, such as during outbreaks of emerging infectious threats and use this information to inform clinical trials.
- Enable collection of real-world treatment experience directly from healthcare providers in a systematic, accurate, and detailed manner. Information from CURE ID can be used to inform ongoing and future clinical trials and potentially drug labeling.

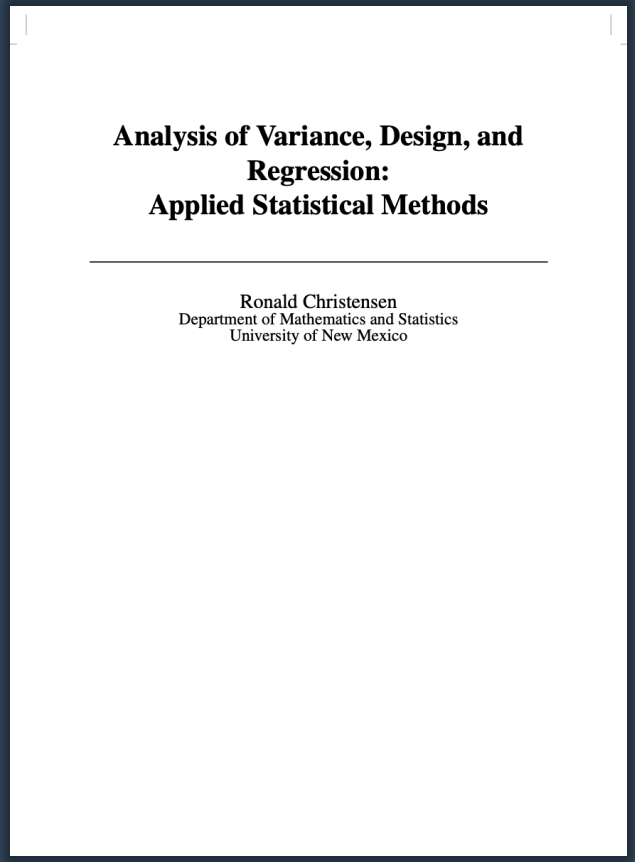
Books of interest



Uta Schmidt-Strasßburger
Improving Oncology Worldwide



Kroese et al.
Data Science and Machine Learning Mathematical and Statistical Methods



Ronald Christensen
Analysis of Variance, Design, and Regression: Applied Statistical Methods

Continuing Medical Education Program
"Master Online Advanced Oncology" (part-time)

Type of study
Continuing medical education programme/part-time (M.Sc.)

Language
english

Credit Points
363 CME points
60 ETCS points

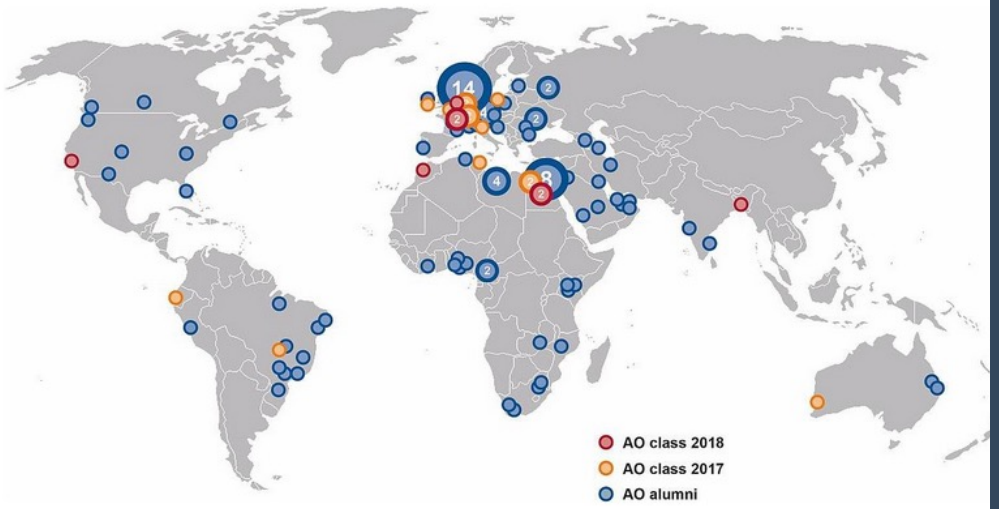
Number of students/year
20

Start of the study programme
Winter semester (1 October)
application deadline 15 May

Regular duration of the study
4 semesters

Internationality

Our students and lecturers are from all over the world. Join the Advanced Oncology Network today and meet at high-ranking international meetings!



History of AI

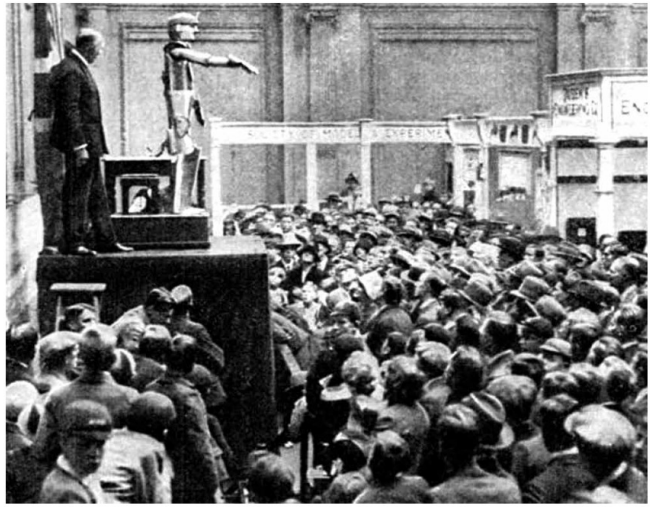
CRITICAL FOCUS

Brian J. Ford

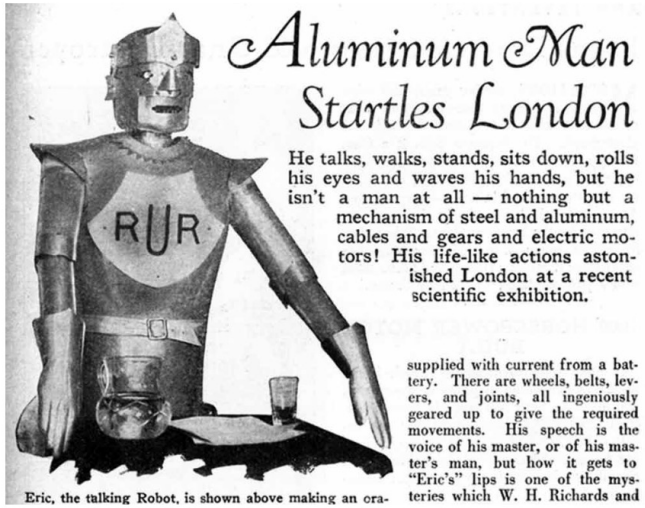
featured work

AI: Artificial, Yes. Intelligent, Not.

n and machine learning are wonderfully efficient, but they pale
ine intelligence and complicated mechanisms of the living cell.



Eric was one of the first autonomous robots and rose to give the opening speech at a major engineering exhibition in London in 1928. American newspapers described this robot as “an almost perfect man.” A working replica was reconstructed by the Science Museum in London in 2017.



