

World Journal of *Gastroenterology*

Weekly Volume 31 Number 24 June 28, 2025



REVIEW

Dutt K, Vasudevan A, Hodge A, Nguyen TL, Srinivasan AR. Cardiometabolic diseases in patients with inflammatory bowel disease: An evidence-based review. *World J Gastroenterol* 2025; 31(24): 107661 [DOI: 10.3748/wjg.v31.i24.107661]

Chen ZL, Wang C, Wang F. Revolutionizing gastroenterology and hepatology with artificial intelligence: From precision diagnosis to equitable healthcare through interdisciplinary practice. *World J Gastroenterol* 2025; 31(24): 108021 [DOI: 10.3748/wjg.v31.i24.108021]

MINIREVIEWS

Wang JY, Yi B, Li CY, Xu HQ, Tang SH. Pay attention to the value of liver regeneration in the re-compensation of decompensated cirrhosis. *World J Gastroenterol* 2025; 31(24): 106564 [DOI: 10.3748/wjg.v31.i24.106564]

Wang QC, Jiao J, Zhang CQ. Application of artificial intelligence in portal hypertension and esophagogastric varices. *World J Gastroenterol* 2025; 31(24): 108508 [DOI: 10.3748/wjg.v31.i24.108508]

ORIGINAL ARTICLE**Retrospective Study**

Gao Z, Wang XY, Shen ZG, Liu JH, Wang XY, Wu SK, Jin X. Real-world comparison of chemotherapy plus bevacizumab with or without immunotherapy as first-line therapy in colorectal cancer. *World J Gastroenterol* 2025; 31(24): 108298 [DOI: 10.3748/wjg.v31.i24.108298]

Clinical Trials Study

Zhu JH, Liu X, Zhou W, Xu XN, Sheng WD, Han YL, Qiu XO, Liu YW, Qian YY, Liao Z, Li ZS. Carbonated soft drink for gastric preparation for magnetically controlled capsule endoscopy: An open-label randomized controlled trial. *World J Gastroenterol* 2025; 31(24): 105823 [DOI: 10.3748/wjg.v31.i24.105823]

Basic Study

Baek G, Singh R, Ha SE, Cho H, Padmanabhan S, Vishwanath V, Kim MS, Seon D, You J, Lee MY, Ro S. miR-10a-5p and miR-10b-5p restore colonic motility in aged mice. *World J Gastroenterol* 2025; 31(24): 104437 [DOI: 10.3748/wjg.v31.i24.104437]

Schulze S, Keshvari S, Miller GC, Bridle KR, Hume DA, Irvine KM. Perisurgical colony stimulating factor one treatment ameliorates liver ischaemia/reperfusion injury in rats. *World J Gastroenterol* 2025; 31(24): 108234 [DOI: 10.3748/wjg.v31.i24.108234]

LETTER TO THE EDITOR

Sonbare DJ. Approaches to laparoscopic anatomic liver resection: Does one size fit all? *World J Gastroenterol* 2025; 31(24): 104907 [DOI: 10.3748/wjg.v31.i24.104907]

Semash K, Dzhanbekov T. Redefining the treatment paradigm for esophageal gastrointestinal stromal tumors: The emerging role of endoscopic resection. *World J Gastroenterol* 2025; 31(24): 106440 [DOI: 10.3748/wjg.v31.i24.106440]

ABOUT COVER

Editorial Board Member of *World Journal of Gastroenterology*, Zoltán Rakonczay Jr, DSc, MD, PhD, Professor, Department of Pathophysiology, University of Szeged, Szeged 6701, Hungary. rakonczay.zoltan@med.u-szeged.hu

AIMS AND SCOPE

The primary aim of *World Journal of Gastroenterology* (WJG, *World J Gastroenterol*) is to provide scholars and readers from various fields of gastroenterology and hepatology with a platform to publish high-quality basic and clinical research articles and communicate their research findings online. WJG mainly publishes articles reporting research results and findings obtained in the field of gastroenterology and hepatology and covering a wide range of topics including gastroenterology, hepatology, gastrointestinal endoscopy, gastrointestinal surgery, gastrointestinal oncology, and pediatric gastroenterology.

INDEXING/ABSTRACTING

The WJG is now abstracted and indexed in Science Citation Index Expanded (SCIE), MEDLINE, PubMed, PubMed Central, Scopus, Reference Citation Analysis, China Science and Technology Journal Database, and Superstar Journals Database. The 2025 edition of Journal Citation Reports® cites the 2024 journal impact factor (JIF) for WJG as 5.4; Quartile: Q1. The WJG's CiteScore for 2024 is 8.1.

RESPONSIBLE EDITORS FOR THIS ISSUE

Production Editor: *Wen-Bo Wang*, Production Department Director: *Xiang Li*, Cover Editor: *Jia-Ru Fan*.

NAME OF JOURNAL

World Journal of Gastroenterology

ISSN

ISSN 1007-9327 (print) ISSN 2219-2840 (online)

LAUNCH DATE

October 1, 1995

FREQUENCY

Weekly

EDITORS-IN-CHIEF

Andrzej S Tarnawski

EXECUTIVE ASSOCIATE EDITORS-IN-CHIEF

Xian-Jun Yu, Jian-Gao Fan, Hou-Bao Liu

EDITORIAL BOARD MEMBERS

<http://www.wjgnet.com/1007-9327/editorialboard.htm>

PUBLICATION DATE

June 28, 2025

COPYRIGHT

© 2025 Baishideng Publishing Group Inc

PUBLISHING PARTNER

Shanghai Pancreatic Cancer Institute and Pancreatic Cancer Institute, Fudan University
Biliary Tract Disease Institute, Fudan University

INSTRUCTIONS TO AUTHORS

<https://www.wjgnet.com/bpg/gerinfo/204>

GUIDELINES FOR ETHICS DOCUMENTS

<https://www.wjgnet.com/bpg/GerInfo/287>

GUIDELINES FOR NON-NATIVE SPEAKERS OF ENGLISH

<https://www.wjgnet.com/bpg/gerinfo/240>

PUBLICATION ETHICS

<https://www.wjgnet.com/bpg/GerInfo/288>

PUBLICATION MISCONDUCT

<https://www.wjgnet.com/bpg/gerinfo/208>

POLICY OF CO-AUTHORS

<https://www.wjgnet.com/bpg/GerInfo/310>

ARTICLE PROCESSING CHARGE

<https://www.wjgnet.com/bpg/gerinfo/242>

STEPS FOR SUBMITTING MANUSCRIPTS

<https://www.wjgnet.com/bpg/GerInfo/239>

ONLINE SUBMISSION

<https://www.f6publishing.com>

PUBLISHING PARTNER'S OFFICIAL WEBSITE

<https://www.shca.org.cn>
<https://www.zs-hospital.sh.cn>



Revolutionizing gastroenterology and hepatology with artificial intelligence: From precision diagnosis to equitable healthcare through interdisciplinary practice

Zhi-Li Chen, Chao Wang, Fang Wang

Specialty type: Gastroenterology and hepatology

Provenance and peer review: Invited article; Externally peer reviewed.

Peer-review model: Single blind

Peer-review report's classification

Scientific Quality: Grade A, Grade B, Grade B

Novelty: Grade A, Grade B, Grade B

Creativity or Innovation: Grade A, Grade B, Grade B

Scientific Significance: Grade A, Grade B, Grade B

P-Reviewer: Zhang YG; Zhao X

Received: April 3, 2025

Revised: April 21, 2025

Accepted: June 4, 2025

Published online: June 28, 2025

Processing time: 84 Days and 18.3 Hours



Zhi-Li Chen, Chao Wang, Fang Wang, Department of Pathogen Biology, College of Basic Medical Sciences, Jilin University, Changchun 130021, Jilin Province, China

Zhi-Li Chen, Chao Wang, Fang Wang, State Key Laboratory for Diagnosis and Treatment of Severe Zoonotic Infectious Diseases, Jilin University, Changchun 130021, Jilin Province, China

Chao Wang, Fang Wang, Jilin Provincial Engineering Laboratory of Precision Prevention and Control for Common Diseases, Jilin University, Changchun 130021, Jilin Province, China

Co-first authors: Zhi-Li Chen and Chao Wang.

