



Applicazioni dell'intelligenza artificiale in oncoematologia

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Università degli Studi di Padova

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Il sottoscritto Raffaella Colombatti

*ai sensi dell'art. 3.3 sul Conflitto di Interessi, pag. 17 del Reg. Applicativo dell'Accordo
Stato-Regione del 5 novembre 2009,*

dichiara

☐ *che negli ultimi due anni ha avuto rapporti diretti di finanziamento con i seguenti
soggetti portatori di interessi commerciali in campo sanitario:*

*- Novartis; Addmedica; Forma Therapeutics, NovoNordisk; Global Blood Therapeutics,
Pfizer; Vertex; Agios*

- Remind general concepts on AI
- Examples of AI use in Pediatric Hematology Oncology
 - to solve unmet needs (disease classification, risk determination, choose best treatment option...)
 - to optimize workflow and diagnostics

TIME



Hi ChatGPT



Hello! How can I assist you today?



What do you think of a TIME cover story with the title, "The AI Arms Race Is Changing Everything?"



As an AI language model, I don't have personal opinions or beliefs, but I can provide some context and information on the subject.

"The AI Arms Race is Changing Everything" could be an attention-grabbing and thought-provoking title for a cover story on AI. A cover story in a widely-read publication like TIME could help raise public awareness about the potential risks and benefits of this trend, and stimulate discussions on how to ensure that AI is developed and deployed in a responsible and ethical manner.

It's important to note that the title of the story could also be interpreted as sensationalist or alarmist, and may not accurately reflect the complexities

by
ANDREW R. CHOW
& BILLY PERRIGO
(humans)

THE 100 MOST INFLUENTIAL PEOPLE IN ARTIFICIAL INTELLIGENCE

TIME 100/AI



+
ELON
MUSK'S
FIGHT
FOR THE
FUTURE
OF AI
By WALTER
ISAACSON

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COMING SOON NEJM AI – A NEW JOURNAL

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NEJM Group, the publisher of the *New England Journal of Medicine*, is planning a new journal, *NEJM AI*, to identify and evaluate state-of-the-art applications of artificial intelligence to clinical medicine. In addition to original research, *NEJM AI* will provide reviews, policy perspectives, and accessible educational material targeted at practicing physicians and clinician leaders interested in applying AI, computer scientists seeking to translate algorithmic advances to clinical practice, and policy makers and regulators.

The past decade has seen a resurgence of artificial intelligence (AI) in medicine enabled by new advancements in machine learning, from deep learning systems for computer vision to the latest conversational agents based on large language models. There are FDA-approved devices that use AI to read a broad range of imaging modalities, programs that provide diagnostic assistance, and software that helps outline possible treatments and provide prognostic data for clinicians. Although many such

EDITORIAL

AI IN MEDICINE

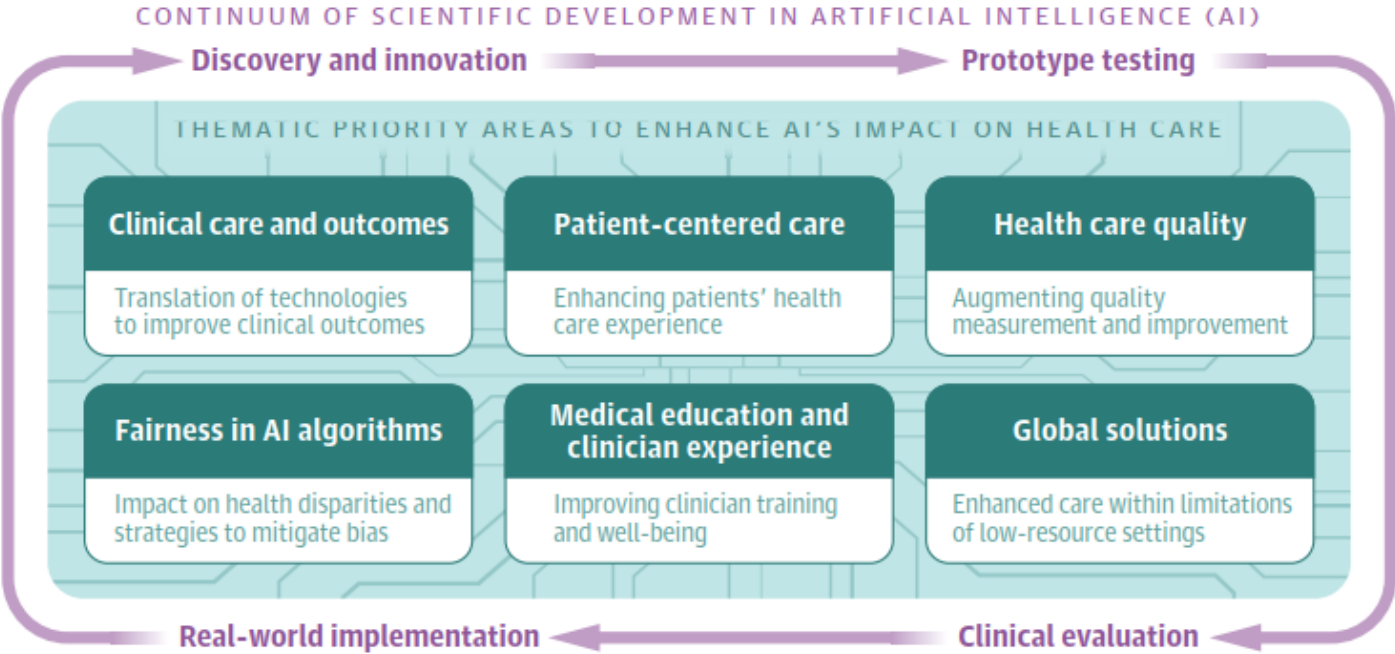
AI in Medicine—*JAMA's* Focus on Clinical Outcomes, Patient-Centered Care, Quality, and Equity

Rohan Khera, MD, MS; Atul J. Butte, MD, PhD; Michael Berkwits, MD, MSCE; Yulin Hswen, ScD, MPH;
Annette Flanagan, RN, MA; Hannah Park; Gregory Curfman, MD; Kirsten Bibbins-Domingo, PhD, MD, MAS

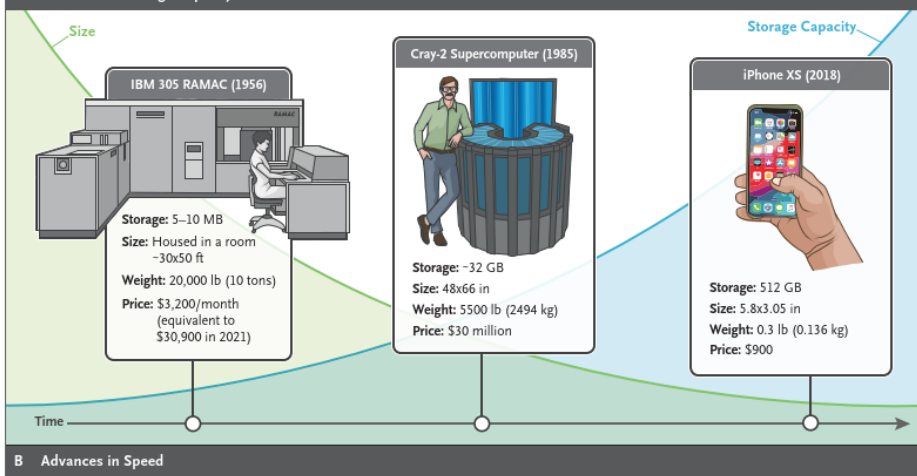
11th August 2023

JCO[®] Clinical Cancer Informatics
An American Society of Clinical Oncology Journal

Figure. The Continuum of Scientific Development in Artificial Intelligence and Thematic Priority Areas



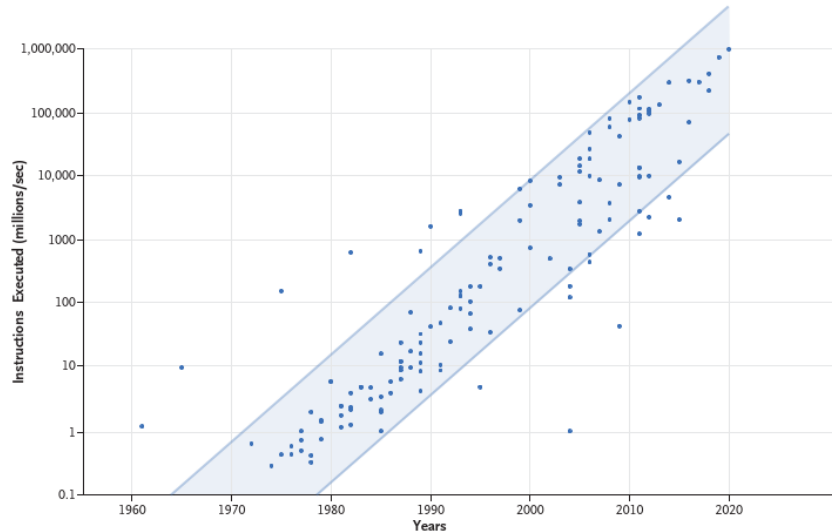
A Advances in Storage Capacity



DATA

Increased Capacity of Data Storage

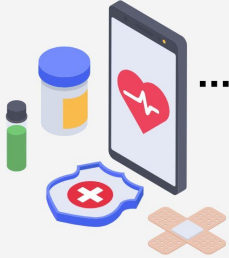
B Advances in Speed



Increased Speed of Data processing

Digital health and care technologies

Telemedicine



Wearable devices

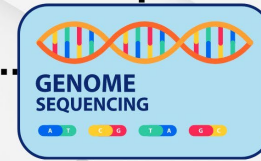
Personalised medicine



Electronic health records (EHRs)



Healthcare
Innovation
Consortium



Genome
sequencing

Shared care record (SCR)