Aluminum Man Startles London

He talks, walks, stands, sits down, rolls his eyes and waves his hands, but he isn't a man at all — nothing but a mechanism of steel and aluminum, cables and gears and electric motors! His life-like actions astonished London at a recent scientific exhibition.

RUR

supplied with current from a battery. There are wheels, belts, levers, and joints, all ingeniously geared up to give the required movements. His speech is the voice of his master, or of his master's man, but how it gets to "Eric's" lips is one of the mysteries which W. H. Richards and

Eric, the talking Robot, is shown above making an ora-

Press reports aroused international interest in Eric, who was designed to respond to verbal commands and could move his limbs and eyes. After being exhibited in London in 1928, the original Eric toured the world, but within a decade, he disappeared and was never seen again.

QUAREP-LiMi

featured work

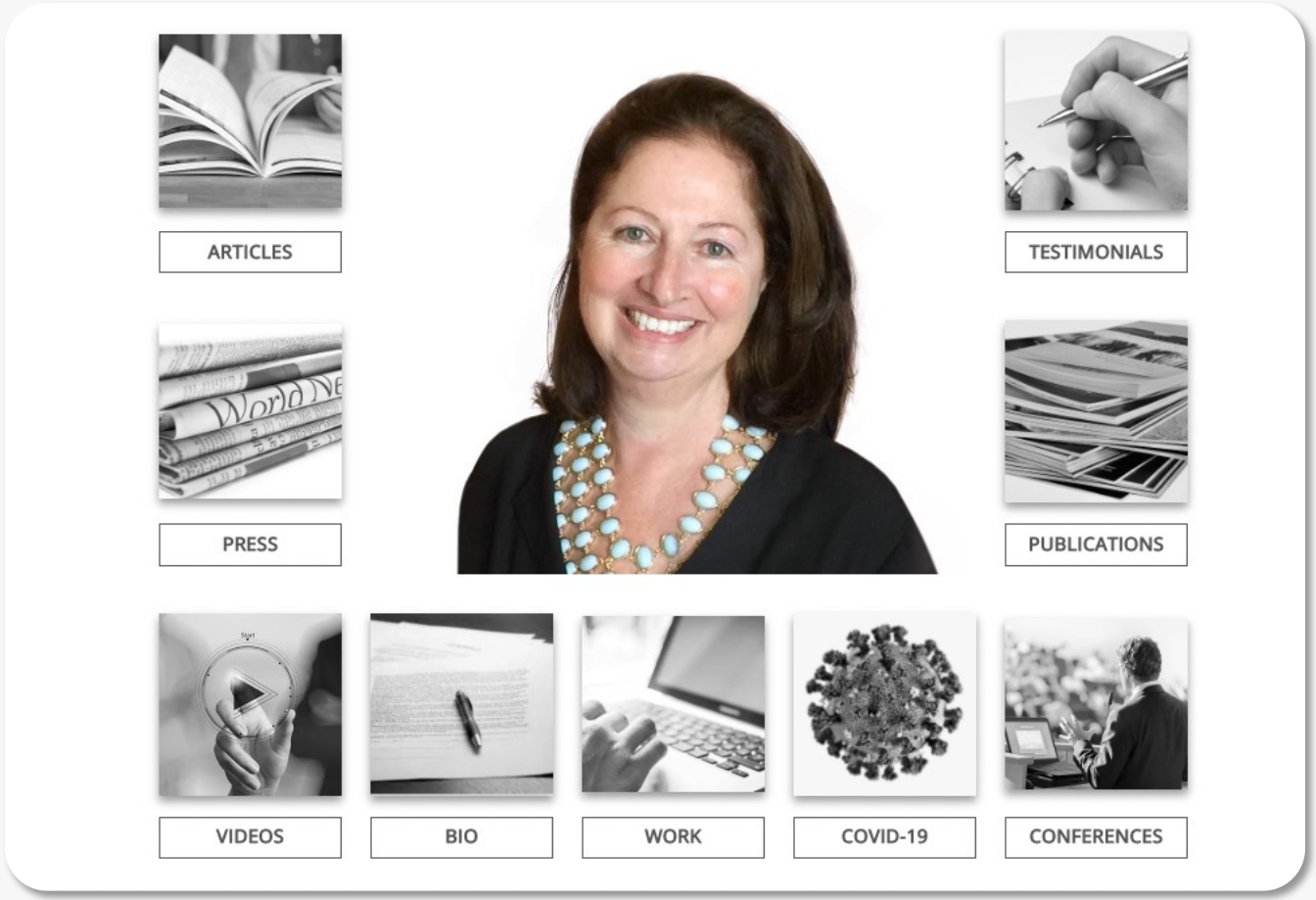
Quality Assessment and Reproducibility for Instruments & Images in Light Microscopy

The QUAREP-LiMi is a group of enthusiastic light microscopists from Academia and Industry all interested in improving qu
on-line Webi
has grown t
communities
standardizat
agencies (se

Please select the Working Group(s) you would like to join *

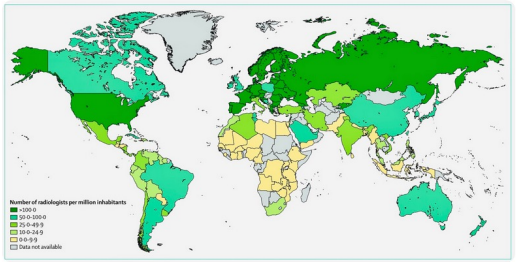
- [ ] WG 1 - Ilumination power
- [ ] WG 2 - Detection system performance
- [ ] WG 3 - Uniformity of field - flatness
- [ ] WG 4 - System chromatic aberration and co-registration
- [ ] WG 5 - Lateral and axial resolution
- [ ] WG 6 - Stage and focus
- [ ] WG 7 - Metadata
- [ ] WG 8 - White paper
- [ ] WG 9 - Over all planning + funding
- [ ] WG 10 - Image Quality
- [ ] WG 11 - Microscopy publication standards
- [ ] WG 12 - Image Visualization and Analysis
- [ ] WG 13 - Phototoxicity
- [ ] Currently not actively want to join a WG

Margaretta Colangelo



feature

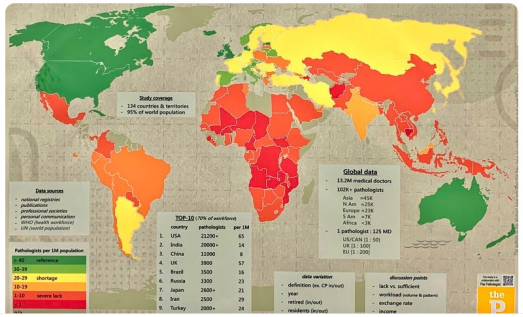
How AI Can Help Address The Global Shortage of Radiologists



There's a global shortage of radiologists. Today, over 2/3 of the people on earth do not have access to radiologists. The are big disparities between counties and within countries. AI can help radiologists triage patients and reduce delays by identifying and flagging abnormal medical images. AI can also help doctors assess which patients are are higher risk for some diseases. This article includes examples of AI /DL applications that are helping to address the radiologist shortage.