Corresponding author: Fang Wang, Doctor, Professor, Department of Pathogen Biology, College of Basic Medical Sciences, Jilin University, No. 126 Xinmin Street, Changchun 130021, Jilin Province, China. wf@jlu.edu.cn

Abstract

Artificial intelligence (AI) is driving a paradigm shift in gastroenterology and hepatology by delivering cutting-edge tools for disease screening, diagnosis, treatment, and prognostic management. Through deep learning, radiomics, and multimodal data integration, AI has achieved diagnostic parity with expert clinicians in endoscopic image analysis (e.g., early gastric cancer detection, colorectal polyp identification) and non-invasive assessment of liver pathologies (e.g., fibrosis staging, fatty liver typing) while demonstrating utility in personalized care scenarios such as predicting hepatocellular carcinoma recurrence and optimizing inflammatory bowel disease treatment responses. Despite these advancements challenges persist including limited model generalization due to fragmented datasets, algorithmic limitations in rare conditions (e.g., pediatric liver diseases) caused by insufficient training data, and unresolved ethical issues related to bias, accountability, and patient privacy. Mitigation strategies involve constructing standardized multicenter databases, validating AI tools through prospective trials, leveraging federated learning to address data scarcity, and developing interpretable systems (e.g., attention heatmap visualization) to enhance clinical trust. Integrating generative AI, digital twin technologies, and establishing unified ethical/regulatory frameworks will accelerate AI adoption in primary care and foster equitable healthcare access while interdisciplinary collaboration and

evidence-based implementation remain critical for realizing AI's potential to redefine precision care for digestive disorders, improve global health outcomes, and reshape healthcare equity.

Key Words: Artificial intelligence; Precision medicine; Gastroenterology; Hepatology; Multimodal data integration; Deep learning; Microbiome

©The Author(s) 2025. Published by Baishideng Publishing Group Inc. All rights reserved.

Core Tip: This review highlights artificial intelligence (AI)-driven innovations in gastroenterology and hepatology, demonstrating breakthroughs in endoscopic/image analysis, multi-omics integration, and precision therapy. AI achieves diagnostic parity with experts in detecting early cancers and fibrosis, while addressing challenges like data fragmentation and bias through standardized databases, federated learning, and explainable systems. The study emphasizes interdisciplinary collaboration and ethical frameworks to advance equitable healthcare access and redefine digestive disease management.

Citation: Chen ZL, Wang C, Wang F. Revolutionizing gastroenterology and hepatology with artificial intelligence: From precision diagnosis to equitable healthcare through interdisciplinary practice. *World J Gastroenterol* 2025; 31(24): 108021

URL: <https://www.wjgnet.com/1007-9327/full/v31/i24/108021.htm>

DOI: <https://dx.doi.org/10.3748/wjg.v31.i24.108021>

INTRODUCTION

The development of artificial intelligence (AI) applications in medicine dates back to the mid-20th century, and the combination of its technological evolution and medical needs has driven several key breakthroughs. Early explorations were represented by expert systems, such as the MYCIN system developed in 1975, which first realized rule-based diagnosis of infectious diseases[1]. This phase of research laid the foundation for subsequent AI logical reasoning in medicine, but the scope of application was limited due to the scale of data and computational power at that time. Machine learning technology emerged from the 1990s to the beginning of the 21st century. Machine learning algorithms such as support vector machines (SVMs) have emerged in medical data classification, and in a 2004 machine learning study exploring the impact of genetic polymorphisms on breast cancer risk, SVMs became the optimal model at the time for distinguishing between breast cancer and normal controls by comprehensively analyzing the three key single nucleotide polymorphism loci with a prediction accuracy of 69%, revealing the multi-gene single nucleotide polymorphism combination's synergistic advantage for cancer risk assessment[2]. Meanwhile, research on artificial neural networks continued to advance, with Lecun *et al*'s team realizing handwritten character recognition through LeNet, a convolutional neural network (CNN) architecture, in 1998, providing the basis for medical image analysis[3]. After 2010, the explosive development of deep learning technology completely changed the landscape of medical AI. 2012 AlexNet's breakthrough performance in the ImageNet competition pushed the widespread application of CNN in medical imaging[4].

The current medical AI technology system covers machine learning, deep learning and natural language processing technologies, and the algorithms include SVM, decision trees, random forests, logistic regression, CNN, recurrent neural networks, long and short-term memory networks, transformer, generative adversarial networks (GAN) and other algorithms. Machine learning algorithms have played an important role in medical image analysis and disease diagnosis. For example, algorithms such as SVM and random forests excel at processing structured data and can be used for disease risk prediction and diagnostic support. In the lung nodule segmentation task, the dice similarity coefficient of the fully automated lung nodule segmentation model constructed on the basis of random forest can reach 0.986[5]. Deep learning models, especially CNN and Transformer, have made significant progress in medical image analysis and multimodal data fusion. Among them, CNNs still dominate the field of medical image parsing[6]. In 2017, deep CNNs can reach a level comparable to experts in skin cancer classification[7]. Vision transformer achieves global feature extraction through the self-attention mechanism and demonstrates performance beyond traditional CNNs in analysis such as computed tomography three-dimensional (3D) reconstruction and full-slice pathology images[8-11]. Natural language processing technologies are important in medical text processing and information extraction, which cover several healthcare scenarios such as clinical practice, hospital management, personal care, public health and drug development[12]. Natural language processing facilitates the translation of cancer treatment from laboratory to clinic by mining unstructured text data in electronic medical records. It empowers oncologists to construct evidence-based research frameworks in case identification, staging, and outcome quantification. In this way, natural language processing lays a technological foundation for the advancement of an efficient and precise cancer diagnosis and treatment system[13].

Global cancer statistics for 2022 show that cancers of the digestive tract are one of the major threats to human life and health, with esophageal, gastric, liver, and colorectal cancers having the seventh, fifth, third, and second highest mortality rates in the world, respectively[14,15]. And due to the lack of specific symptoms and early diagnostic markers in the early stages, there is a large number of potential patients who remain undiagnosed, resulting in the majority of patients often being diagnosed at a late stage[16-18]. Improving early detection of gastroenterological cancers is urgently needed. Benign ulcerative colorectal diseases, such as ulcerative colitis (UC), Crohn's disease, ischemic colitis, and intestinal tuber-

culosis, still require accurate diagnostic typing and appropriate therapeutic strategies by clinicians due to the fact that such diseases have similar phenotypes and but different etiologies and therapeutic strategies, however, AI may be able to accomplish the nuanced typing of the diseases with the advantage of its algorithm[19]. Therefore, there is an important need for the introduction of AI techniques in gastroenterological diseases. Moreover, current studies have shown that AI technologies exhibit great potential in the early detection, diagnosis, treatment planning, and prognosis prediction of gastrointestinal cancers, *e.g.*, AI is able to improve the sensitivity and specificity of tumor screening through medical image analysis and support intraoperative assessment of the depth of tumor invasion and prediction of the treatment response to optimize personalized treatment plans[20]. Furthermore, applying AI to pathology has significantly improved diagnostic efficiency and accuracy, surpassing the performance of human experts[18]. The application of AI in gastrointestinal diseases is summarized as shown in Figure 1. Although AI technology is reshaping the diagnosis and treatment paradigm of digestive diseases, and its application has crossed over from single-modality assisted diagnosis to multidimensional, chain-wide intelligent decision-making systems, there are still some unresolved issues, such as the crisis of trust of patients in AI, the issue of patient privacy, and ethical norms. In summary, this paper will systematically review the breakthrough progress of AI in the diagnosis and treatment of digestive diseases, focusing on the dissection of its translational value in early warning, precise staging, treatment optimization and prognostic management, as well as elaborate the current problems and possible future solutions for the large-scale promotion of AI in digestive diseases, and further explore the key challenges of multimodal data fusion, interpretability enhancement, data privacy protection and clinical landing of the future development direction. We expect that this review will provide the latest research progress and unique contributions on AI in gastroenterology and hepatology, break through the original limitations through emerging AI tools or algorithms such as multimodal data integration, interpretable AI systems, or new ethical frameworks adopted by AI, and provide a comprehensive overview for clinical researchers and AI enthusiasts, as well as insights and ideas to further ground the clinical translation of AI.