Telehealth



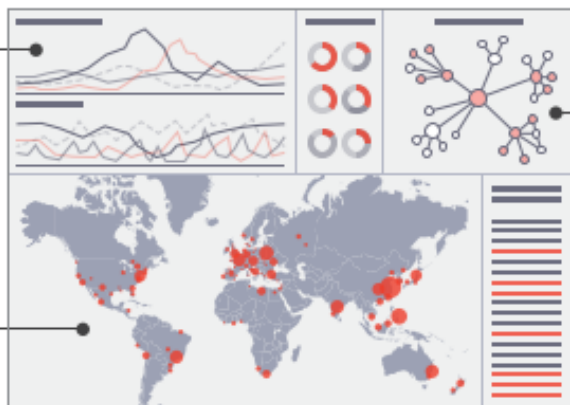
Mobile health apps



Public Health

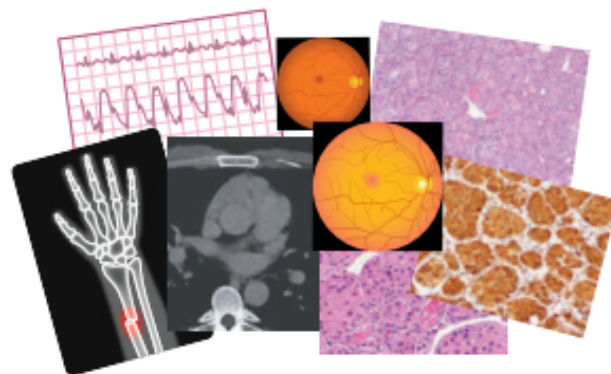
Identification of outbreaks by monitoring Internet traffic

Tracking of cases, outcomes, and relationships to local factors



Contact tracing within an outbreak

Image Analysis



Clinical-Trial Performance

Decision support in trial design

Patient identification, recruitment, and retainment

Outcome and side-effect monitoring



Retrieval of Medical Information

Use of multiple information sources about a patient to make a diagnosis

Internet search engines

EMR decision support



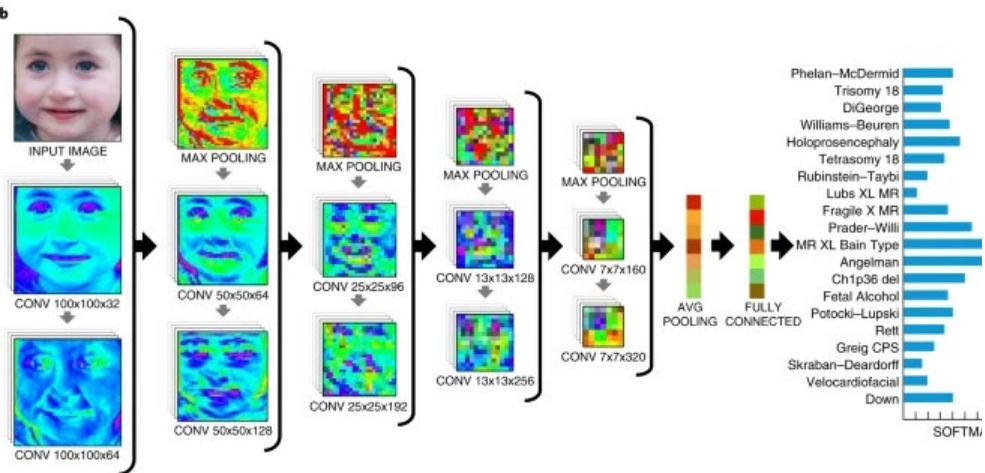
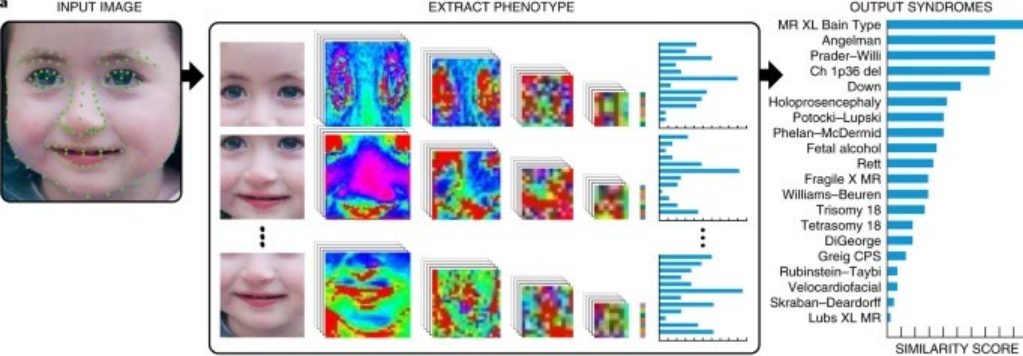
Operational Organization

Operating-room scheduling

Billing and collections

Patient follow-up





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Smart Phenotyping. Better Genetics.

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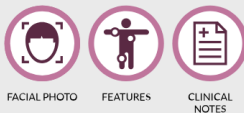
What is Next-Generation Phenotyping (NGP)?

Technologies that use artificial intelligence frameworks, such as FDNA's DeepGestalt¹, to capture, structure and analyze human phenotypic data to generate unique and comprehensive genomic insights and identify causative variants.

¹ Gurovich et al (2019) Identifying rare genetic syndromes using deep learning. Nature Medicine. DOI:10.1038/s41591-018-0279-0

FACE2GENE
Smart Phenotyping. Better Genetics.

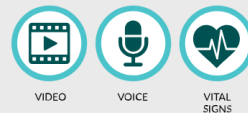
CURRENTLY AVAILABLE

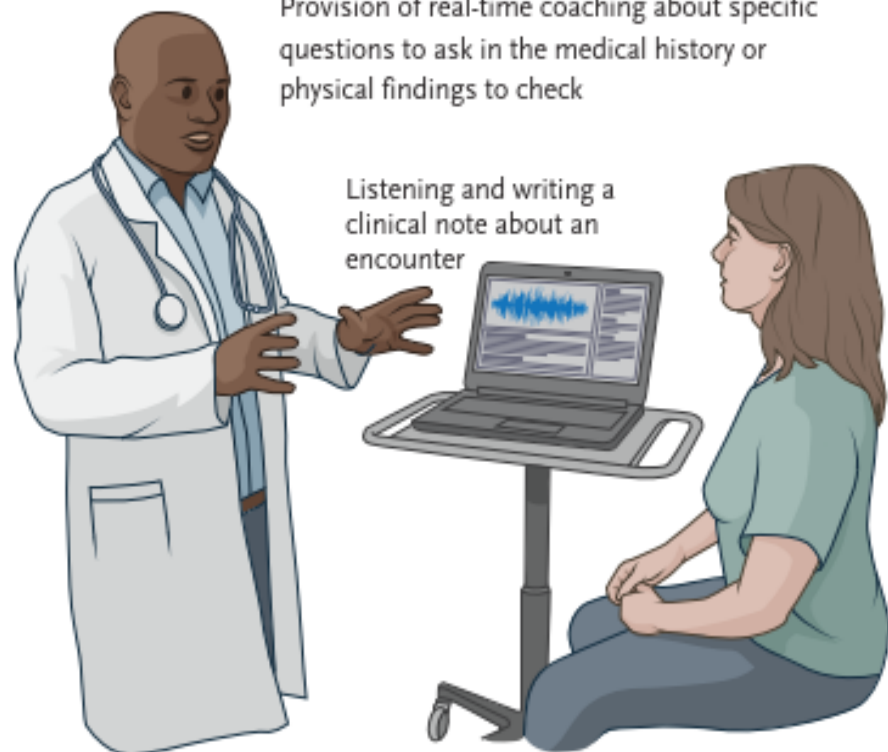


NEAR TERM



FUTURE





Provision of real-time coaching about specific questions to ask in the medical history or physical findings to check

Listening and writing a clinical note about an encounter

Serving as a teacher and an assessor in medical education

Creating realistic "flight simulators" for simple and complex patient encounters



Artificial Intelligence in Clinical Oncology: From Data to Digital Pathology and Treatment

Kirthika Senthil Kumar, PhD^{1,2,3}; Vanja Miskovic, PhD^{4,5}; Agata Blasiak, PhD^{1,2,3,6}; Raghav Sundar, MBBS, PhD^{1,2,7,8,9,10}; Alessandra Laura Giulia Pedrocchi, PhD⁴; Alexander T. Pearson, MD, PhD^{11,12}; Arselä Prelaj, MD^{4,5}; and Dean Ho, PhD^{1,2,3,6}

ARTIFICIAL INTELLIGENCE

Applications of Artificial Intelligence in Pediatric Oncology: A Systematic Review

Siddhi Ramesh, BA¹; Sukarn Chokkara, BA¹; Timothy Shen, BA¹; Ajay Major, MD, MBA²; Samuel L. Volchenbourn, MD, PhD³; Anoop Mayampurath, PhD³; and Mark A. Applebaum, MD³

- Fields of application: classification, prediction of treatment response, dose optimization
- Variety of methods used: neural network, k-nearest neighbor, random forest, naive Bayes, and support vector machines.
- Strengths: matching or outperforming physician comparators via automated analysis and predicting therapeutic response.
- Limitations: significant heterogeneity in reporting standards, clinical applicability, small sample sizes, and missing external validation cohorts
- Conclusions: ML can enhance clinical care in ways that may not otherwise be achievable. ML has enormous potential in improving diagnostics, decision making, monitoring for children with cancer, but the field remains in early stages; future work will be aided by **standards and guidelines** to ensure rigorous methodologic design and maximizing clinical utility

Manuscript	Cancer(s) Evaluated	Task	ML Method	No. of Patients	No. of Images or Samples	Type of Data	CV
Fetit et al ¹¹	CNS tumors (medulloblastoma, pilocytic astrocytoma, and ependymoma)	Classification	SVM	134		MRI data	LOOCV
Faranoush et al ¹²	High-grade glioma and medulloblastoma	Classification	SVM	198		Clinical data	NA
Quon et al ¹³	Diffuse midline glioma, medulloblastoma, pilocytic astrocytoma, and ependymoma	Classification	Neural network	816		MRI	Holdout test set
Dong et al ¹⁴	Ependymoma and medulloblastoma	Classification	KNN, AdaBoost, random forest, and SVM	51		MRI	10-fold CV
Li et al ¹⁵	Ependymoma and pilocytic astrocytoma	Classification	SVM	45	95	MRI	Holdout test set
Zhou et al ¹⁶	Ependymoma, pilocytic astrocytoma, and medulloblastoma	Classification	Tree-based pipeline optimization tool	288		MRI	Five-fold CV

BRAIN TUMORS

Zarinabad et al ²⁹	Ependymoma, medulloblastoma, and astrocytoma	Classification	LDA, SVM, and random forest
Robinson et al ¹⁸	Low- and high-grade pediatric brain tumors	Classification	inForm ML software
Das et al ¹⁹	Medulloblastoma	Classification	SVM
Iv et al ²⁰	Medulloblastoma	Classification	SVM
Das et al ²¹	Medulloblastoma	Classification	SVM
Zhang et al ²²	Medulloblastoma, brain metastatic tumor, and hemangioblastoma	Classification	Logistic regression
Gutierrez et al ²³	Medulloblastoma, pilocytic astrocytoma, and ependymoma	Classification	SVM