Read More

How AI Can Help Address The Global Shortage of Pathologists



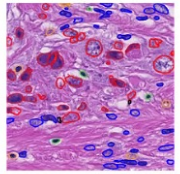
There's a global shortage of pathologists. Today there are slightly more than 102,000 pathologists spread over 130+ countries worldwide. There are big disparities between regions with 2/3 of the pathologist workforce located in just 10 countries. This year, Andrey

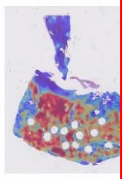
PathML

featured work

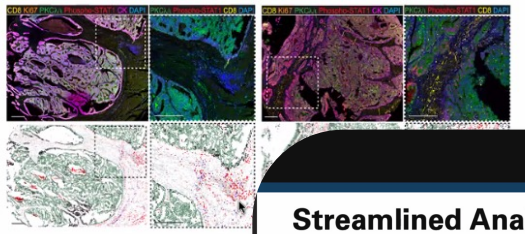
How PathML is Being Used Today

- Prostate cancer research, H&E images
  - Multiple instance learning
  - Cell segmentation and classification

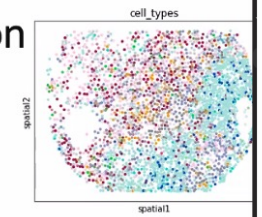




- Colorectal cancer research, 7-channel IF images
  - Cell segmentation and rules-based phenotyping
  - Spatial biology



- Image quantification pipelines used in production at DFCI core facility, CODEX spatial proteomics
  - Improving operational efficiency of key institutional resource



Dana-Farb
Cancer Institu

PathML: An open-source software toolkit for computational pathology research

Summary:

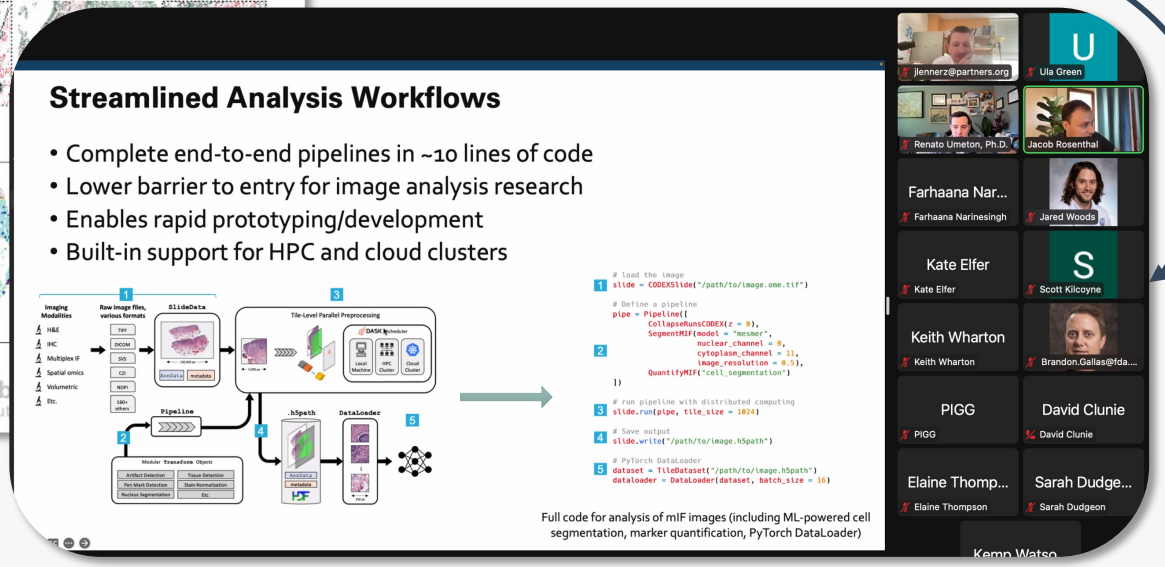
Imaging datasets in cancer research have grown exponentially in size and information density in recent years, driven chiefly by two trends:

- Increasing adoption of digital pathology workflows at departmental and institutional scale (large *n* datasets)
- Emerging technologies in highly multiplexed imaging and spatial omics (high *dimensional* datasets)

The unprecedented scale of today's datasets may enable derivation of insights for cancer research and clinical care, but only if researchers are equipped with the tools to leverage advanced computational approaches from machine learning and computer vision. PathML is a software toolkit designed to lower the barrier to entry for computational pathology, enabling researchers to develop streamlined, scalable, fully customized end-to-end image analysis pipelines, with a unified framework for brightfield, multiplexed immunofluorescence, and spatial omics images and support for 160+ file formats. Developed at Dana-Farber Cancer Institute and Weill Cornell Medicine, PathML is currently being used by 7+ research groups and 2 imaging core facilities across the two institutions. PathML is an open-source project freely available on GitHub, with complete documentation, tutorials, and example vignettes and more than 15,000 downloads worldwide. We welcome anyone interested in collaborating or learning more to contact us at PathML@dfci.harvard.edu or visit www.pathml.org for more information.

Presentation recording:

June 6th presentation
Available on website



MedTech Color Collaborative Community Annual Report

featured work

1

MedTech Color Collaborative Community Annual Report

MedTech Color Collaborative Community Annual Report

Collaborative Community Overview

MedTech Color has convened this Collaborative Community to create a forum in which a diverse cross-section of MedTech industry stakeholders can work together to identify issues and opportunities for improvement of current practices, share and curate existing knowledge, and develop evidence-based solutions to address racial and ethnic minority health issues in medical device product development and clinical research. The Collaborative Community will work to develop targeted strategies, including education and awareness activities, guidelines, best practices, and thought leadership to increase the awareness, understanding, access, engagement, and participation of racial and ethnic minorities.

Our community is comprised of volunteers united by our common drive, passion, and dedication for creating more diverse and representative populations in clinical research. The potential to support better patient outcomes by promoting greater diversity in medical device development fuels our mission.