BREAKTHROUGHS IN AI FOR GASTROINTESTINAL DISEASE DIAGNOSIS AND TREATMENT

Recent advancements in AI have catalyzed transformative applications across gastrointestinal disease diagnostics and therapeutics, with machine learning and deep learning emerging as distinct yet complementary paradigms. As summarized in Table 1[21-51], machine learning algorithms including SVM, random forests, and gradient boosting have demonstrated robust performance in structured data analysis, particularly for risk stratification and treatment response prediction. For instance, SVM-based models achieved 98.5% accuracy in differentiating celiac disease from non-celiac duodenitis by analyzing duodenal histopathological features, while ensemble methods improved recurrence risk stratification in Crohn's disease [area under the curve (AUC) = 0.84].

In parallel, Table 2[52-77] highlights the ascendancy of deep learning architectures, notably CNNs and vision transformers in processing high-dimensional imaging and multimodal data. These systems have achieved human-expert parity in endoscopic image interpretation, with CNN models attaining 99% sensitivity for polyp detection and transformer-based frameworks enabling 3D lesion quantification in computed tomography enterography ($\kappa = 0.83$). The integration of attention mechanisms and federated learning has further enhanced model generalizability across heterogeneous datasets, addressing longstanding challenges in rare disease analysis.

AI applications for inflammatory gastrointestinal diseases

AI demonstrates multidimensional value in the management of UC and Crohn's disease. In the field of UC, deep learning-based histologic scoring systems (*e.g.*, PICaSSO histologic remission index) are highly correlated with endoscopic scores (Mayo, PICaSSO) and clinical outcomes (intraclass correlation coefficient = 0.84), with AI-assisted diagnostic sensitivity of 78% and specificity of 91.7%[78]. By quantifying features such as neutrophil extravasation, a CNN can predict Nancy's histologic index score ($\kappa = 0.91$) and accurately determine histologic remission (97% accuracy)[79,80]. AI also predicts the risk of recurrence by the "vascular healing" status in endoscopic images, with a significantly higher recurrence rate in the vasoactive group (23.9%) than in the vascular healing group (3.0%)[81], and a recurrence rate of up to 45% in patients with a rectal cuprocyte mucus area $\leq 12\%$ [82].

In addition, the UC-severity classification and localized extent (SCALE) algorithm enables topological visualization of disease severity by automating the assessment of inflammation distribution in full-length colonoscopy videos (86.5% accuracy, $\kappa = 0.813$)[83].

For Crohn's disease, a multimodal machine learning model integrating magnetic resonance small bowel imaging and biochemical markers noninvasively assessed terminal ileal endoscopic activity with an AUC of 0.84[84]; and a deep learning model (SA-AbMILP) predicted Global Histologic Disease Activity scores from histologic images (65%-89% accuracy), which was in high agreement with the pathologist's findings[85]. For the prediction of postoperative recurrence, the EfficientNet-b5 model analyzed whole slide images of surgical specimens with an AUC as high as 0.995 and found adipocyte atrophy and mast cell infiltration to be key features of recurrence[86].

AI significantly improves the efficiency and accuracy of inflammatory gastrointestinal disease screening. In capsule endoscopy, CNN models can quickly identify ulcers, erosions, and vascular malformations (with 96.9%-99% sensitivity) with processing speeds up to 90 frames/second[87,88]; a sequential CNN model for Crohn's disease ulcer severity has an accuracy of 91% in identifying grade 3 ulcers[89]. In the field of colonoscopy, the FRCNN-AA-CIF model based on the attention mechanism and context fusion has a leakage rate of only 4.22% and the mean of average precision of all categories of detection of 0.817[90]; the ResNet50 migration learning model has an accuracy of 99.8% in the polyp classification task, which is superior to the traditional methods[91,92]. In imaging, 3D-CNN distinguished colon cancer from

Table 1 Recent advances in machine learning applications for gastrointestinal diseases (2022-2025)[21-51]

AI algorithm	Parameters employed/study design	Sample size/control group/ validation	Outcomes	Performance	Ref.
SVM	Multi-center data + TCGA validation	Total $n = 255$ (training 212 + internal validation 43); external: 4 centers + TCGA	OS/DFS risk stratification (low/moderate/high); high-risk stage II/III chemotherapy benefit	AUC training 0.773 (OS)/0.751 (DFS); validation 0.852 (OS)/0.837 (DFS)	Li <i>et al</i> [21]
SVM + APINet/TransFG	Tongue features (color/morphology/coating) + microbiome (16S rDNA); multicenter prospective study	Cohort 1: GC = 328 <i>vs</i> NGC = 304; cohort 2: GC = 937 <i>vs</i> NGC = 1911 (10 centers); external: GC = 294 <i>vs</i> NGC = 521 (7 centers)	Distinguish GC/early GC/precancerous lesions (<i>e.g.</i> , AG); superior to 8 blood biomarkers	Tongue model AUC: 0.89 (initial); 0.88-0.92 (internal); 0.83-0.88 (external); microbiome AUC: 0.94 (genus)/0.95 (species)	Yuan <i>et al</i> [22]
SVM/LR/kNN + feature selection	Liver/PBMC RNA-seq data	Liver = 67; PBMC = 137; external public dataset; controls: Healthy + AH/AC/MASLD/HCV	Precise differentiation of AH/AC/MASLD/HCV; minimal gene sets (33-75 genes)	Liver accuracy: 90% (AH/AC <i>vs</i> healthy), 91% (4-class); External 82%; PBMC accuracy: 75% (4-class)	Listopad <i>et al</i> [23]
SVM/LR/RF	Multiphase CT radiomics ($n = 851$)	Total $n = 215$ (training 150 + external 65)	Multiphase CT prediction (plain scan alternative)	Nomogram C-index 0.913 (95% CI: 0.878-0.956)	Liu <i>et al</i> [24]
SVM	Radiomics features extracted from CT images; integrated rad-score + clinicopathological characteristics	693 GC patients (2 centers); training ($n = 390$), internal validation ($n = 151$), external validation ($n = 152$) cohorts	Rad-scores significantly associated with diffuse-type GC and SRCC ($P < 0.001$)	Lauren nomogram: AUC = 0.895 (training), 0.841 (internal), 0.893 (external). SRCC nomogram: AUC = 0.905 (training), 0.845 (internal), 0.918 (external)	Chen <i>et al</i> [25]
Counterfactual random forest + optimal policy trees	Imatinib duration inferred <i>via</i> counterfactual model; OPTs interpreted counterfactual predictions	Internal: 117 (MSKCC); external: 363 (polish) + 239 (spanish)	OPTs recommended no imatinib for low-risk subgroups: Gastric GIST < 15.9 cm + mitotic count < 11.5/5 mm ² . Any site GIST < 5.4 cm + mitotic count < 11.5/5 mm ²	Sensitivity: 92.7% (internal), 95.4% (Spanish), 92.4% (Polish). Specificity: 33.9% (internal)	Bertsimas <i>et al</i> [26]
Markov decision tree model	Input variables from systematic review/meta-analysis of RCTs comparing DS, EUS-GE, and GJ; prospective cohort study for EUS-GE	15 studies in Markov model	1-month survival: DS (81.2%), EUS-GE (80.4%) > GJ (75.5%). 6-month survival: GJ (25.2%), EUS-GE (23.8%) > DS (21.3%)	EUS-GE and GJ outperformed DS for long-term palliation (6 months)	Chue <i>et al</i> [27]
Decision trees, LASSO, kNN, random forests	Pathomics features extracted from HE-stained WSIs; multicenter retrospective study	584 gastric cancer patients (training: 325, internal validation: 113, external validation 1:73, external validation 2:73)	Pathomics signature independently predicted progression-free survival ($P < 0.001$, HR = 0.34)	Training: AUC = 0.985; Internal validation: AUC = 0.921	Han <i>et al</i> [28]
Optimal classification trees	Input variables: Tumour size, mitotic count, tumour site	Internal: 395 patients (MSKCC + Spanish consortium); external: 556 patients (polish registry)	OCT significantly improved calibration compared to MSK nomogram	Higher C-index for OCT (0.805 <i>vs</i> 0.788); slope = 1.041 (OCT) <i>vs</i> 0.681 (MSK); no significant calibration error for OCT	Bertsimas <i>et al</i> [29]
Gradient-boosting decision tree	Baseline characteristics, endoscopic atrophy	Total: 1099 chronic gastritis patients, training: 879, test: 220	Key predictors: Age, OLGIM/OLGA stage, endoscopic atrophy, history of other malignancies	Harrell's c-index: 0.84 (test set). Stratified risk into 3 categories ($P < 0.001$)	Arai <i>et al</i> [30]
GBM	Prospective cohort study (15-year follow-up); 70% training and 30% validation split	FINRISK 2002 cohort: 7115 individuals (103 incident liver disease, 41 alcoholic liver disease)	Gut microbiome and conventional factors showed comparable predictive power	Liver disease: AUROC = 0.834 (microbiome + conventional) <i>vs</i> 0.768 (conventional); alcoholic liver disease: AUROC = 0.956 (microbiome + conventional) <i>vs</i> 0.875 (conventional)	Liu <i>et al</i> [31]
XGBoost (pre/delta-	Pre/post-treatment MRI	LARC patients $n = 84$;	Delta-radiomics > pre-	Pre-model: AUC 0.93	Wang <i>et al</i>