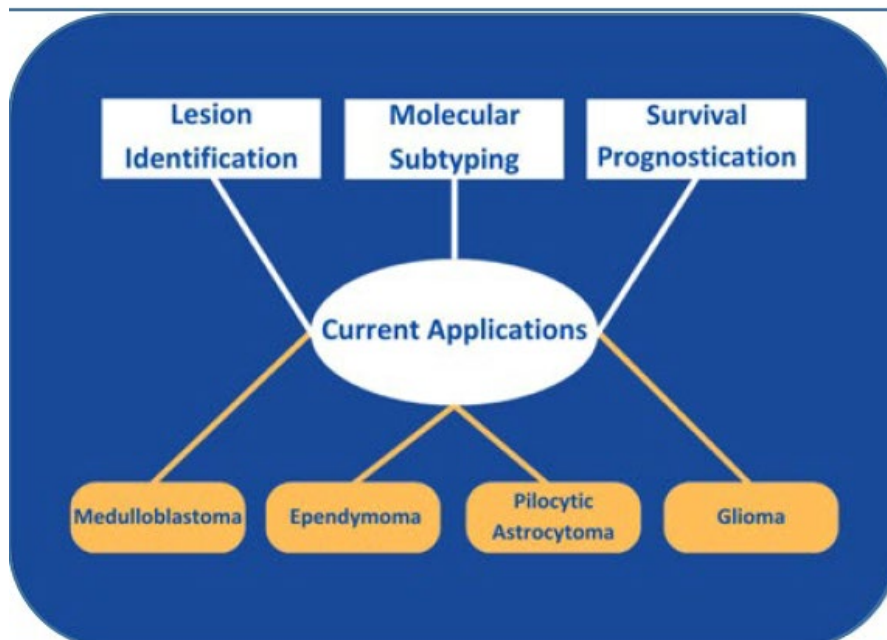
Fetit et al ²⁴	Medulloblastoma, pilocytic astrocytoma, and ependymoma	Classification	Naive Bayes, KNN, decision tree, SVM, neural network, and logistic regression	48		MRI	LOOCV with stratified 10-fold CV
Fetit et al ²⁵	Medulloblastoma, pilocytic astrocytoma, and ependymoma	Classification	Naive Bayes, KNN, decision tree, and SVM	21	21	MRI	LOOCV
Li et al ²⁶	Medulloblastoma and ependymoma	Classification and feature extraction	KNN, SVM, bagging, boosting, neural networks, classification and regression trees, random subspace method, extreme learning machine, naive Bayes, random forests, and partial least square regression.	58	174 MRI slices	MRI images	Holdout test set (70% training set, 30% validation set)
Grist et al ²⁷	Pilocytic astrocytoma, ependymoma, and medulloblastoma	Classification	Neural network, SVM, and random forest	49		MRI	Three-fold CV
Hollon et al ²⁸	Pilocytic astrocytoma, ependymoma, medulloblastoma and other embryonal tumors, ganglioglioma, diffuse midline glioma, hemangioblastoma, choroid plexus papilloma, chordoma, and germinoma	Classification	Decision tree and random forest	25	25 hematoxylin and eosin and stimulated Raman histology images	Raman histology	10-fold CV
Zarinabad et al ²⁹	Pilocytic astrocytoma, medulloblastoma, and ependymoma	Classification	Random forest, naive Bayes, SVM, neural network, and LDA	90		MRS	10-fold CV
Orphanidou-Vlachou et al ³⁰	Posterior fossa tumors (medulloblastomas, pilocytic astrocytomas, and ependymomas)	Classification	PCA, LDA, and neural network	40		MRI	LOOCV, 10-fold cross-validation

Manuscript	Cancer(s) Evaluated	Task	ML Method	No. of Patients	No. of Images or Samples	Type of Data	CV
Chaber et al ³¹	Ewing sarcoma	Classification	Quadratic discriminant analysis classifier	37		FTIR spectroscopy	LOOCV
Chaber et al ³²	Ewing sarcoma	Prediction of treatment outcome	SVM, random forest, and LDA	27		FTIR spectroscopy	LOOCV
Gheisari et al ³³	Neuroblastoma	Classification	SVM, random forest, and neural network	125	1,043 histologic images	Histology	NA
Kong et al ³⁴	Neuroblastoma	Classification	KNN and SVM	36	422	Histology	NA
Gheisari et al ³⁵	Neuroblastoma	Classification	Neural network	125	1,043 histologic images	Histology	10-fold CV
Wills et al ³⁶	Neuroblastoma	Classification	PCA	39	1,114 spectra	Raman spectra	NA
Huang et al ³⁷	Osteosarcoma	Classification	Random forest	12	102 tissue samples	MRI	Five-fold CV
Hu et al ³⁸	Osteosarcoma	Classification	SVM	141	141	XR	NA
Arunachalam et al ³⁹	Osteosarcoma	Prediction of treatment outcome	SVM and neural network	50	Of these, 40 whole-slide images selected from 942 histology glass slides (mean: 19 slides per patient; range: 4-51 slides per patient)	Histology	Five-fold CV
Cuplov et al ⁴⁰	Rhabdomyosarcoma	Dose and treatment toxicity prediction	Gradient-boosted regression	24		Blood	10-fold CV
Banerjee et al ⁴¹	Rhabdomyosarcoma	Classification	Neural network	21		MRI	LOOCV
Virgolin et al ⁴²	Wilms tumor	Dose reconstruction	Random forest	37	37 CT images	CT	NA
Virgolin et al ⁴³	Wilms tumor	Dose-volume metric value generation (radiotherapy)	Logistic regression	142	142 CT images	CT	Five-fold CV

SOLID TUMORS

Manuscript	Cancer(s) Evaluated	Task	ML Method	No. of Patients	No. of Images or Samples	Type of Data	CV
Reiter et al ⁴⁴	Acute B-lymphoblastic leukemia	Classification	Gaussian mixture model and SVM	337	337 bone marrow samples	Flow cytometry	NA
Fathi et al ⁴⁵	Acute leukemia	Classification	Neural network with PCA and group method of data handling	243	346 CBCs total (each with 9 features): 172 ALL CBCs; 74 AML CBCs; 110 healthy CBC's	Clinical data	NA
Kesler et al ⁴⁶	ALL	Prediction	Random forest	70		Clinical data (MRI and cognitive testing)	10-fold CV
Glass et al ⁴⁷	ALL	Classification	Neural network along with spatially normalized proportional volume maps and a gradient magnitude threshold	228	636 images	MRI	NA
Al-Fahad et al ⁴⁸	ALL	Classification (cognitive abilities of patients with ALL)	SVM and random forest	200		MRI-based volumetric measures, morphometry statistics, behavioural, and demographic variables.	80%-20% shuffle-split with 10 iterations
Doan et al ⁴⁹	ALL	Classification	Neural network and linear SVM	30	30 bone marrow samples	Flow cytometry	NA
Pan et al ⁵⁰	ALL	Disease relapse or disease progression	Random forest	336		Clinical variables data	10-fold CV
Pedreira et al ⁵¹	ALL	Dose reconstruction	Neural network estimation	158		Laboratory and clinical variables data	LOOCV
Kashef et al ⁵²	ALL	Classification (treatment outcome)	Decision tree, SVM, LDA, multilayer perceptron, gradient-boosting machine, random forest, and extreme gradient boosting	241		Clinical and medical data	10-fold CV

Current state of radiomics in pediatric neuro-oncology practice: a systematic review



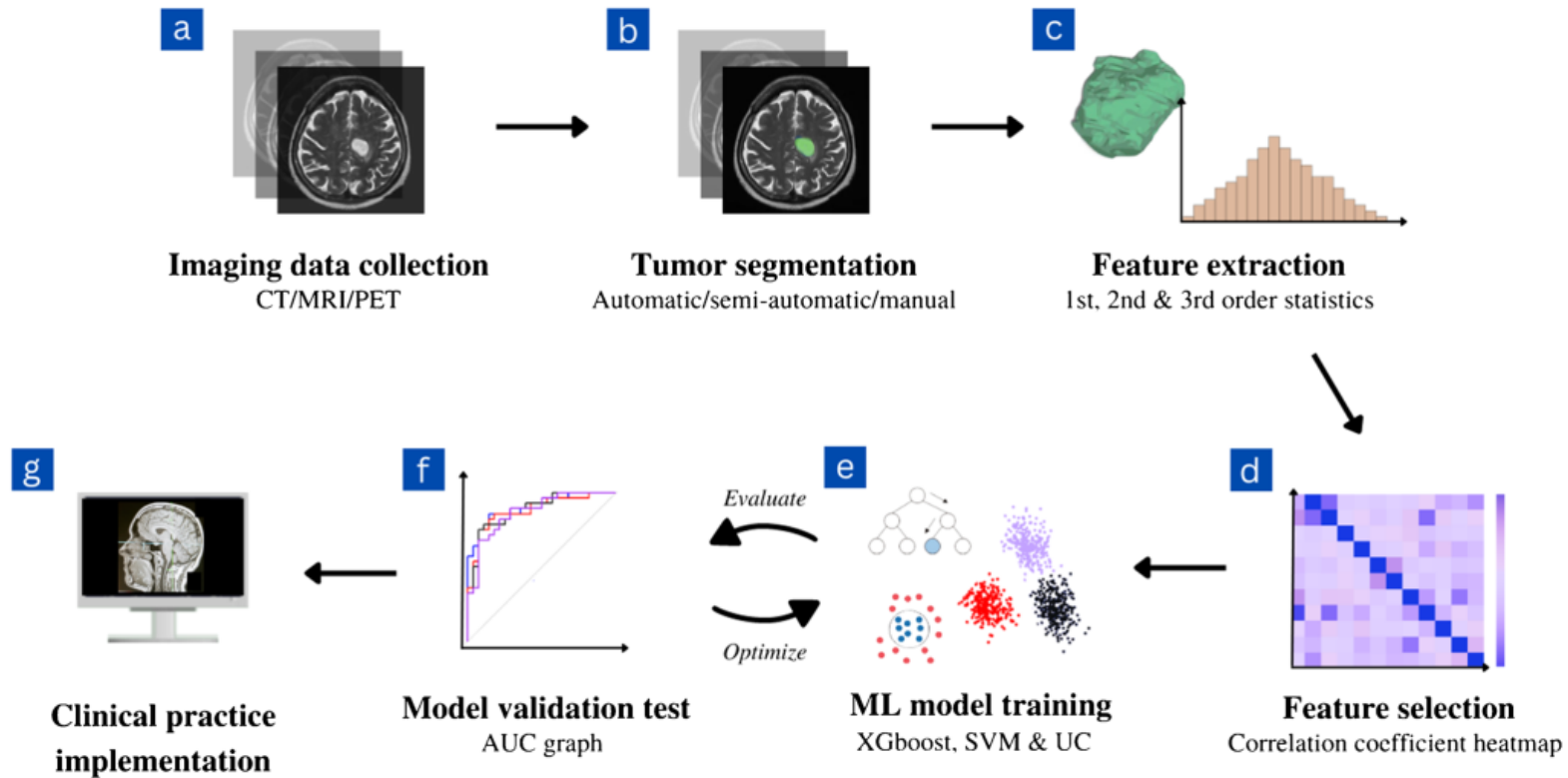


Fig. 1 The typical radiomics workflow has 6 key steps. **a** Collecting radiological images from various modalities. **b** Segmenting the region of interest. **c** Extracting topographical and shape features. **d** Selecting some of the extracted features. **e** Using the features to train machine

learning models. **f** Evaluating performance using sensitivity, specificity and area under the curve. **g** Incorporating the model into clinical practice