Thank you to the MedTech Color Collaborative Community Sponsors

AMA AMERICAN MEDICAL ASSOCIATION

Medtronic

Edwards

DEERFIELD Advancing Healthcare®

Veranex Transforming Your MedTech Innovation

mdgroup

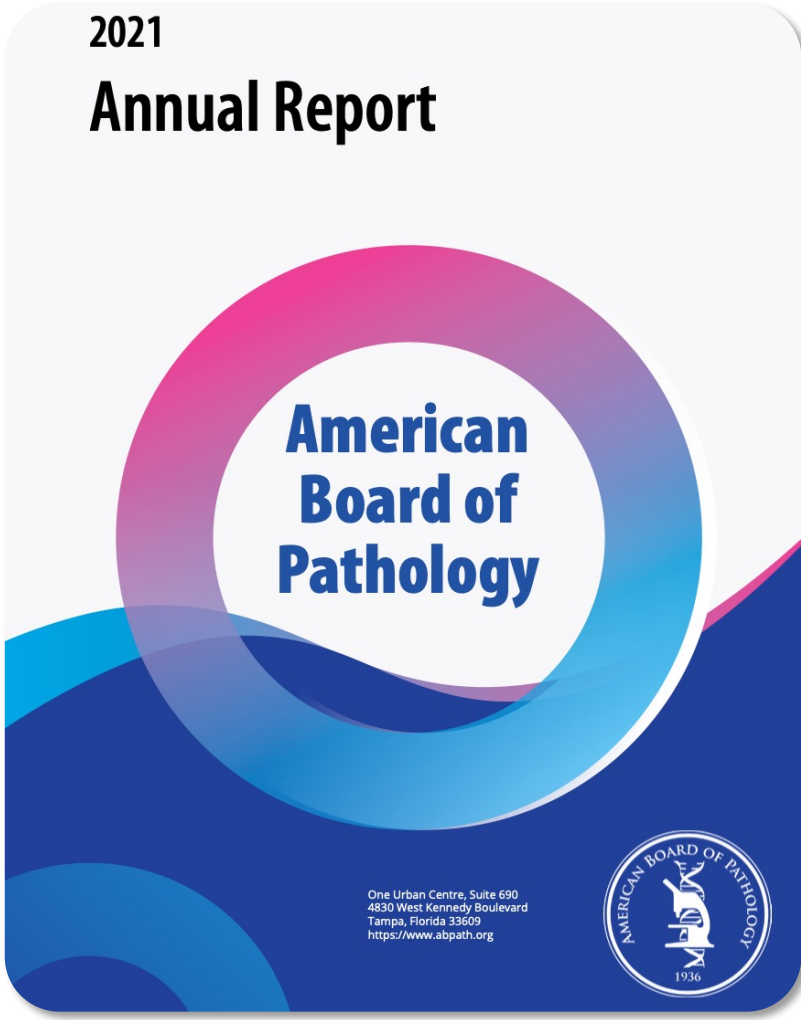
MDMA MEDICAL DEVICE MANUFACTURERS ASSOCIATION

Otsuka

Johnson & Johnson

ResMed

American Board of Pathology
Annual Report



2021 Subspecialty Examinations

	Total Candidates		First-Time Takers			Repeaters		
	#	% Pass	#	# Pass	% Pass	#	# Pass	% Pass
BB/TM	48	81	45	38	84	3	1	33
CH	-	-	-	-	-	-	-	-
CI	35	77	30	25	83	5	2	40
CYP	124	86	117	103	88	7	4	57
DP	45	87	43	38	88	2	1	50
FP	38	95	33	31	94	5	5	100
HEM	112	94	108	103	95	4	2	50
MMB	18	100	17	17	100	1	1	100
MGP	52	94	52	49	94	-	-	-
NP	31	90	31	28	90	-	-	-
PP	22	91	21	20	95	1	0	0
FPClinMB*	-	-	-	-	-	-	-	-

**FPClinMB = Focus Practice Designation-Clinical Microbiology*

The Commonwealth Fund
Meeting America's Public Health Challenge

featured work

Congress should:

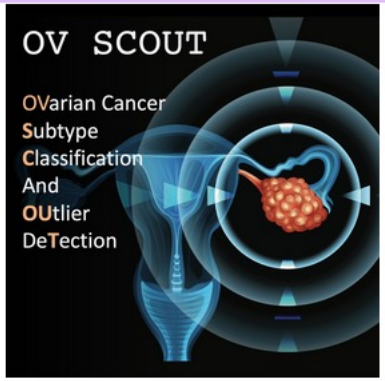
- Establish a position, such as an undersecretary for public health at the U.S. Department of Health and Human Services (HHS), to oversee and coordinate the development of the national public health system.
- Provide adequate and reliable public health infrastructure funding, paired with expectations that states, localities, tribes, and territories meet standards for protecting their communities.
- Fund a modern public health information technology system and provide HHS with the authority to make it work.

The Administration should:

- Set parameters for use of available funds to systematically build public health infrastructure, with an initial focus on workforce and data systems.
- Support revision of accreditation standards for state, local, tribal, and territorial health departments to focus on basic capabilities for public health protection.
- Establish a council to coordinate federal public health action with states, localities, tribes, and territories.
- Reconvene the National Prevention and Public Health Council to guide an all-of-government approach to the drivers of health.
- Embrace ethics, integrity, and transparency in decision-making in public health.

States, localities, tribes, and territories should:

Other project updates pushed to July



5/25/22

OV SCOUT

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5/24/22

Advancing Cancer Research Through Collaboration

Read More

5/24/22

CPIM: WSI for nonclinical development

Read More

5/19/22

SEER 2.0

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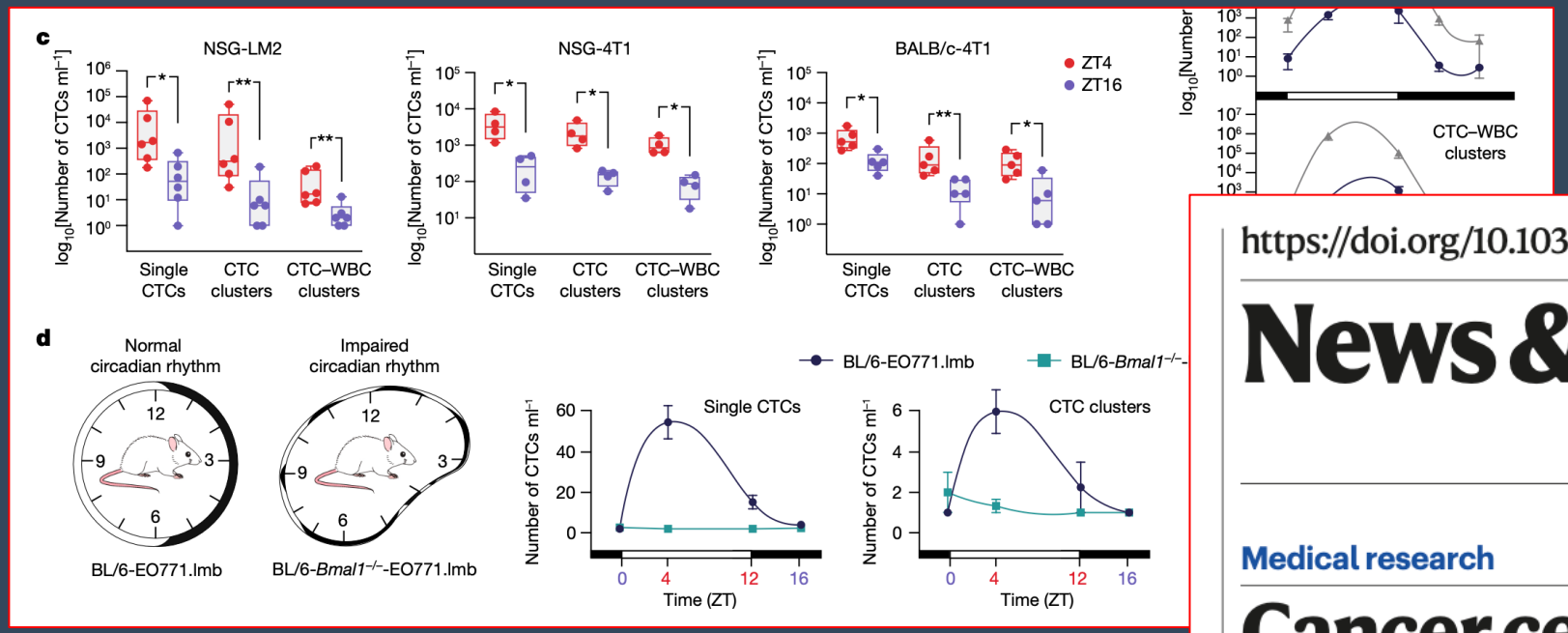
Pre-Analytics • 3/9/22