radiomics) + SMOTE	radiomics ($n = 105$); multisequence MRI integration	validation: 5/10-fold CV + independent; no control	radiomics	± 0.06 (train)/0.79 (test); delta-model: AUC 0.96 ± 0.03 (train)/0.83 (test)	[32]
sPLS-DA	Multi-site microbiome (saliva/esophagus/stomach); 16S rRNA analysis	EoE: Saliva = 29, biopsy = 25; controls: Non-EoE = 20 (saliva)/5 (biopsy)	Saliva model distinguishes EoE/non-EoE; esophageal microbiota detects disease activity	Saliva: CE 24%, validation Acc 78.6% (sensitivity 80%/specificity 75%); esophagus: CE 8% (activity detection)	Facchin <i>et al</i> [33]
sPLS-DA + LR	Genome-wide 5hmC features ($n = 64$); protein biomarkers	Healthy = 165; LC = 62; HCC = 135; longitudinal cohort	HCC diagnosis/recurrence prediction; tumor burden monitoring	Wild-score AUC = 93.24% (HCC vs non-HCC); HCC score AUC = 92.75% (HCC vs LC)	Cai <i>et al</i> [34]
LR + mixed-effects model	Multicohort clinical/serologic/genetic data; JAK-STAT/IL6 pathway	IBD patients = 12083 (4 cohorts); within-case design	Female/CD colonic location/surgery linked to EIMs; MHC/CPEB4 associations; therapeutic targets (TNE/JAK-STAT)	MHC OR = 2.5 ($P = 1.4E-15$); CPEB4 OR = 1.5 ($P = 2.7 \times 10^{-8}$); serologic panel OR = 1.7 ($P = 3.6 \times 10^{-19}$)	Khrom <i>et al</i> [35]
LR + RF + kNN + SVM + NN	Recursive feature elimination; single-center retrospective	Total $n = 864$ (IIIA + $n = 457$ vs low-risk $n = 407$); 3-fold imputation/CV	NN outperforms others (Acc 68.8%); best in medical complications (AUC = 0.695)	NN: Overall Acc 0.688/AUC = 0.672; medical AUC = 0.695; surgical AUC = 0.653; cologne score Acc 0.510	Jung <i>et al</i> [36]
RF vs cv-Enet/glmboost/ensemble	Multicenter preoperative features; elastic-net regularization	Development = 3182 (39 centers); validation = 260; no control	RF optimal prediction; surgical decision support	RF AUC = 0.844 (0.841-0.848) (development); similar in validation	Pera <i>et al</i> [37]
LR + Cox regression models	Endoscopic features (whitish/irregular) + Histology (marked IM); retrospective multicenter	Total $n = 182$ (malignant = 48); progression cohort = 98; ROC/KM validation	Misdiagnosis predictors (single/large/IM); progression predictors (whitish/margin/multi-diagnosis)	AUC 0.871 (sensitivity 68.7%/specificity 92.5%)	Zou <i>et al</i> [38]
RF + Swin transformer tongue model	Questionnaire features ($n = 10$) + tongue images; multicenter	Total $n = 2229$ (9 centers); validation AUC > 0.8	Key factors: Age/TCM constitution/tongue features/diet/anxiety; dynamic nomogram	RF Acc 85.65%; tongue model Acc 73.33% (validation)	Yu <i>et al</i> [39]
LR	Tumor location/ulceration/biopsy features; H-L test/DCA validation	Training = 516; validation = 220 (7:3 split); no control	4 fibrosis predictors; severe fibrosis prediction model	Raining AUC = 0.819; validation AUC = 0.812; DCA clinical benefit	Zeng <i>et al</i> [40]
Stepwise logistic regression	Demographics/history/Lab markers (AFP/AST/albumin); prospective multicenter	Total $n = 1723$; HCC events = 109; median follow-up 2.2 years; no control	Key factors: Male/cirrhosis duration/family history/age/obesity/AFP/AST	Incidence 24/100 person-years; multivariate OR 1.08-2.73 ($P < 0.05$)	Reddy <i>et al</i> [41]
Multivariate logistic regression	Radiomic features (peritumoral enhancement/necrosis); transcriptomic sequencing	Development = 470; validation: Control = 145 + HAIC = 143; multicenter	Imaging subtypes guide HAIC benefit; immune pathway correlation	Training AUC = 0.83; control AUC = 0.84; HAIC AUC = 0.73	Ma <i>et al</i> [42]
LR	Multiphase CT radiomics (peritumoral); RNA sequencing	Total $n = 773$ (training 334 + internal 142 + external 141 + survival 121 + RNA35); 4 centers	MVI prediction + survival stratification (early recurrence/OS); glucose metabolism genes	Hybrid model AUC: 0.86 (internal)/0.84 (external); survival $P < 0.01$	Xia <i>et al</i> [43]
Multivariate logistic regression	LI-RADS visualization score (A/B/C); obesity class II-III	Total $n = 2053$ (A = 1685, B = 262, C = 106); longitudinal = 1546; multicenter	Alcohol/MASLD cirrhosis + obesity linked to limited visualization; 19.6% worsened/53.1% improved	Baseline limited rate 18%; obesity OR = 2.1 ($P < 0.001$)	Schoenberger <i>et al</i> [44]
Regularized LR + GBM	RCT secondary analysis; mailed outreach; prior screening behavior	Total $n = 1200$ (training 960 + test 240); 3 screening rounds; no control	Surveillance adherence stratification; key variables: Prior screening/primary care contact	AUROC 0.66-0.77 (increasing); 41%-47% completion rate	Singal <i>et al</i> [45]
LASSO logistic regression	Pre/intraoperative variables; multicenter international	Total $n = 2192$ (train 70% + valid 30%); 12 centers	Dual prediction (PHLF/CCI > 40); online risk calculators	PHLF AUC = 0.80 (calib. slope = 0.95); CCI AUC = 0.76	Wang <i>et al</i> [46]
LDpred2 PRS + QCancer-10 integration	Genetic/non-genetic factors; Cox proportional hazards	United Kingdom Biobank $n = 434587$;	C-index improvement (M + 7.3%/F + 6.5%); high-risk	Integrated C-index: 0.730 (M)/0.687 (F);	Briggs <i>et al</i> [47]