Table 1 Radiomics quality score (RQS) checklist

RQS checkpoint	RQS item number and name	Description and (points)
First	Item 1: image protocol quality	Well-documented protocol (+1) AND/OR publicly available protocol (+1)
Second	Item 2: multiple segmentation	Testing feature robustness to segmentation variability, e.g., different physicians/algorithms/software (+1)
	Item 3: phantom study	Testing feature robustness to scanner variability, e.g., different vendors/scanners (+1)
	Item 4: multiple time points	Testing feature robustness to temporal variability, e.g., organ movement/expansion/shrinkage (+1)
Third	Item 5: feature reduction	Either feature reduction OR adjustment for multiple testing is implemented (+3); otherwise, (−3)
	Item 6: multivariable analysis	Non-radiomic feature are included in/considered for model building (+1)
	Item 7: Biological correlates	Detecting and discussing correlation of biology and radiomic features (+1)
	Item 8: cut-off analysis	Determining risk groups by either median, pre-defined cut-off, or continuous risk variable (+1)
	Item 9: discrimination statistics	Discrimination statistic and its statistical significance are reported (+1); a resampling technique is also applied (+1)
	Item 10: calibration statistics	Calibration statistic and its statistical significance are reported (+1); a resampling technique is also applied (+1)
	Item 11: prospective design	Prospective validation of a radiomics signature in an appropriate trial (+7)
	Item 12: validation	Validation is missing (−5) OR internal validation (+2) OR external validation on single dataset from one institute (+3) OR external validation on two datasets from two distinct institutes (+4) OR validation of a previously published signature (+4) validation is based on three or more datasets from distinct institutes (+5)
	Item 13: comparison to “gold standard”	Evaluating model’s agreement with/superiority to the current “gold standard” (+2)
	Item 14: potential clinical application	Discussing model applicability in a clinical setting (+2)

ore 2023**Table 3** Radiomics quality score (RQS) for the included studies**Fig. 3** Quality Assessment of Diagnostic Accuracy Studies-2 score by author (a) and domain (b)

Diagnostic performance of artificial intelligence for pediatric pulmonary nodule detection in computed tomography of the chest

Rida Salman¹, HaiThuy N Nguyen², Andrew C Sher¹, Kristina A Hallam³, Victor J Seghers¹, Marla B K Sammer⁴

Affiliations + expand

PMID: 37301051 DOI: 10.1016/j.clinimag.2023.05.019

Abstract

Purpose: To test the performance of a commercially available adult pulmonary nodule detection artificial intelligence (AI) tool in pediatric CT chests.

Methods: 30 consecutive chest CTs with or without contrast of patients ages 12-18 were included. Images were retrospectively reconstructed at 3 mm and 1 mm slice thickness. AI for detection of lung nodules in adults (Syngo CT Lung Computer Aided Detection (CAD)) was evaluated. 3 mm axial images were retrospectively reviewed by two pediatric radiologists (reference read) who determined the location, type, and size of nodules. Lung CAD results at 3 mm and 1 mm slice thickness were compared to reference read by two other pediatric radiologists. Sensitivity (Sn) and positive predictive value (PPV) were analyzed.

Results: The radiologists identified 109 nodules. At 1 mm, CAD detected 70 nodules; 43 true positive (Sn = 39 %), 26 false positive (PPV = 62 %), and 1 nodule which had not been identified by radiologists. At 3 mm, CAD detected 60 nodules; 28 true positive (Sn = 26 %), 30 false positive (PPV = 48 %) and 2 nodules which had not been identified by radiologists. There were 103 solid nodules (47 measuring < 3 mm) and 6 subsolid nodules (5 measuring < 5 mm). When excluding 52 nodules (solid < 3 mm and subsolid < 5 mm) based on algorithm conditions, the Sn increased to 68 % at 1 mm and 49 % at 3 mm but there was no significant change in the PPV measuring 60 % at 1 mm and 48 % at 3 mm.

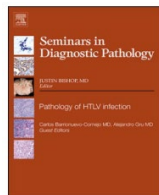
Conclusion: The adult Lung CAD showed low sensitivity in pediatric patients, but better performance at thinner slice thickness and when smaller nodules were excluded.

Keywords: Artificial intelligence; Lung Computer Aided Detection; Lung nodules; Pediatric.



Article

Automated Bone Marrow Cell Classification for Haematological Disease Diagnosis Using Siamese Neural Network



Digital pathology and artificial intelligence as the next chapter in diagnostic hematopathology

Elisa Lin ^a, Franklin Fuda ^a, Hung S Luu ^a, Andrew M. Cox ^b, Fengqi Fang ^c, Junlin Feng ^d, Mingyi Chen ^{a,*}

MODERN PATHOLOGY



Journal homepage: <https://modernpathology.org/>

Research Article

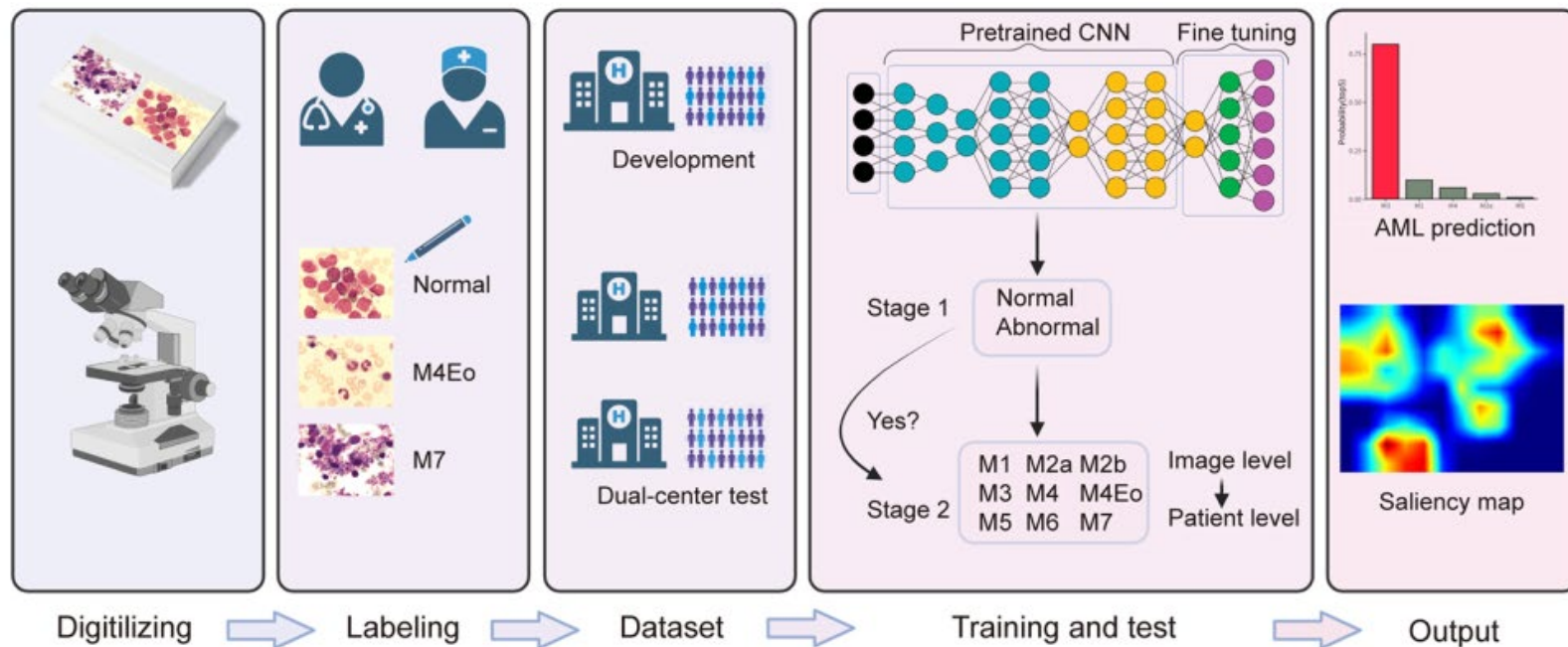
MarrowQuant 2.0: A Digital Pathology Workflow Assisting Bone Marrow Evaluation in Experimental and Clinical Hematology

Workflow optimization:
Increased Accuracy
Reduced time



AMLnet, A deep-learning pipeline for the differential diagnosis of acute myeloid leukemia from bone marrow smears