Yin and Yang Study

Diamantopoulou et al. ETH Zurich

The metastatic spread of breast cancer accelerates during sleep



https://doi.org/10.1038/d41586-022-01639-6

News & views

Medical research

Cancer cells spread aggressively during sleep

Harrison Ball & Sunitha Nagrath

The deadly spread of cancer occurs predominantly during

featured papers

Drews et al. (UK, Spain, Berlin, …)

A pan-cancer compendium of chromosomal instability

Article

A pan-cancer compendium of chromosomal instability

https://doi.org/10.1038/s41586-022-04789-9

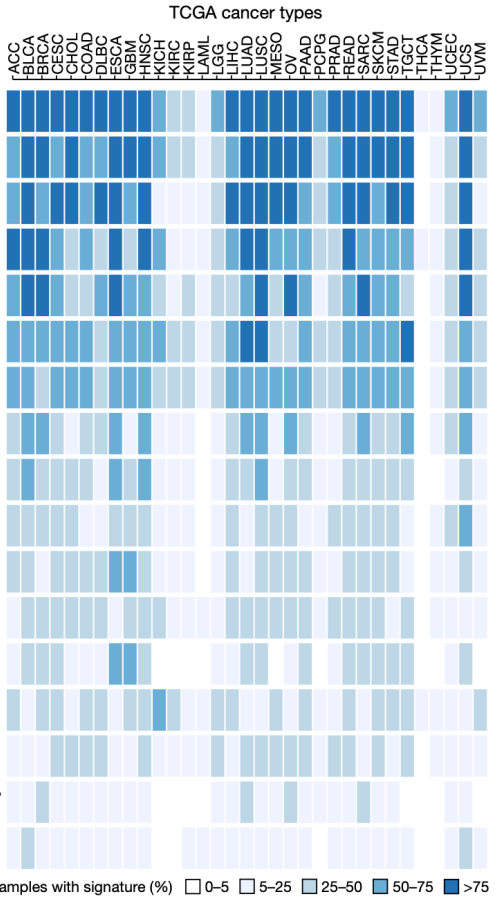
Received: 31 July 2020

Accepted: 21 April 2022

Published online: 15 June 2022

Ruben M. Drews[1], Barbara Hernando[2], Maxime Tarabichi[3,4], Kerstin Haase[3,5], Tom Lesluyes[3], Philip S. Smith[1], Lena Morrill Gavarró[1], Dominique-Laurent Couturier[1,6], Lydia Liu[3,7], Michael Schneider[1], James D. Brenton[1,8,9], Peter Van Loo[3], Geoff Macintyre[1,2,10]✉ & Florian Markowetz[1,10]✉

Signature	Pan-cancer prevalence (%)	Putative cause	Confidence	Pattern of change
CX1	80	Chromosome missegregation via defective mitosis and/or telomere dysfunction	★★★	Whole-arm/chromosome changes
CX2	69	IHR	★★★	Short-to-medium-sized, oscillating, single-copy changes
CX3	63	IHR with replication stress and impaired damage sensing	★★★	Long-sized, single-copy changes
CX4	58	PI3K–AKT-mediated toleration of whole-genome duplication	★★★	Medium-sized, clustered and oscillating, two-copy changes
CX5	56	IHR with replication stress	★★★	Medium-sized, two-to-three-copy changes
CX6	51	Chromosome missegregation via defective mitosis	★★★	Whole-arm/chromosome changes
CX7	50	Unknown	☆☆☆	Long-sized, less than one-copy change
CX8	38	Replication stress	★★★	Short-to-medium-sized, oscillating, low-level amplifications
CX9	32	Replication stress	★☆☆	Short-to-medium-sized, clustered, mid-level amplifications
CX10	29	Impaired NHEJ with replication stress	★★☆	Short-to-medium-sized, clustered and oscillating, two-copy changes
CX11	28	Replication stress	★★☆	Short-sized, clustered and oscillating, mid-level amplifications
CX12	27	Unknown	☆☆☆	Very short oscillating changes
CX13	26	Replication stress	★☆☆	Short-to-medium-sized, clustered, high-level amplifications
CX14	26	Chromosome missegregation via defective mitosis	★★☆	Whole-arm/chromosome, less than one-copy changes
CX15	25	Unknown	☆☆☆	Long-sized, less than one-copy changes
CX16	17	Unknown	★☆☆	Very short, clustered and oscillating, two-to-three-copy changes
CX17	16	Unknown	★★☆	Short-to-long-sized, one-to-three-copy changes



featured papers

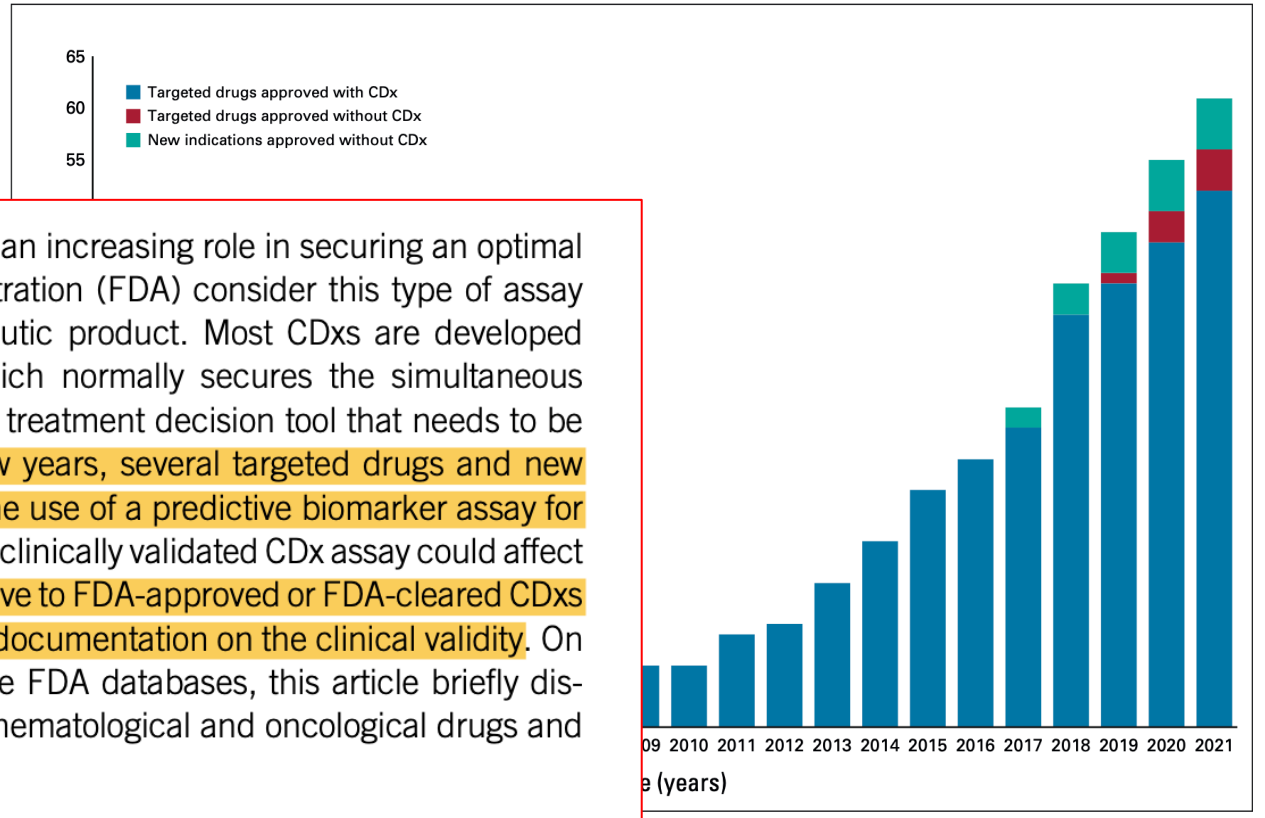
Jan Trøst Jørgenson (Denmark)