		case-control/survival validation	group 3.47 × (M)/2.77 × (F)	sensitivity/specificity: 47.8%/80.3% (M), 42.7%/80.1% (F)	
Multivariable logistic + Cox regression	Multicenter FS screening; long-term follow-up (median 17 years)	Intervention = 40085 (13 centers)	High-ADR group: Distal CRC HR = 0.34 (incidence)/0.22 (mortality); all-site CRC HR = 0.58/0.52	High vs low-ADR: Distal CRC HR 0.34 vs 0.55 (incidence), 0.22 vs 0.54 (mortality)	Cross <i>et al</i> [48]
RRR + elastic net models	Inflammatory markers (CRP/IL6/GDF15) + metabolic markers (BMI/waist/C-peptide); case-control	Total <i>n</i> = 1368 (cases 684 + controls 684); NHS = 818F + HPFS = 550M	Sex-specific: Median OR = 1.34 (inflammation)/1.25 (metabolic); NS in F; 11 key metabolites	Variance explained: 24% (inflammation)/27% (metabolic)	Bever <i>et al</i> [49]
RSF/GBM/Deep hit	Multivariable analysis + clinical feature selection; time-dependent C-index	CRC patients = 2157; stratified 5-fold CV (5 repeats)	Deep hit best discrimination; RSF best calibration; SHAP key factors (R0 resection/TNM)	Deep hit C-index 0.789 (0.779-0.799); RSF brier 0.096 (0.094-0.099)	Yang <i>et al</i> [50]
Multivariable logistic regression	Cell search CTCs detection; prospective CTCs + retrospective HGP; excluded neoadjuvant/extrahepatic	Total <i>n</i> = 177 (dHGP = 34, 19%); multivariable validation; no external cohort	CTC-negativity predicts dHGP (OR = 2.7); dHGP better survival	OR = 2.7 (1.1-6.8), <i>P</i> = 0.028	Meyer <i>et al</i> [51]

SVM: Support vector machine; TCGA: The Cancer Genome Atlas; OS: Overall survival; DFS: Disease-free survival; AUC: Area under the curve; APINet: Attentive pairwise interaction neural network; TransFG: Transformer architecture for fine-grained recognition; GC: Gastric cancer; NGC: Non-gastric cancers; AG: Atrophic gastritis; LR: Logistic regression; kNN: K-nearest neighbors; PBMC: Peripheral blood mononuclear cells; RNA-seq: Ribonucleic acid sequencing; AH: Alcohol-associated hepatitis; AC: Alcohol-associated cirrhosis; MASLD: Metabolic dysfunction-associated steatotic liver disease; HCV: Hepatitis C virus; CT: Computed tomography; SRCC: Signet ring cell carcinoma; CI: Confidence interval; RF: Random forest; OPT: Optimal policy trees; MSKCC: Memorial Sloan Kettering Cancer Center; GIST: Gastrointestinal stromal tumours; RCT: Randomized controlled trials; DS: Duodenal stenting; EUS-GE: Endoscopic ultrasound-guided gastroenterostomy; GJ: Gastrojejunostomy; HE: Hematoxylin and eosin; WSI: Whole slide image; LASSO: Least absolute shrinkage and selection operator; HR: Hazard ratio; MSK: Memorial Sloan Kettering; GBM: Gradient boosting machine; OLGIM: Operative link on gastritis-intestinal metaplasia assessment; OPGA: Operative link on gastritis assessment; AUROC: The area under the receiver operating characteristic curve; XGBoost: eXtreme gradient boosting; SMOTE: Synthetic minority oversampling technique; sPLS-DA: Sparse partial least squares-discriminant analysis; MRI: Magnetic resonance imaging; CV: Cross validation; EoE: Eosinophilic oesophagitis; Acc: Accuracy; CE: Classification error; NN: Neural network; JAK: Janus kinase; STAT: Signal transducers and activators of transcription; IL-6: Interleukin-6; LC: Liver cirrhosis; HCC: Hepatocellular carcinoma; IBD: Inflammatory bowel disease; CD: Crohn's disease; EIM: Extraintestinal manifestations; MHC: Major histocompatibility complex; CPEB4: Cytoplasmic polyadenylation element binding protein 4; TNF: Tumor necrosis factor; OR: Odds ratio; IM: Intestinal metaplasia; ROC: Receiver operating characteristic curve; KM: Kaplan-Meier; TCM: Traditional Chinese medicine; H-L: Hosmer-Lemeshow; DCA: Decision curve analysis; AFP: Alpha-fetoprotein; AST: Aspartate aminotransferase; HAIC: Hepatic arterial infusion chemotherapy; MVI: Microvascular invasion; LI-RADS: Liver imaging, reporting and data system; PHLF: Posthepatectomy liver failure; CCI: Comprehensive complication index; M: Male; F: Female; ADR: Adenoma detection rate; CRC: Colorectal cancer; FS: Flexible sigmoidoscopy; CRP: C-reactive protein; GDF15: Growth differentiation factor 15; BMI: Body mass index; NS: Neither signature; RSF: Random survival forest; SHAP: SHapley Additive exPlanations; TNM: Tumor-node-metastasis; CTCs: Circulating tumour cells; HGP: Histopathological growth pattern; dHGP: Desmoplastic histopathological growth pattern.

acute diverticulitis by computed tomography images (sensitivity 83.3%, specificity 86.6%), and AI support enabled radiologists to increase the sensitivity to 85.6%[93]. For data-scarce scenarios, computed tomography colon segmentation adopts a guided sequential scenario training strategy, which requires only 10 cases of annotation to achieve a dice coefficient of 97.15%, and its cross-layer feature comparison learning mechanism enables polyp detail retention to exceed 98.28%[94]. The most clinically translatable value is the hybrid architecture of 3D-CNN and random forest: By modeling spatial continuity, this model achieves a physician-level agreement of $\kappa = 0.83$ for the severity classification of 7.5-mm-level lesions in computed tomography enterography images, with a 91.51% accuracy in localizing moderate-to-severe lesions[95].

AI has also made breakthroughs in gastritis, celiac disease and small bowel disease. Multi-stage semantic segmentation model (AI-G) has an accuracy of 91% in gastric biopsy diagnosis, with significant cross-institutional validation robustness [96]; CNN can differentiate between *Helicobacter pylori* gastritis and autoimmune gastritis (with 100% diagnostic concordance)[97]. For celiac disease, the SVM model distinguishes between celiac disease and non-celiac duodenitis based on images of the duodenal lamina propria with 98.5% accuracy[98]. These innovations signal that AI is breaking through the traditional qualitative diagnostic framework and driving the transition of the diagnostic paradigm from qualitative detection to accurate quantitative assessment through interpretable feature engineering and anatomical constraint algorithms.

Recent advances in AI-enabled upper gastrointestinal tumor diagnosis and treatment

Deep learning-based endoscopic image analysis system significantly improves the efficiency and detection rate of upper gastrointestinal tumors. The study showed that the sensitivity of the GRAIDS system in diagnosing upper gastrointestinal cancer by analyzing more than 1 million endoscopic images (0.942) was comparable to that of expert endoscopists (0.945) and significantly better than that of non-experts ($P < 0.0001$), and its negative predictive value (0.978) was close to the level of experts (0.980), which demonstrated that AI can effectively assist grassroots hospitals in improving diagnostic capabilities[99]. For the determination of the depth of infiltration of early gastric cancer, the diagnostic model F1 value of

Table 2 Emerging deep learning approaches in gastrointestinal disease management (2022-2025)[52-77]