A



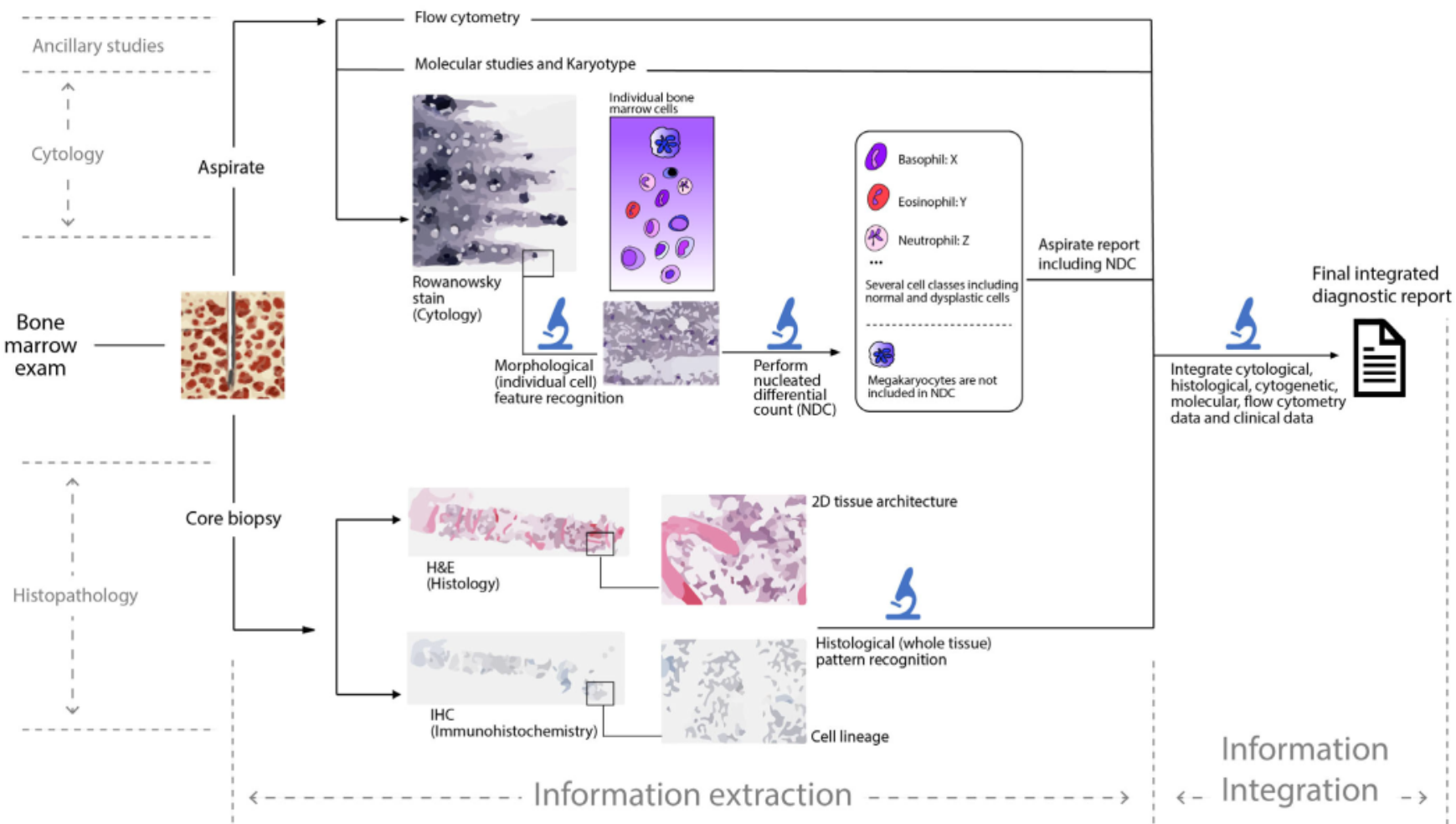


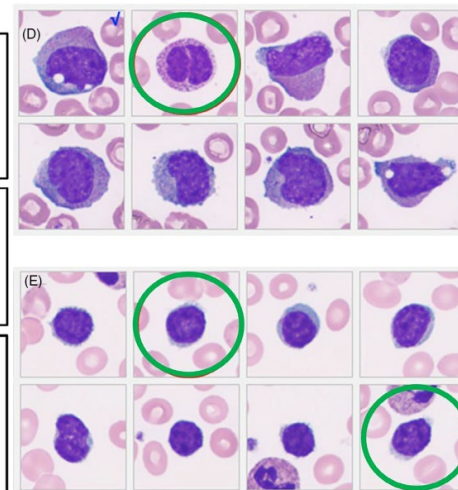
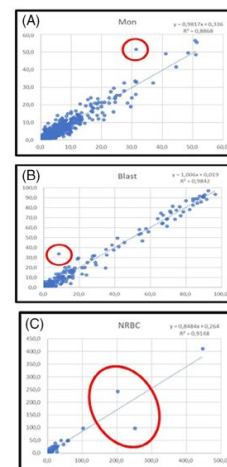
TABLE 1 A summary of examples of object detection models in bone marrow pathology.

Study	Purpose	Number of slides/cells	Highlight
Chandradevan et al. ²⁵	Detect and classify BMA cells to create NDC	10 000 manually annotated cells from 17 patients	Faster R-CNN for cell detection, and VGG16 for cell classification
Liu et al. ²⁶	Bone marrow cell detection and classification	70 BMA WSIs	Faster R-CNN for detection and classification. Integrated in an augmented reality system.
Tayebi et al. ²⁷	Bone marrow cell detection and classification	More than 1 million cells with data augmentation	YOLOv4 for detection and classification. Provides a histogram of cell types.
Lewis et al. ²⁸	Bone marrow cell detection and classification	28 914 manually labelled cells from 36 WSIs.	Faster R-CNN for detection and classification
Lee et al. ³⁰	Detection and classification of normal versus dysplastic cell lineage	34 MDS + 24 Normal	
Tang et al. ³¹	Normal/reactive vs. abnormal lymphocytes	15 353 cell images from 53 WSIs	Based on Morphogo
Sirinukunwattana et al. ²⁹	Megakaryocyte detection from histopathology images	131 WSIs of MPN patients	Slide-level morphological fingerprinting of megakaryocytes
van Eekelen et al. ³²	Quantification of bone marrow cellularity	130 WSIs	A VGG-like structure for segmentation

Artificial intelligence and the blood film: Performance of the MC-80 digital morphology analyzer in samples with neoplastic and reactive cell types

Gina Zini^{1,2} | Francesca Mancini³ | Elena Rossi^{1,2} | Stefania Landucci³ |
Giuseppe d'Onofrio¹

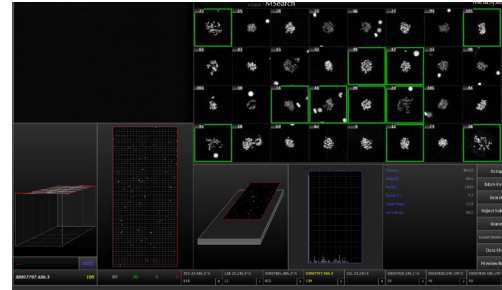
- Excellent morphological reproducibility and similarity with microscope images of cells in normal and dysplastic samples
- Role in remote reviewing, training and education, harmonization and comparability of results, peer film reviewing and consultation



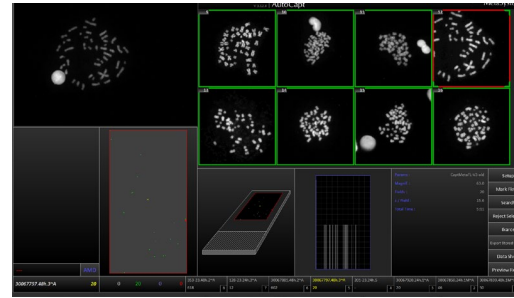
Ricerca di alterazioni cromosomiche acquisite mediante analisi citogenetica classica, ibridazione in situ fluorescente (FISH) in metafase e nei nuclei in interfase e multicolor FISH (mFISH).

Uso di microscopi a fluorescenza, di un sistema automatico, e l'acquisizione delle metafasi e dei nuclei e di software dedicati per la cariotipizzazione, l'analisi FISH e multi-FISH.

Citogenetica Classica

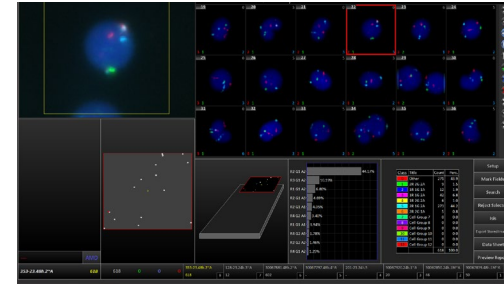


Ricerca e riconoscimento di metafasi

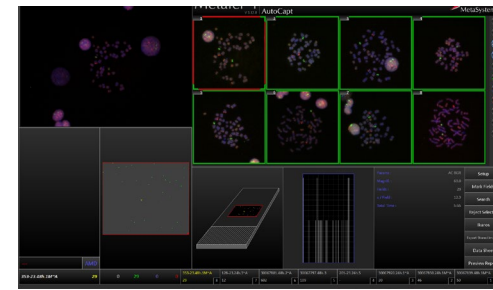


Acquisizione di metafasi

FISH



Ricerca e acquisizione di nuclei



Ricerca e acquisizione di metafasi

Applicazione di Deep Learning per ottimizzazione workflow in Citodiagnostica

- Implementazione del sistema con algoritmi di intelligenza artificiale (Deep Learning) utili alla **separazione e classificazione automatica dei cromosomi (cariotipizzazione automatica)**,
- minimizzazione delle operazioni ripetitive svolte dagli operatori,
- **ottimizzazione delle risorse e potenziamento dell'attività produttiva di laboratorio** (risparmio di almeno il 40/50% di tempo nell'esecuzione di un caso di citogenetica classica).

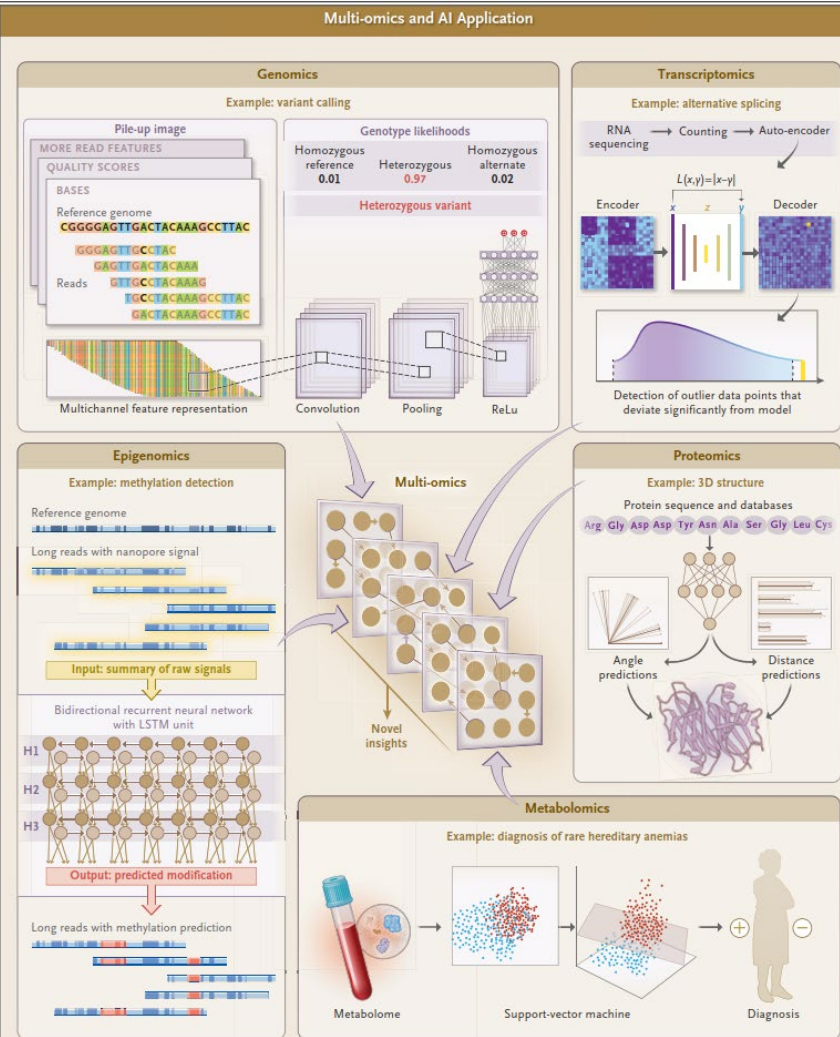
REVIEW ARTICLE

AI IN MEDICINE

Jeffrey M. Drazen, M.D., *Editor*, Isaac S. Kohane, M.D., Ph.D., *Guest Editor*,
and Tze-Yun Leong, Ph.D., *Guest Editor*