Missing companion diagnostic for US FDA Approved

abstract

Within hematology and oncology, companion diagnostics (CDxs) play an increasing role in securing an optimal therapy for individual patients, and the US Food and Drug Administration (FDA) consider this type of assay essential for the safe and effective use of a corresponding therapeutic product. Most CDxs are developed prospectively using the drug-diagnostic codevelopment model, which normally secures the simultaneous approval of both drugs and diagnostics. A CDx assay is an important treatment decision tool that needs to be available simultaneously with the drug. However, within the past few years, several targeted drugs and new indications have been approved by the FDA without a CDx, despite the use of a predictive biomarker assay for patient selection during clinical development. A missing analytical and clinically validated CDx assay could affect the correct use of these drugs and ultimately patient safety. An alternative to FDA-approved or FDA-cleared CDxs could be to use a laboratory-developed test, which will normally miss documentation on the clinical validity. On the basis of the information available from different publicly available FDA databases, this article briefly dis- isses the issue of missing CDx assays in relation to the approval of hematological and oncological drugs and indications.

Oncol 6:e2200100. © 2022 by American Society of Clinical Oncology



ed CDx-drug combinations within hematology and oncology from 1998 to present. The figure also includes new drugs and indications that have been approved without a CDx assay. CDx, companion diagnostic.

featured papers

Lips et al. *Amsterdam UK etc...

Genomic analysis defines clonal relationships of ducal carcinoma in situ and recurrent invasive breast cancer

nature genetics

ARTICLES

https://doi.org/10.1038/s41588-022-01

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Genomic analysis defines clonal relationships of ductal carcinoma in situ and recurrent invasive breast cancer

Esther H. Lips[1,24], Tapsi Kumar[2,3,4,24], Anargyros Megalios[5,24], Lindy L. Visser[1], Michael Sheinman[6], Angelo Fortunato[7,8], Vandna Shah[5], Marlous Hoogstraat[6], Emi Sei[3], Diego Mallo[7,8], Maria Roman-Escorza[5], Ahmed A. Ahmed[5], Mingchu Xu[2],

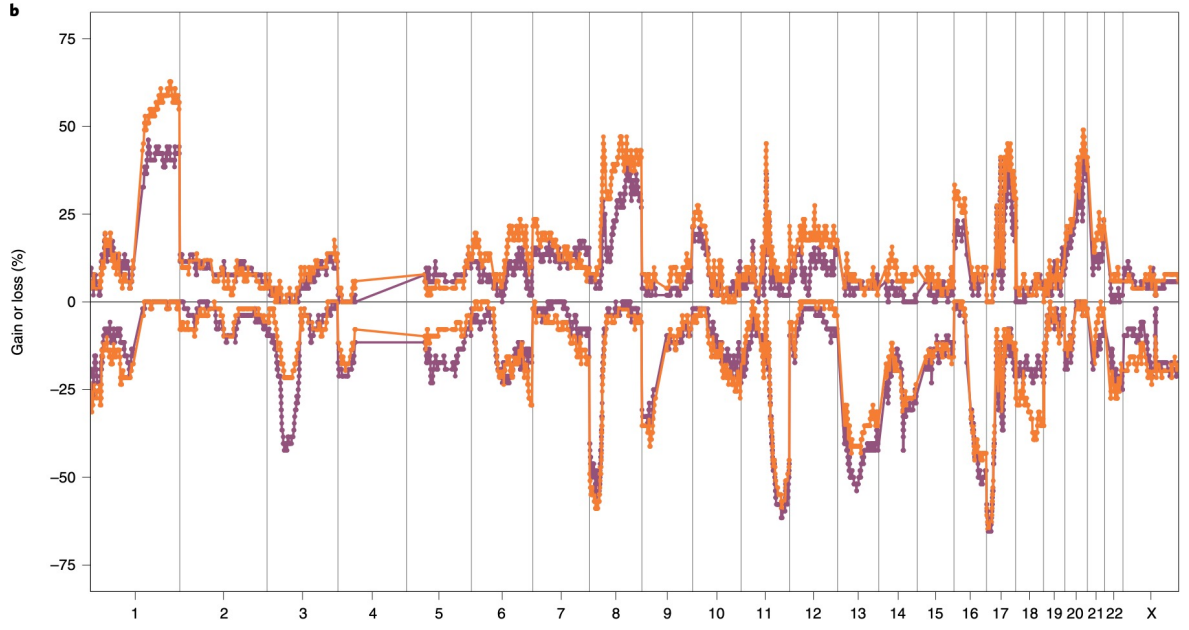

Fig. 6 | Mutations and copy number alterations in primary DCIS and subsequent clonally related invasive recurrences. a, Oncoplots for primary DCIS samples (left) and invasive recurrences (right) based on WES and targeted sequencing. Of the 45 genes covered by all sequencing platforms, only genes mutated in more than 3% of the primary DCIS or invasive recurrence samples are shown. We removed C>T mutations with allele frequency < 0.1 and fewer than three entries in the COSMIC database. **b**, Frequency plot of genome-wide copy number alterations in clonally related DCIS and invasive recurrences ($n = 55$) showing primary DCIS (purple) and its paired ipsilateral invasive recurrence (orange). The *y* axis shows the percentage of samples with gains (above zero line) and losses (below zero line). The genomic position is indicated by chromosome 1 on the left and up to chromosome X on the right with chromosome boundaries indicated by vertical lines.

featured papers

Maier-Hein et al. (German/Swiss/Czech)

BIAS: Transparent reporting of biomedical image analysis challenges

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Medical Image Analysis

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BIAS: Transparent reporting of biomedical image analysis challenges

Lena Maier-Hein[a,*], Annika Reinke[a], Michal Kozubek[b], Anne L. Martel[c,d], Tal Arbel[e], Matthias Eisenmann[a], Allan Hanbury[f,g], Pierre Jannin[h], Henning Müller[i,j], Sinan Onogur[a], Julio Saez-Rodriguez[k,l,m], Bram van Ginneken[n], Annette Kopp-Schneider[o], Bennett A. Landman[p]

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Mund et al.