AI algorithm	Parameters employed/study design	Sample size, control group, validation	Outcomes	Performance	Ref.
CNN	14 EUS anatomical sites; multicenter validation	Training: 1812 patients/6230 images; internal: 47 patients/1569 images; external: 131 patients/85322 images	Outperformed novices in 11 sites; high expert agreement (kappa 0.84-0.98)	Internal Acc 92.1-100%; external sensitivity 89.45%-99.92%/specificity 93.35%-99.79%	Tian <i>et al</i> [52]
NNLS deconvolution + GCNN	Methylation atlas (TSMAs) + genome-wide density; multi-modal strategy	5 tumor types + WBC training; validation = 239 low-depth cfDNA	Multi-modal improves TOO in low-depth cfDNA	Validation Acc 69%	Nguyen <i>et al</i> [53]
CNN + survival MLP	CT + clinical multimodal data; 5-fold CV	GC patients = 1061; vs 3 SOTA methods; no control	Multimodal > single-modality; optimal OS/PFS prediction	OS C-index 0.849; PFS 0.783 (surpass SOTA)	Hao <i>et al</i> [54]
CNN	HE features for HER2 status; trastuzumab response	Surgical = 300; biopsy = 101; treated = 41; no control	HER2 amplification prediction; treatment response (CR + PR vs SD + PD)	Surgical AUC 0.847 (amplification)/0.903 (2+); biopsy 0.723; treatment 0.833	Wu <i>et al</i> [55]
DCNN	HE whole-slide imaging; fibrosis stage comparison	Non-HCC = 639; HCC = 46; paired training/unpaired validation	Detect HCC risk in mild fibrosis; saliency maps reveal nuclear atypia/immune infiltration	Training Acc 81.0% (AUC = 0.80); validation 82.3% (AUC = 0.84)	Nakatsuka <i>et al</i> [56]
Faster R-CNN model	Preoperative CT/MRI analysis; multicenter retrospective cohort (2012-2020)	Total <i>n</i> = 1141 (PCCCL = 62, CHCC = 1079); 4:1 split (train-val vs test); CHCC cases (<i>n</i> = 1079) as negative control	Differential diagnosis of rare PCCCL	Accuracy: 0.962 (95%CI: 0.931-0.992); AP: PCCCL 0.908, CHCC 0.907; Recall: 0.95	Liu <i>et al</i> [57]
Transformer	End-to-end biomarker prediction; multicenter validation	Total <i>n</i> > 13k (16 CRC cohorts); resection training/biopsy validation	Solved biopsy MSI diagnosis; improved interpretability	MSI detection: Sensitivity 0.99/NPV > 0.99	Wagner <i>et al</i> [58]
CNN + SMOTE/SVM	Pathomics/radiomics/immune score (CD3 +/CD8 +)/clinical; digital pathology	Lung metastasis = 103; internal validation	Path/radio features vs immunoscore (neg); triple independent prognosis	Integrated model: OS = 0.860/DFS = 0.875; Calib/DCA validated	Wang <i>et al</i> [59]
INSIGHT (CNN) + wise MSI (self-attention) two-stage	Tumor tile classification + ResNet pre-trained + attention pooling; multicenter	Chinese multicenter cohort; vs 5 DL methods	Outperforms SOTA in MSI prediction; high pathologist consistency	Wise MSI AUC 0.954 (0.948-0.960)	Chang <i>et al</i> [60]
CNN + RNN	Multicenter blinded trial; real-time monitoring + second observer	Total <i>n</i> = 946 (adenomas = 989); multicenter	CADe > human in adenoma detection (sensitivity 94.6% vs 96.0%); changed 2.3% follow-up	ADR + 1.1%/case; Non-neoplastic + 4.9%; time + 42.6% (6.6 minutes)	Sinonquel <i>et al</i> [61]
ANN	Pathological image analysis; retrospective multicenter	Training = 496 (GDPH); external validation = 150 (SYSMH)	Avoided 34.9% unnecessary surgeries; outperformed United States guidelines	Training AUC = 0.979; validation AUC = 0.978	Su <i>et al</i> [62]
Multitask transformer	Preop MRI multiparametric features; 7-center retrospective	Total <i>n</i> = 725 (train 234 + internal 58); external = 212/111/110	PA-TACE benefit in high-MVI/low-survival group (<i>P</i> < 0.001)	RFS C-index: Training 0.763/validation 0.628-0.728	Wang <i>et al</i> [63]
Multistage DL models	Longitudinal MRI (pre/post-TA) + clinical variables; multicenter retrospective	Total <i>n</i> = 289 (train 254 + external 35); 3 hospitals	DL clinical improved ER prediction (AUC = 0.740); High/low-risk RFS <i>P</i> = 0.04	DL clinical AUC: 0.740 vs 0.571/0.648/0.689	Kong and Li[64]
CNN	Clinical data + MRI radiomics; 6 time-frame prediction	Early HCC = 120 (recurrence = 44); retrospective (2005-2018)	Imaging model > clinical (AUC 0.76 vs 0.68, <i>P</i> = 0.03)	Imaging model AUC 0.71-0.85; KM <i>P</i> < 0.05 (2-6 years)	Iseke <i>et al</i> [65]
RSF/ANN/decision	Inflammatory markers + ALBI +	Total <i>n</i> = 808 (train 2:1 split)	ANN optimal (5	Training AUC 0.85	Zhang <i>et</i>

tree	AFP + tumor size + INR; single-center retrospective		years AUC = 0.85); High-risk OS HR = 7.98 (5.85-10.93)	(0.82-0.88); validation 0.82 (0.74-0.85); $P < 0.0001$	<i>al</i> [66]
DL	DCE-MRI + clinical/radiologic features; retrospective multicenter	Total $n = 355$ (train 251 + internal 62 + external 42); 2 centers	Proliferative HCC prediction; fusion model improves recurrence stratification	DL + clinical + radiologic model AUC: Training 0.99/internal 0.87/external 0.80	Qu <i>et al</i> [67]
DenseNet169 + MLP	Multiphase 25D CT + clinical features + RNA-seq; multicenter retrospective	Total $n = 620$ (TCIA + 3 centers); internal + 2 external test sets	Stratified RFS/OS ($P < 0.001$); high score links <i>WNT/MYC/KRAS</i> activation	DLER MLP 0.891 vs DLER 0.797 vs clinical model 0.752	Guo <i>et al</i> [68]
scSE-CatBoost	Multi-site endoscopic images; CNN + scSE feature extraction	Total $n = 302$ (An Nan Hospital); RUT validation	Real-time <i>Helicobacter pylori</i> detection; NPV 100%	Acc 0.90; sensitivity 1.00/specificity 0.81; AUC = 0.88	Lin <i>et al</i> [69]
Transformer + MIL	HE WSIs; dual-task (subtype + TMB prediction)	EC = 529/918; CRC = 594/1495; vs 7 SOTA methods	Strong subtype-TMB association (fisher $P < 0.001$); guides immunotherapy	Outperformed SOTA in both tasks	Wang <i>et al</i> [70]
GAN + ViT distillation	HE/HPS staining; multi-task prognosis (OS/TTR/TRG)	Internal = 258 CLM; two public datasets	TRG dichotomization. Acc 86.9-90.3%; 3-class Acc 78.5-82.1%	OS C-index 0.804 (± 0.014); TTR C-index 0.735 (± 0.016)	Elforaici <i>et al</i> [71]
Transfer learning	HE WSIs analysis	Segmentation = 100 WSI; validation: 4 cohorts (3 internal +1 external) + 6-month series = 217	Fine-tuning improved F1 0.797-0.949 ($P < 0.00001$); 100% visual overlay accuracy	Detection model AUC 0.959-0.978 ($P < 0.00001$)	Khan <i>et al</i> [72]
DBMIA-Net	GIA + EIA modules; adaptive channel graph convolution	5 public datasets (CVC-Clinic DB); vs SOTA methods	Enhanced generalization	94.12% dice (vs PraNet + 4.22%); leading in 6 metrics	Zhang <i>et al</i> [73]
UC-former vision transformer	Multicenter retrospective study; mayo endoscopic score prediction	Total $n = 768$ UC patients/15120 images; internal + 3 external validations	Surpassed senior endoscopists; strong multicenter stability	Internal Acc 90.8%; external Acc 82.4%-85.0%	Qi <i>et al</i> [74]
MIST	Self-supervised contrastive learning + dual-stream MIL	Total $n = 480/666$ WSI (Drum Tower); external = 273 WSI (Nanjing First)	Acc comparable to pathologists (0.784 vs 0.806)	External Acc 0.784	Cai <i>et al</i> [75]
ResTransUNet	Global context (transformer) + local features (CNN); LiTS2017/3Dircadb/Chaos/Sliver07	LiTS2017/3Dircadb/Chaos/Sliver07	Solved small/discontinuous region segmentation; outperformed SOTA	LiTS2017 dice 0.9535/VOE 0.0804/RVD -0.0007	Ou <i>et al</i> [76]
GCN	Pathological micronecrosis analysis + multicenter datasets; GCN feature fusion	Total $n = 752/3622$ slides; internal (FAH-ZJUMS) + external (TCGA-LIHC)	Improved prognostic stratification; precise necrosis localization	Internal + 8.18%; External + 9.02%; superior C-index vs baseline	Deng <i>et al</i> [77]