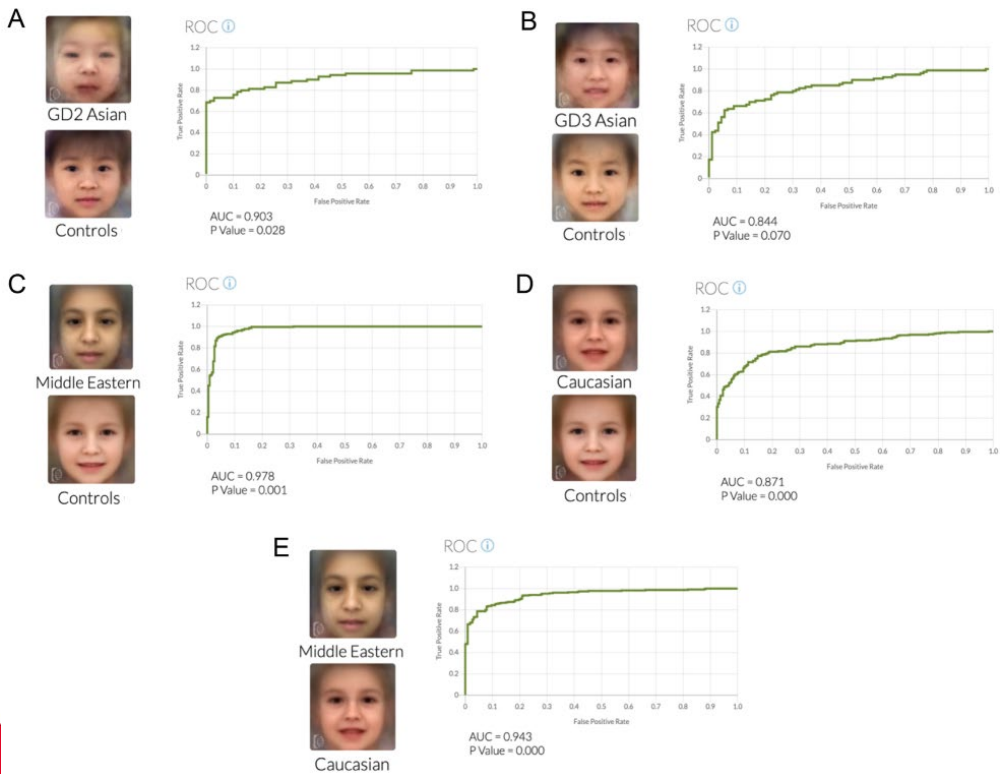
Artificial Intelligence in Molecular Medicine

Bruna Gomes, M.D., and Euan A. Ashley, M.B., Ch.B., D.Phil.










Investigation of a dysmorphic facial phenotype in patients with Gaucher disease types 2 and 3

Emily Daykin ^a, Nicole Fleischer ^b, Magy Abdelwahab ^c, Nehal Hassib ^d, Raphael Schiffmann ^e, Emory Ryan ^a, Ellen Sidransky ^{a,*}



Automated Matching of Patients to Clinical Trials: A Patient-Centric Natural Language Processing Approach for 2023 Pediatric Leukemia

Samuel Kaskovich, MD¹; Kirk D. Wyatt, MD² ; Tomasz Oliwa, PhD³ ; Luca Graglia, MS⁴ ; Brian Furner, MS⁴ ; Jooho Lee, PhD⁴ ; Anoop Mayampurath, PhD⁵ ; and Samuel L. Volchenbom, MD, PhD⁴ 

JCO® Clinical Cancer Informatics
An American Society of Clinical Oncology Journal

CONTEXT

Key Objective

To develop a tool for processing free-text clinical trial inclusion and exclusion criteria and matching patients to relevant clinical trials.

Knowledge Generated

The automated tool for criteria extraction and patient-trial matching demonstrated acceptable performance and significantly reduced manual workload. However, the tool failed to identify key criteria extracted by human abstractors.

Relevance

Automated clinical trial inclusion and exclusion criteria extraction can be combined with manual subject matter review to optimize clinical trials matching performance while reducing human workload.

MatchGraft.AI

Making transplants safer!



MatchGraft.AI

- Can predict each patient's absolute individual risk to develop severe acute GvHD depending on different potential donors, graft manipulations, prophylaxis and conditioning regimens.
- Is a machine learning (ML) based algorithm that uses artificial intelligence (AI).
- Enables physicians to select the best - matched donor, adapt SCT conditioning, and adjust GvHD prophylaxis
- Improves automatically with extended use
- Takes numerous established and experimental biological parameters into account, while also compensating for missing parameters
- Assesses and evaluates interactions of numerous parameters, which is humanly impossible
- Revolutionizes bone marrow transplantation donor - patient matching



2-4 Ottobre 2023

Deep Learning Staging of Liver Iron Content From Multiecho MR Images



healthcare

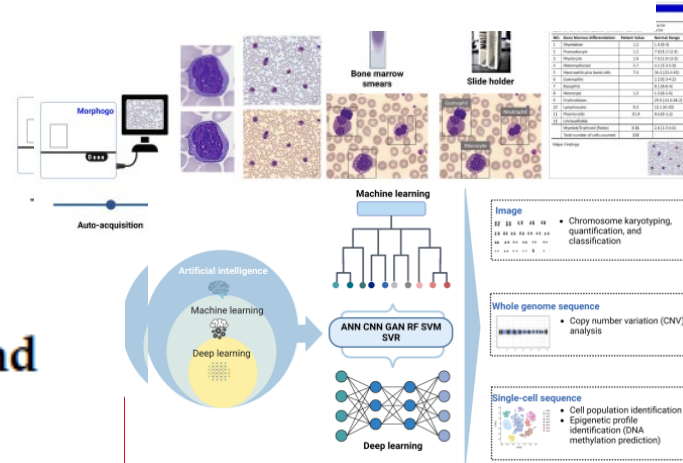


Cell Type	Diameter	Lifespan in Blood	Number of Cells	Function
Red cells	6-8	120 days	Male: $4.5 - 6.5 \times 10^6$ Female: $3.9 - 5.6 \times 10^6$	Conveyance of oxygen and carbon dioxide
Platelets	0.5-3.0	10 days	$140 - 400 \times 10^3$	Hemostasis
Phagocytes				
Neutrophils	12-15	6-10 h	$1.9 - 7.6 \times 10^3$ (46-76%)	Protection against organisms such as bacteria and fungi
Monocytes	12-20	20-40 h	$0.2 - 0.8 \times 10^3$ (2.5-8.5%)	Protection against organisms such as bacteria and fungi
Eosinophils	12-15	Days	$0.04 - 0.44 \times 10^3$ (0.5%)	Protection against parasites
Basophils	12-15	Days	$0.01 - 0.1 \times 10^3$ (<1.5%)	Release histamine for inflammatory responses
Lymphocyte B T	7-9 (resting) 12-20 (active)	Weeks or years	$1.5 - 3.5 \times 10^3$ (10-41%)	B-cells: Reduces antibodies and antibody activation of T-cells T-cells: Protection against viruses, immune functions.



Article

A New Artificial Intelligence Approach Using Extreme Learning Machine as the Potentially Effective Model to Predict and Analyze the Diagnosis of Anemia



1 Review Artificial Intelligence-Assisted Diagnostic Cytology and Genomic Testing for Hematologic Disorders

Validating AI in Haematological Diseases

Our goals



ENHANCE

Diagnostic capacity



EVALUATE

Treatment alternatives



PREDICT

Disease outcomes and
treatment response



ESTIMATE

Drug repurposing

Pilots

Myelodysplastic
syndromes

LEARN MORE

Multiple
Myeloma

LEARN MORE

Sickle Cell
Disease

LEARN MORE



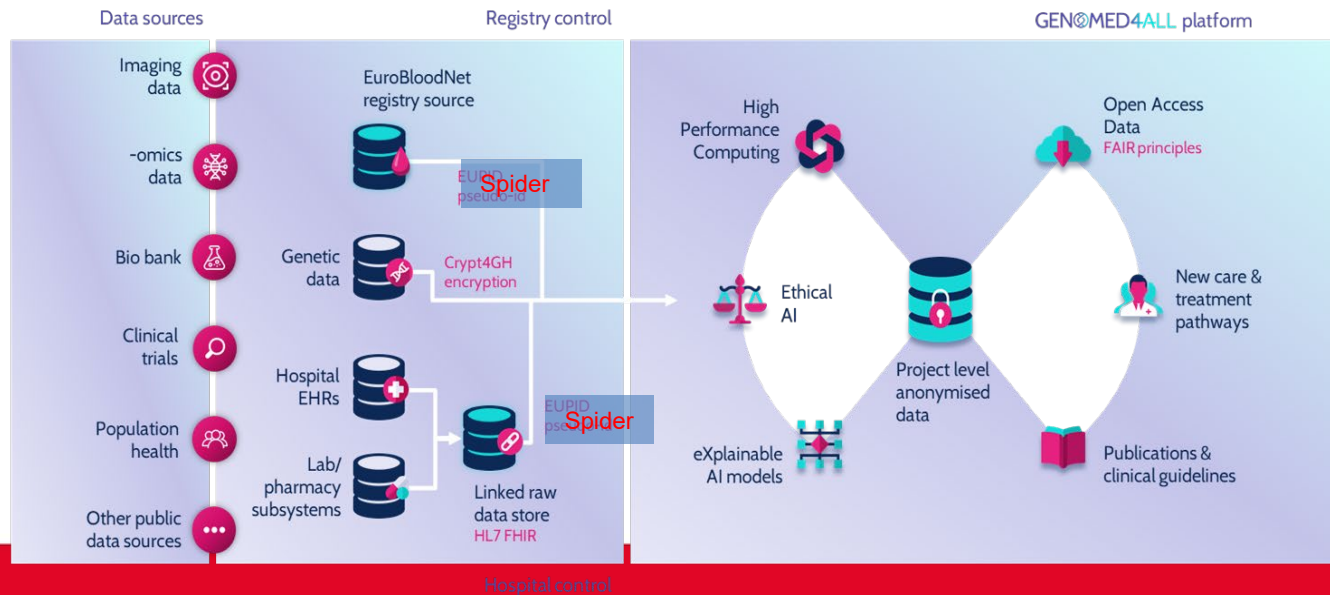
«Genomics and Personalized Medicine for all through Artificial Intelligence in Haematological Diseases»