Unbiased spatial proteomics with single-cell resolution in tissues

Molecular Cell

CellPress

Technology review

Unbiased spatial proteomics with single-cell resolution in tissues

Andreas Mund,[1,4] Andreas-David Brunner,[2,3,4] and Matthias Mann[1,2,*]
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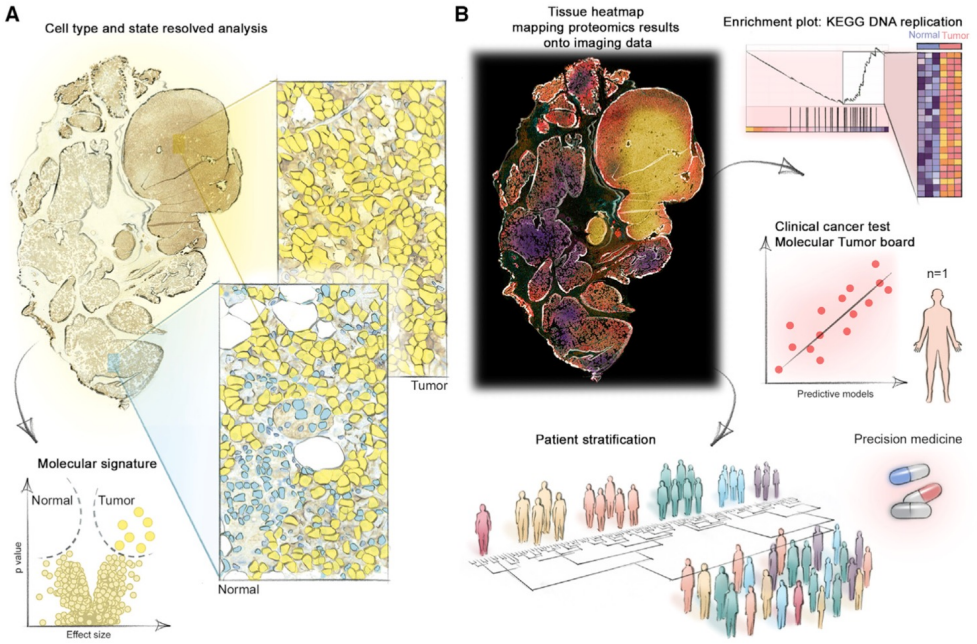


Figure 5. Clinical applications of spatial proteomics for patient phenotyping
(A) High-resolution tissue maps allow machine-learning-based accurate cell segmentation and classification. Spatial proteomics analysis reveals disease-specific molecular signatures in their native tissue context, directly from normal or tumor FFPE tissue slices.
(B) Combining unbiased proteomics with high-content imaging generates a phenotype map including the tissue microenvironment. Out of the detailed and quantitative proteomic map of the tissue, matrices, profiles, enrichment plots, and neighborhood analysis can be generated to define phenotypic relationships and mine the spatial correlations in the data to provide diagnostic decision support.

featured papers

Nacev et al. (MSKCC)

Clinical sequencing of soft tissue and bone sarcomas delineates diverse genomic landscapes and potential therapeutic targets

nature COMMUNICATIONS

ARTICLE

https://doi.org/10.1038/s41467-022-30453-x OPEN

Clinical sequencing of soft tissue and bone sarcomas delineates diverse genomic landscapes and potential therapeutic targets

...njamin A. Nacev[1,2,3,15], Francisco Sanchez-Vega[4,14,15], Shaleigh A. Smith[4,5], ...a R. Antonescu[6], Evan Rosenbaum[1,2], Hongyu Shi[7], Cerise Tang[6,8], Nicholas D. Socci[5,9], Satshil Rana[6], ...Gularte-Mérida[4], Ahmet Zehir[6], Mrinal M. Gounder[1,2], Timothy G. Bowler[1], Anisha Luthra[5,10], ...

Because a pan-cancer MSK-IMPACT analysis identified *TERT* promoter mutations in a subset of sarcomas[22], we investigated *TERT* alteration frequency as a function of sarcoma subtype (Fig. 4C). We identified oncogenic *TERT* amplifications in 44% (8/18) of intimal sarcoma (INTS) and *TERT* promoter mutations in 79% (38/48) of MRLS, 46% (24/52) of SFT, and 35% (5/14) of dedifferentiated chondrosarcoma (DDCHS). In DDLS, oncogenic *TERT* promoter alterations were present in 16% of samples (27/167) and were almost entirely amplifications ($n = 24$). *TERT* copy

featured papers

Park et al. (Seoul, Korea; Lunit)

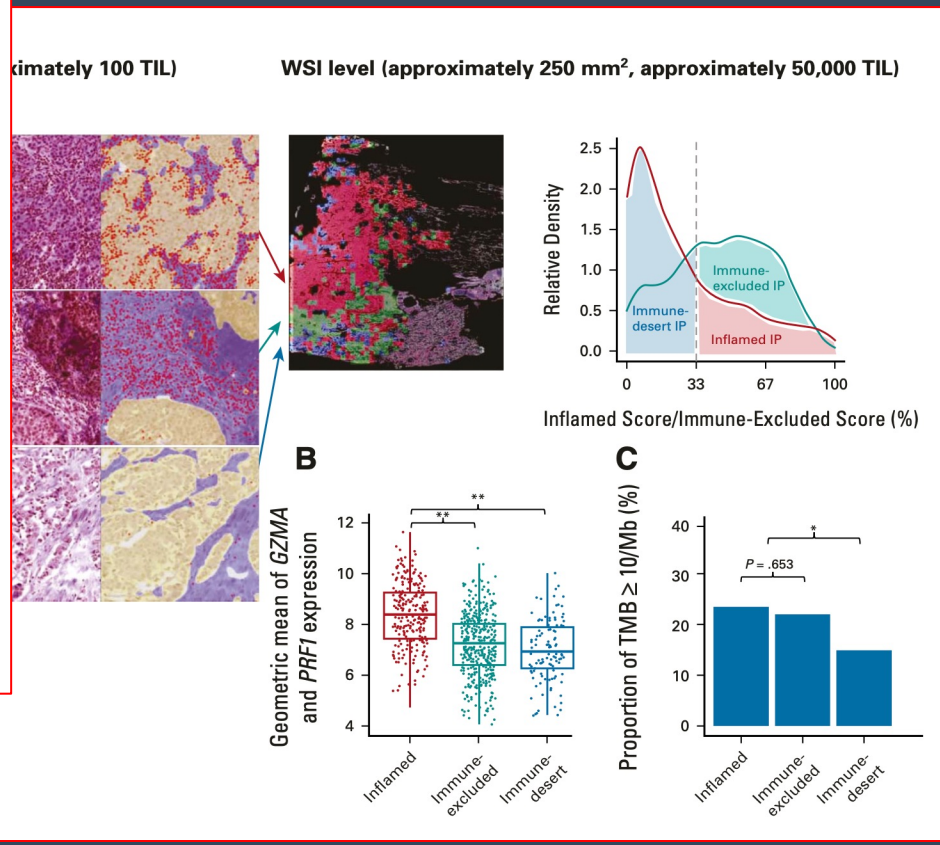
Artificial Intelligence-Powered spatial analysis of TILs as complementary biomarker for immune checkpoint inhibition in NSCL

original reports

featured papers

Artificial Intelligence–Powered Spatial Analysis of Tumor-Infiltrating Lymphocytes as Complementary Biomarker for Immune Checkpoint Inhibition in Non–Small-Cell Lung Cancer