CNN: Convolutional neural network; EUS: Endoscopic ultrasonography; Acc: Accuracy; NNLS: Non-negative least square matrix factorization; WBC: White blood cells; TSMA: Tumor-specific methylation atlas; GCNN: Graph convolutional neural network; TOO: Tissue-of-origin; cfDNA: Cell free DNA; MLP: Multilayer perceptron; CT: Computed tomography; CV: Cross validation; GC: Gastric cancer; SOTA: State-of-the-art methods; OS: Overall survival; PFS: Progression-free survival; HE: Hematoxylin and eosin; HER2: Human epidermal growth factor receptor 2; CR: Complete response; PR: Partial response; SD: Stable disease; PD: Progressive disease; AUC: Area under the curve; DCNN: Deep convolutional neural networks; HCC: Hepatocellular carcinoma; MRI: Magnetic resonance imaging; PCCCL: Primary clear cell carcinoma of the liver; CHCC: Common hepatocellular carcinoma; CRC: Colorectal cancer; MSI: Microsatellite instability; NPV: Negative predictive value; SMOTE: Synthetic minority oversampling technique; SVM: Support vector machine; CD: Cluster of differentiation; DCA: Decision curve analysis; DL: Deep learning; RNN: Recurrent neural network; ANN: Artificial neural network; CADE: Computer-aided detection; ADR: Adenoma detection rates; GDPH: Guangdong Provincial People's Hospital; SYSMH: Sun Yat-Sen Memorial Hospital; MVI: Microvascular invasion; PA-TACE: Postoperative adjuvant transcatheter arterial chemoembolization; RFS: Recurrence-free survival; TA: Thermal ablation; ER: Early recurrence; KM: Kaplan-Meier; HR: Hazard ratio; ALBI: Albumin-bilirubin; AFP: Alpha-fetoprotein; INR: International normalized ratio; DCE-MRI: Dynamic contrast enhanced-magnetic resonance imaging; RNA-seq: Ribonucleic acid sequencing; TCIA: The cancer image archive; DLER: Deep learning model for early recurrence prediction; scSE: Spatial and channel squeeze and excitation block; RUT: Rapid urease test; TMB: Tumor mutational burden; MIL: Multiple instance learning model; GAN: Generative adversarial network; ViT: Vision transformers; HPS: Hematoxylin phloxine saffron; TRG: Tumor regression grade; TTR: Time-to-recurrence; WSI: Whole-slide image; GIA: Global information aggregation; EIA: Edge information aggregation; CVC-clinic DB: Colorectal cancer-clinic dataset; UC: Ulcerative colitis; MIST: Multiple instance learning network based on swin transformer; VOE: Volume overlap error; RVD: Relative volume difference; GCN: Graph convolutional neural networks; FAH-ZJUMS: The First Affiliated Hospital of Zhejiang University School of Medicine Datasets; TCGA-LIHC: The Cancer Genome Atlas liver hepatocellular carcinoma.

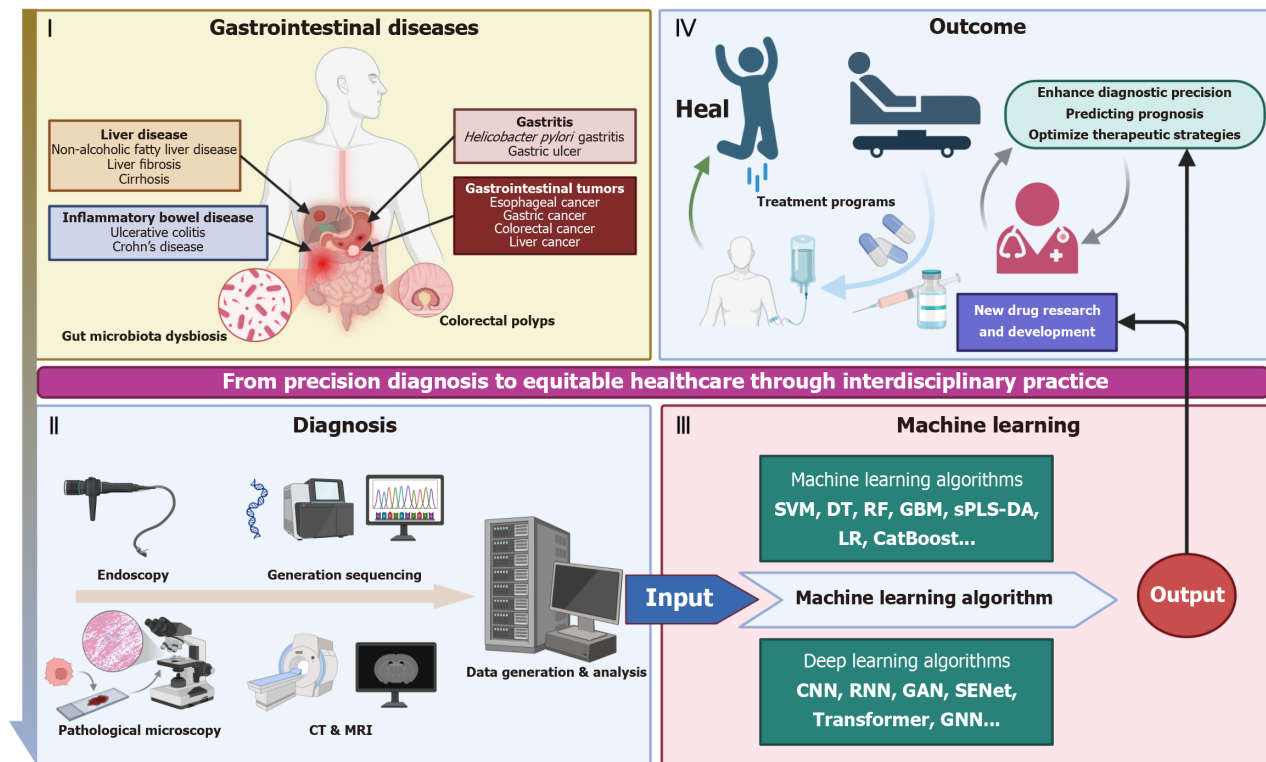


Figure 1 Artificial intelligence in gastrointestinal diseases. Section I (gastrointestinal diseases) includes liver diseases (metabolic dysfunction-associated steatotic liver disease, liver fibrosis, cirrhosis), inflammatory bowel disease (ulcerative colitis, Crohn's disease), gastritis (*Helicobacter pylori* gastritis, erosive mucosal changes), gastrointestinal tumors (esophageal cancer, gastric cancer, colorectal cancer, liver cancer), and colorectal polyps, with gut microbiota dysbiosis as a contributing factor. Section II (diagnosis) involves techniques such as endoscopy, generation sequencing, pathological microscopy, computed tomography and magnetic resonance imaging, followed by data generation and analysis. Section III (machine learning) presents algorithms: Machine learning algorithms (support vector machines, decision tree, random forest, gradient boosting machine, sparse partial least squares-discriminant analysis, logistic regression, CatBoost) and deep learning algorithms (convolutional neural network, recurrent neural network, generative adversarial network, squeeze-and-excitation network, transformer, graph neural network), which process input data. Section IV (outcome) demonstrates the therapeutic cycle: Treatment programs lead to healing or hospital care, promoting new drug research and development. Ultimately, it enhances diagnostic precision, predicts prognosis, and optimizes therapeutic strategies, embodying the journey from precision diagnosis to equitable healthcare via interdisciplinary practice. CT: Computed tomography; MRI: Magnetic resonance imaging; SVM: Support vector machines; DT: Decision tree; RF: Random forest; GBM: Gradient boosting machine; sPLS-DA: Sparse partial least squares-discriminant analysis; LR: Logistic regression; CNN: Convolutional neural network; RNN: Recurrent neural network; GAN: Generative adversarial network; SENet: Squeeze-and-excitation network; GNN: Graph neural network.