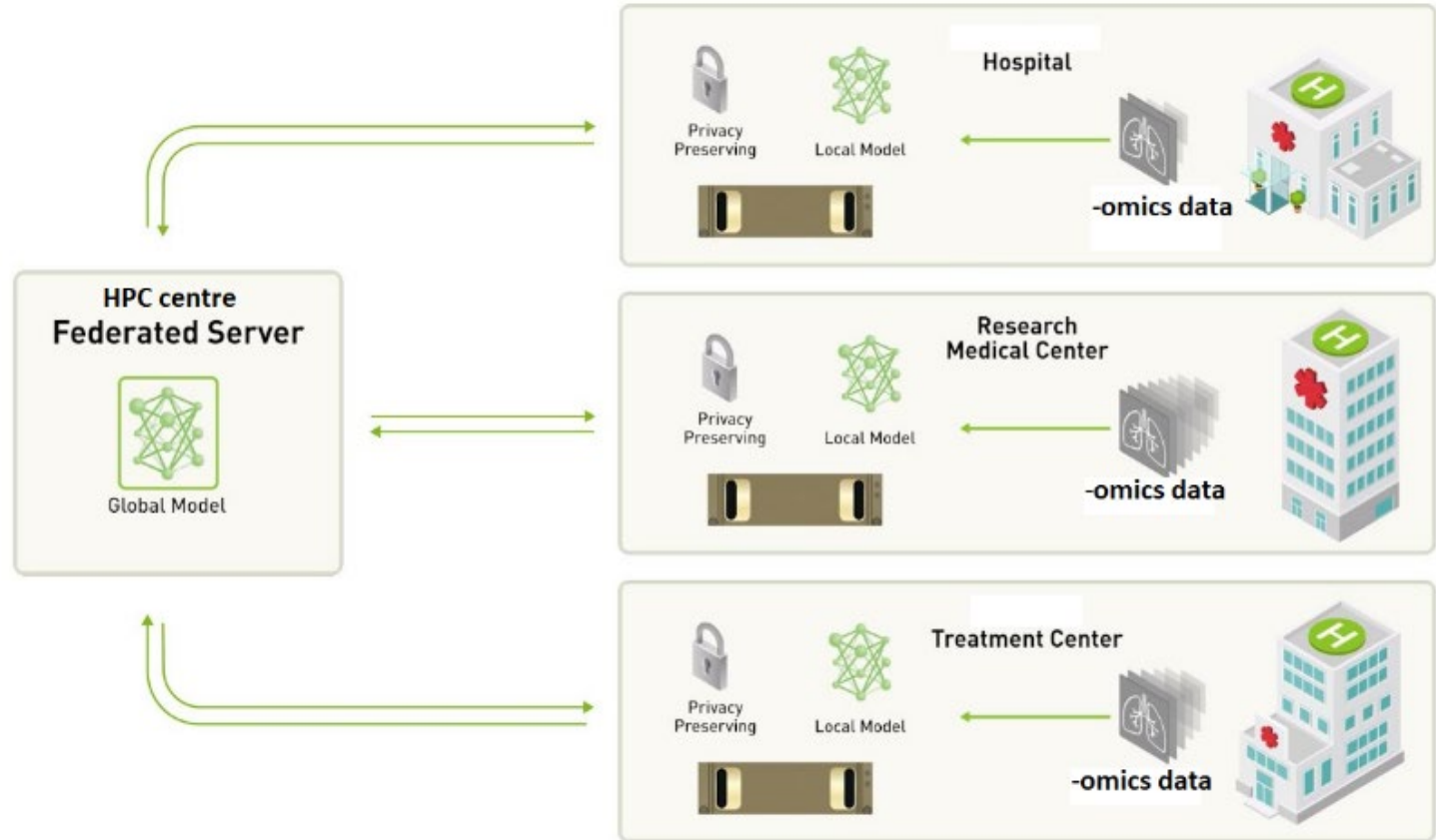
- The variety of assays and technologies has created a need to develop strategies for analyzing, integrating and interpreting the massive amounts of data they generate.
- Experiences with the use of AI techniques suggest that they might be particularly appropriate to analyze “big data”.

- GENOMED4ALL will support the pooling of genomic and clinical data through a secure and privacy respectful data sharing platform based on the novel Federated Learning scheme

OMOP



Federated Learning platform approach: A privacy respectful secure machine learning framework



Real-World Validation of Molecular International Prognostic Scoring System for Myelodysplastic Syndromes

CONTEXT

Key Objective

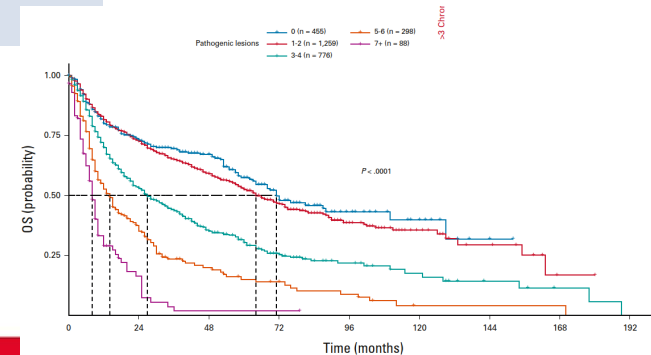
Are gene mutations relevant to improve the prediction of clinical outcomes in patients with myelodysplastic syndromes and to define the probability of response to currently available treatments?

Knowledge Generated

Molecular International Prognostic Scoring System (IPSS-M, including both clinical and genomic features) improves prognostic discrimination across all clinical end points compared with the currently available scores. In patients treated with allogeneic stem-cell transplantation, IPSS-M significantly improves the prediction of the risk of disease relapse and the probability of post-transplantation survival. In patients treated with hypomethylating agents, IPSS-M fails to stratify individual probability of response.

Relevance (C.F. Craddock)

The IPSS-M represents an important new prognostic model in patients with myelodysplastic syndromes and informs the rational selection of treatment strategies including stem-cell transplantation.*



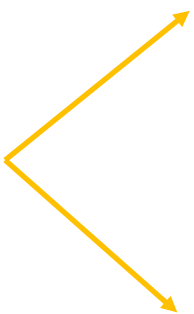
Synthetic hematological data over federated computing frameworks



Haematological diseases at the forefront of rare disease research

Can aid in solving problems due to:

- Data Availability
- Data Quality
- Data Privacy



Acute Myeloid
Leukemia
(Adults)

Sickle Cell
Disease
(Children-Adults)

Synthetic Data Generation by Artificial Intelligence to Accelerate Research and Precision Medicine in Hematology

JCO® Clinical Cancer Informatics

Saverio D'Amico, MEng¹; Daniele Dall'Olio, PhD²; Claudia Sala, PhD³; Lorenzo Dall'Olio, PhD²; Elisabetta Sauta, PhD¹; Matteo Zampini, PhD¹; Gianluca Asti, MSc¹; Luca Lanino, MD^{1,4}; Giulia Maggioni, MD^{1,4}; Alessia Campagna, MD¹; Marta Ubezio, MD¹; Antonio Russo, MD¹; Maria Elena Bicchieri, PhD¹; Elena Riva, BSc¹; Cristina A. Tentori, MD^{1,4}; Erica Travaglino, BSc⁴; Pierandrea Morandini, MEng¹; Victor Savevski, MEng¹; Armando Santoro, MD^{1,4}; Iñigo Prada-Luengo, PhD⁵; Anders Krogh, PhD⁵; Valeria Santini, MD⁶; Shahram Kordasti, MD^{7,8}; Uwe Platzbecker, MD⁹; Maria Diez-Campelo, MD¹⁰; Pierre Fenaux, MD¹¹; Torsten Haferlach, MD¹²; Gastone Castellani, PhD^{2,3}; and Matteo Giovanni Della Porta, MD^{1,4}

PURPOSE Synthetic data are artificial data generated without including any real patient information by an algorithm trained to learn the characteristics of a real source data set and became widely used to accelerate research in life sciences. We aimed to (1) apply generative artificial intelligence to build synthetic data in different hematologic neoplasms; (2) develop a synthetic validation framework to assess data fidelity and privacy preservability; and (3) test the capability of synthetic data to accelerate clinical/translational research in hematology.

METHODS A conditional generative adversarial network architecture was implemented to generate synthetic data. Use cases were myelodysplastic syndromes (MDS) and AML: 7,133 patients were included. A fully explainable validation framework was created to assess fidelity and privacy preservability of synthetic data.

CONCLUSION Synthetic data mimic real clinical-genomic features and outcomes, and anonymize patient information. The implementation of this technology allows to increase the scientific use and value of real data, thus accelerating precision medicine in hematology and the conduction of clinical trials.

CONTEXT

Key Objective

Are synthetic data able to recapitulate real clinical-genomic features and clinical outcomes, and to guarantee privacy preservability? Can this technology accelerate clinical/translational research in hematology?

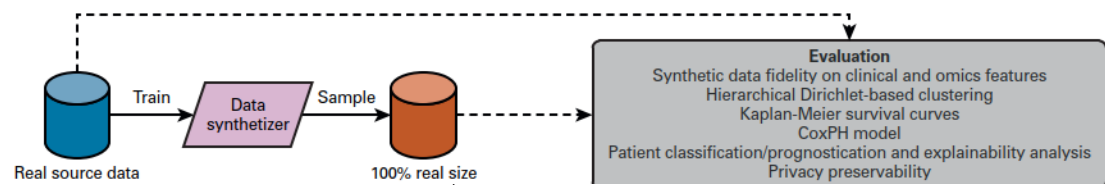
Knowledge Generated

We developed a new technology on the basis of generative artificial intelligence that allows to generate synthetic patient cohorts with high clinical fidelity and privacy performances. We created a prototype web portal for synthetic data generation to help clinicians to be familiar with this new technology.