Sehhoon Park, MD, PhD[1]; Chan-Young Ock, MD, PhD[2]; Hyojin Kim, MD, PhD[3]; Sergio Pereira, PhD[2]; Seonwook Park, PhD[2]; Minuk Ma, MS[2]; Sangjoon Choi, MD[4]; Seokhwi Kim, MD, PhD[5]; Seunghwan Shin, MD[2]; Brian Jaehong Aum, PhD[2]; Kyunghyun Paeng, MS[2]; Donggeun Yoo, PhD[2]; Hongui Cha, PhD[1]; Sunyoung Park, PhD[1]; Koung Jin Suh, MD[6]; Hyun Ae Jung, MD, PhD[1]; Se Hyun Kim, MD, PhD[6]; Yu Jung Kim, MD, PhD[6]; Jong-Mu Sun, MD, PhD[1]; Jin-Haeng Chung, MD, PhD[3]; Jin Seok Ahn, MD, PhD[1]; Myung-Ju Ahn, MD, PhD[1]; Jong Seok Lee, MD, PhD[6]; Keunchil Park, MD, PhD[1]; Sang Yong Song, MD, PhD[4]; Yung-Jue Bang, MD, PhD[7]; [illegible]n-La Choi, MD, PhD[4]; Tony S. Mok, MD[8]; and Se-Hoon Lee, MD, PhD[1,9]



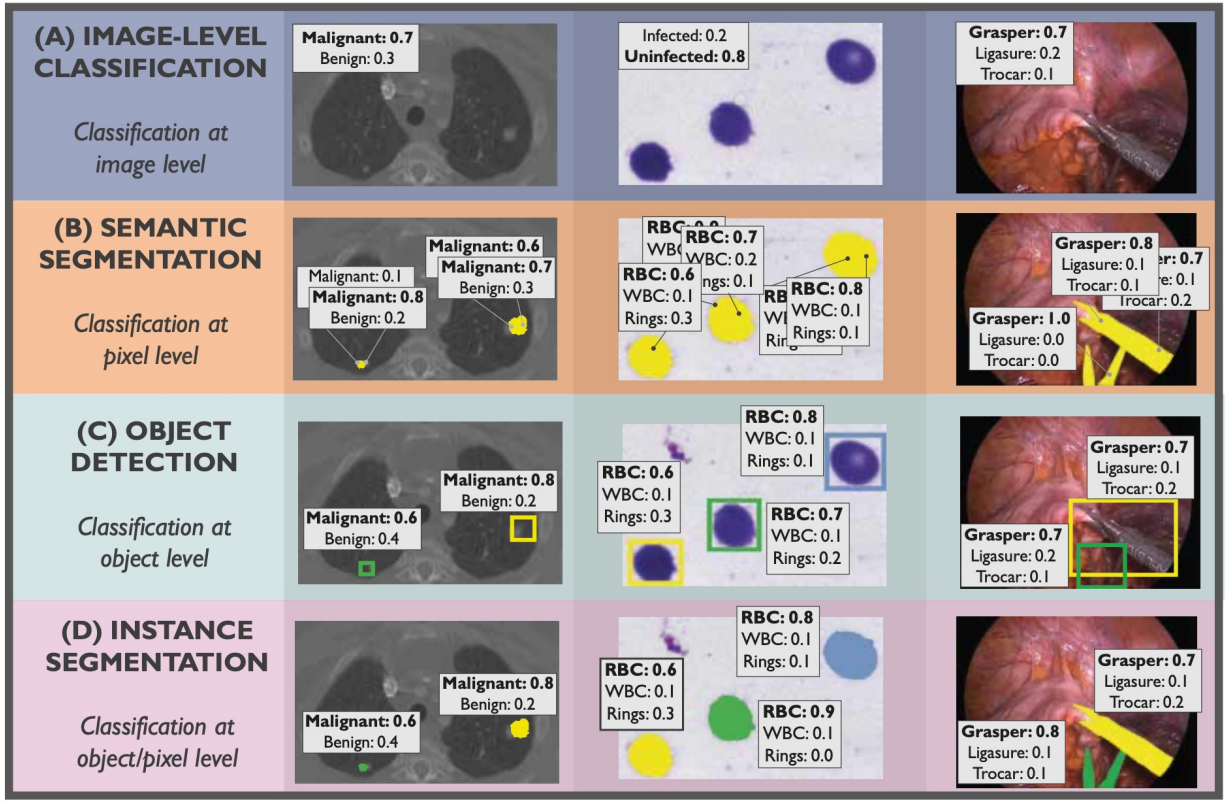
Reinke et al. (DKFZ, and many others)

Common limitations of image processing metrics: a picture story

Common Limitations of Image Processing
A Picture Story

ANNIKA REINKE*, German Cancer Research Center (DKFZ), Germany and Heidelberg
MINU D. TIZABI, German Cancer Research Center (DKFZ), Germany
CAROLE H. SUDRE, University College London, UK and King's College London, UK
MATTHIAS EISENMANN, German Cancer Research Center (DKFZ), Germany
TIM RÄDSCH, German Cancer Research Center (DKFZ), Germany and understandAI

Problem categories addressed by this paper



featured papers

Sherman et al.

Genome-wide mapping of somatic mutation rates uncovers drivers of cancer

nature biotechnology

ARTICLES

https://doi.org/10.1038/s41587-022-01353-8

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Genome-wide mapping of somatic mutation rates uncovers drivers of cancer

Maxwell A. Sherman[1,2,3,4,10], Adam U. Yaari[1,4,5,10], Oliver Priebe[1,4,6,10], Felix Dietlein[4,7,9], Po-Ru Loh[3,4] ✉ and Bonnie Berger[1,2,4,8] ✉

Identification of cancer driver mutations that confer a proliferative advantage is central to understanding cancer; however, searches have often been limited to protein-coding sequences and specific non-coding elements (for example, promoters) because of the challenge of modeling the highly variable somatic mutation rates observed across tumor genomes. Here we present Dig, a method to search for driver elements and mutations anywhere in the genome. We use deep neural networks to map cancer-specific mutation rates genome-wide at kilobase-scale resolution. These estimates are then refined to search for evidence of driver mutations under positive selection throughout the genome by comparing observed to expected mutation counts. We mapped mutation rates for 37 cancer types and applied these maps to identify putative drivers within intronic cryptic splice regions, 5′ untranslated regions and infrequently mutated genes. Our high-resolution mutation rate maps, available for web-based exploration, are a resource to enable driver discovery genome-wide.

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Thank you

Next month's steering committee on

July 27, 2022 at 3:00-4:00 PM Eastern Time

Things to expect by then

1) Update MDUFA/VALID act
2) Updates from projects and workgroups
3) Please send links/papers/other