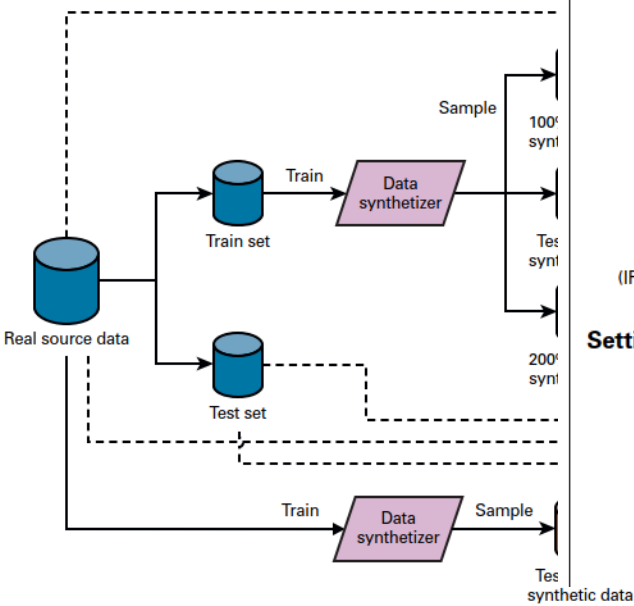
Relevance

This technology allows the resolution of lack/incomplete information and data augmentation starting from real patients. Synthetic data generate new knowledge to accelerate both translational research and the conduction of clinical trials.

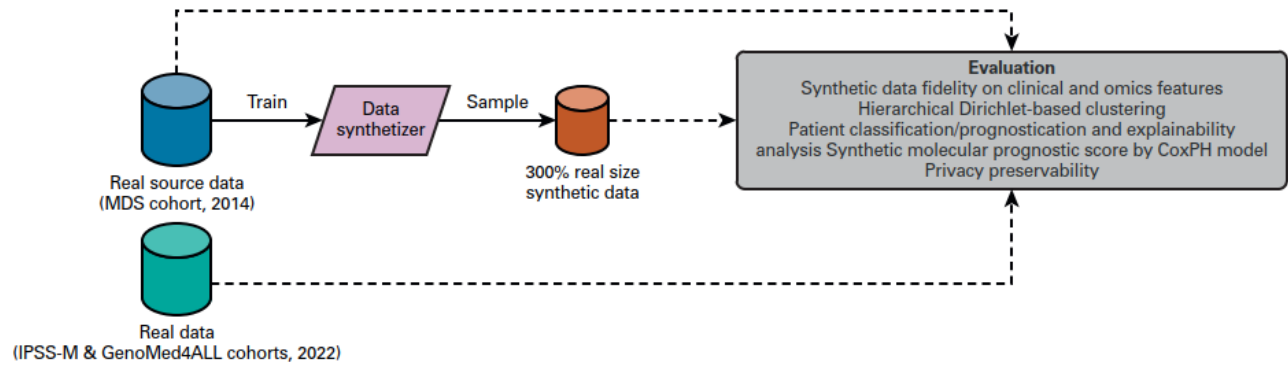
Setting A: Create a synthetic reliable and private copy of the real data



Setting B: Assessment of generated patients, data aug and generalizability of the generative model across difi



Setting C: Accelerating translational research



Setting D: Accelerating clinical research and design/conduction of clinical trials

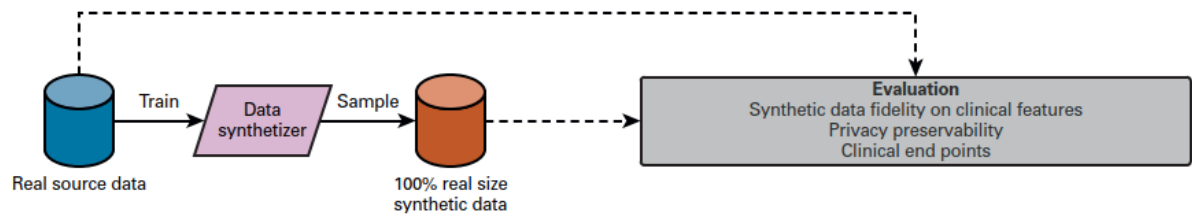


FIG 1. Overview of experimental settings to validate synthetic data. Setting A: Create a synthetic reliable and private copy of the real data. Setting B: Assessment of generated patients, data augmentation, privacy preservability, and generalizability of the generative model across different clinical settings. Setting C: Accelerating translational research. Setting D: Accelerating clinical research and design/conduction of clinical trials.

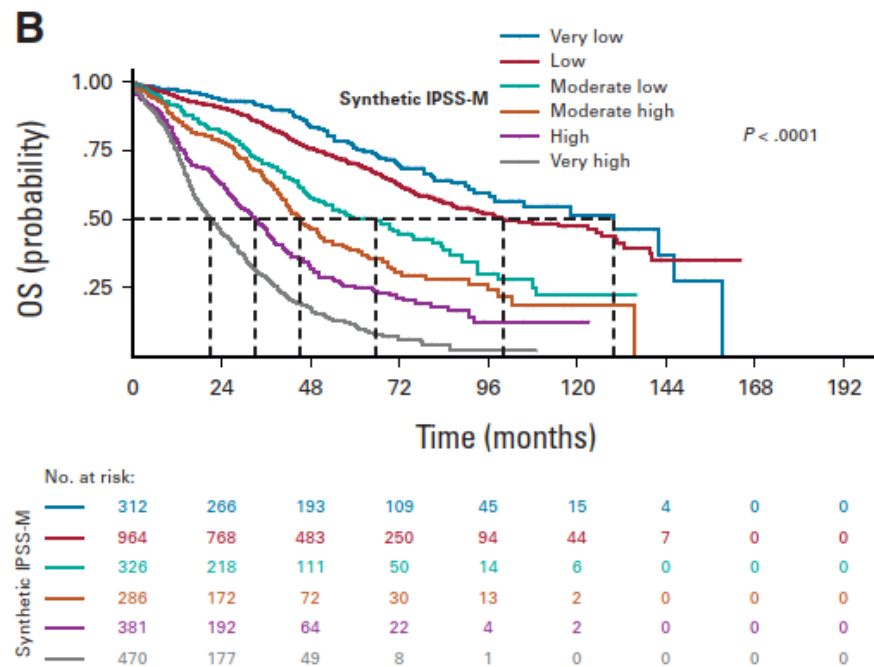
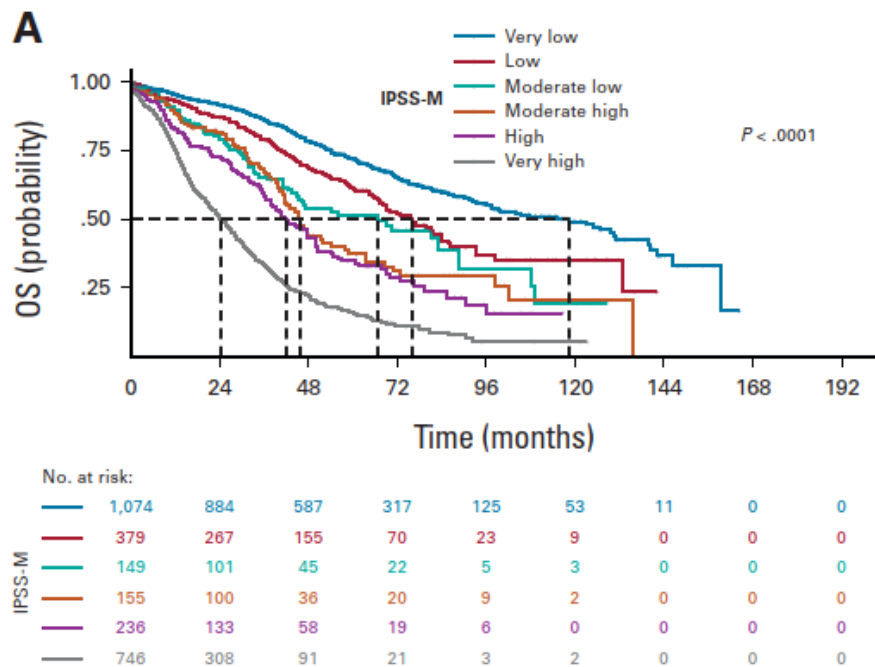
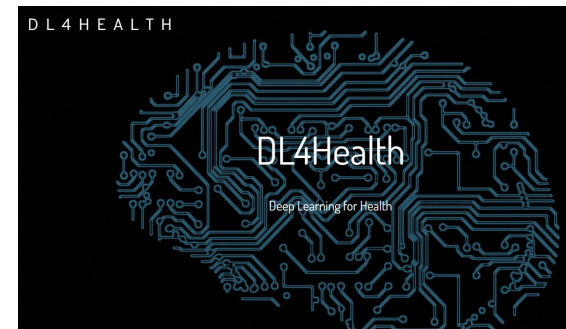


FIG 5. Survival analysis on synthetic molecular prognostic score generated (synthetic IPSS-M) performed in setting C. (A) Kaplan-Meier probability estimates of OS for synthetic patients with MDS are represented and stratified by IPSS-M risk categories as defined by Bernard et al.²¹ P value is from log-rank test. (B) Kaplan-Meier probability estimates of OS for synthetic patients with MDS are represented and stratified by synthetic IPSS-M risk categories. P value is from log-rank test. (C) Percentage of patients in each IPSS-M risk category (both synthetic and original) with the HRs for each outcome, and the median survival for each patient class, where values could be calculated. HR, hazard ratio; IPSS-M, Molecular International Prognostic Scoring System; LFS, leukemia-free

Progetto inteso a sviluppare un approccio innovativo per l'individuazione di **fattori che influiscono sul processo decisionale clinico, organizzativo ed assistenziale**, con lo sviluppo di un prototipo in Onco-ematologia Pediatrica



Prototipo informatizzato, che, alimentato dai **dati sanitari esistenti (cartelle, anagrafiche, laboratorio, flussi informatici aziendali....)**, opportunamente anonimizzati, consente di essere interrogato per valutare trend, cambiamenti, fenomeni che non sarebbero visibili analizzando in unico database



Map the current landscape of AI applications for Childhood Cancer to understand how AI can help improve care pathways in the EU



Unconnected data silos still exist and this fragmentation is often caused by the lack of a common approach for the definition, application and interconnection of data in the healthcare realm. We believe AI can be key in bringing a solution to these challenges.



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DEGLI STUDI
DI PADOVA

Conclusions

- AI involvement in medicine is an opportunity to improve diagnosis and clinical medicine
- Many examples of its application in pediatric hematology oncology are becoming available
- Need of a «training» on AI for physicians
- Need of multidisciplinary teams