AI collaborating with endoscopists (0.776) was higher than that of AI alone (0.768) or physician majority vote (0.662), confirming that human-machine synergy can compensate for the limitations of a single method[100]. In addition, AI-assisted white light endoscopy reduced the leakage rate of gastric tumors from 27.3% to 6.1% ($P = 0.015$), which significantly improved the efficiency of identifying microscopic lesions[101]. In the evaluation of Barrett's esophagus for heterozygous hyperplasia, the AI system surpassed most pathologists in diagnostic accuracy (76.4%) of whole slide images, with an AUC of 0.94 and a sensitivity of 0.92 for the prediction of heterozygous hyperplasia[102]. For the prediction of peritoneal recurrence in gastric cancer, the deep learning model based on preoperative computed tomography images had an AUC of 0.843 in external validation, and the predictive results of this model further indicated that adjuvant chemotherapy was associated with improved disease-free survival in stage II and stage III disease[103]. In addition, the AutoML model (GBM algorithm) based on the SEER database predicted liver metastases of gastrointestinal mesenchymal tumors with an AUC of 0.795, and feature significance analysis showed that tumor size and location were key predictors[104]. These findings indicate that the deep integration of AI and endoscopy technology is reshaping the diagnosis and treatment landscape of upper gastrointestinal tumors. Through high-precision image recognition and real-time decision support, AI can not only alleviate the pressure of the shortage of professionals in primary care, but also promote the standardization of the diagnostic process and reduce the risk of misdiagnosis caused by differences in human experience.

AI fused with multi-omics further breaks through the limits of molecular typing, metastatic mechanisms and immunotherapy response prediction in gastric and esophageal cancer. Based on the dynamic features of mitochondrial adenosine triphosphate metabolism, membrane potential and lactate/pyruvate/glucose metabolism, the researchers constructed a MitoScore quantitative assessment system by integrating 10 machine learning algorithms, which can accurately differentiate the immune-metabolic subtypes of gastric cancer. Data analysis showed that high MitoScore subgroups presented abnormal activation of glycolytic pathways and were significantly associated with tumor aggressiveness phenotype and poor patient prognosis[105]. A SVM model was constructed to predict the response of gastric cancer patients to Sintilimab combined with SOX treatment based on the screening of six key markers (*DUOX2*, *HSPB1*, *S100A14*, *C1QA*, *TGFB1*, and

LTF) by combining the multiplex immunohistochemical data and the deep-learning feature extraction technique, which The AUC values were 0.93 and 0.84 in the exploratory cohort ($n = 107$) and validation cohort ($n = 46$), respectively, showing good predictive efficacy[106]. In addition, the MetImage technology based on metabolomics encoded liquid chromatograph mass spectrometer data into images, and the AI model constructed using the convolutional neuron network algorithm screened esophageal squamous carcinoma with a sensitivity of 85%, specificity of 92%, and AUC of 0.95[107].

AI plays an important role in the optimization of treatment strategies for upper gastrointestinal tumors. A study based on a counterfactual random forest model using predictors of recurrence (mitotic count, tumor size, and tumor site) and imatinib duration to infer the likelihood of recurrence in a given patient at 7 years for each imatinib treatment duration suggested that gastric-derived gastrointestinal stromal tumors (< 15.9 cm and low mitotic count) does not require imatinib treatment, avoiding the 29%-35% of patients who receive ineffective treatment[26]. Moreover, the best model for machine learning to predict imatinib adherence showed cognitive function and the presence or absence of therapeutic drug monitoring as key influencing factors[108].

AI enabled colorectal tumor diagnosis and treatment: Recent advances and clinical translation

AI becomes a real-time aid in colonoscopy traditional colonoscopy suffers from the limitation of a high rate of adenoma leakage (15%-30%), which has been significantly improved by deep learning-based computer-aided detection (CADe) systems through real-time polyp identification. For example, a multicenter randomized controlled trial (RCT) showed an approximately twofold reduction in adenoma missed diagnosis (AMR) in the AI-assisted colonoscopy group compared to the control group (15.5% *vs* 32.4%), with a particularly significant advantage in the detection of tiny polyps (≤ 5 mm) and nonpolypoid lesions [odds ratio (OR) = 0.34-0.24][109]. Another United States multicenter study (CADET-CS trial) further validated that the AMR and SSL leakage rates in the AI-assisted group decreased to 20.12% and 7.14%, respectively, while the number of first-pass adenomas detected increased significantly (1.19 *vs* 0.90)[110]. In addition, the gastrointestinal Genius system improved adenoma detection rate by 8.3% in a large RCT (COLO-DETECT) without the need for extended operating time[111]. These results suggest that AI has become a central tool for optimizing the quality of colonoscopy by reducing the number of perceptual errors.

Digital pathology combined with AI algorithms demonstrated high accuracy in tissue classification and tumor detection. A multi-class tissue segmentation model developed in one study achieved a composite Dice score of 0.895 in colorectal biopsies with a tumor detection sensitivity of 0.987[112]. For lymph node metastasis prediction, a deep learning model based on hematoxylin-eosin (HE)-stained images had an AUC of 0.764 in stage T1 colorectal cancer, which reduces unnecessary surgery by 15.1%[113]. In addition, the Deep-immune score, which quantifies the immune microenvironment by AI, was significantly associated with patient survival, with a 5-year survival rate of up to 87.4% in the high-scoring group, in which a high Deep-immune score was associated with high levels of cluster of differentiation (CD) 3T cell infiltration in the stromal region[114]. More importantly, AI simplifies the microsatellite instability (MSI) screening process. The MSIntuit pre-screening tool based on HE images has a sensitivity of 96%-98%, reducing the need for immunohistochemical validation by almost 50%[115]. Label-free infrared imaging combined with CNN has an AUC of 0.90 for classification of MSI, which provides rapid support for precise treatment[116]. Multi-omics integration models (*e.g.*, TMO-Net) fusing multimodal data from genomics and pathology optimize cancer typing accuracy, while non-invasive screening techniques based on respiratory volatomics achieve more than 89% sensitivity (AUC = 0.91) by detecting volatile organic compound markers[117,118]. These technologies not only improve diagnostic efficiency, but also provide support for individualized treatment at the molecular level.

Imaging and multimodal data integration, AI in imaging analysis optimizes treatment prediction by integrating multimodal data. Multimodal AI models integrating imaging, pathology and genomic data provide new tools for individualized treatment of colorectal tumors. The radio pathomics integrated prediction system combines magnetic resonance imaging radiomics with HE pathologic features to predict pathological complete remission from neoadjuvant radiotherapy for rectal cancer, with an AUC of 0.872 in the validation cohort, which was significantly better than the unimodal model ($P < 0.0001$)[119]. AI has significantly improved the prediction of treatment response by integrating imaging histology and clinical data. One study utilized random forest and gradient boosting algorithms to predict response to radiotherapy for colorectal cancer with an accuracy of 93.8%[120]. Another multi-omics analysis combined with spatial interaction mapping developed the CCIM-Net model, which effectively predicts chemosensitivity and guides combination therapy targeting *FOLR2* macrophages[121].

The application of AI technology to surgical planning for colorectal tumors has also seen breakthroughs. An automated computed tomography-based tumor segmentation model accurately assessed the total tumor volume of colorectal liver metastases with an intraclass correlation coefficient of 0.98[122]. For colorectal cancer liver metastases, the game-theory-based Shapley's additive interpretation AI model recommended individualized margin widths (6 mm-12 mm), with an AUC of 0.78 in the validation cohort, confirming the association between an optimal margin width of 7 mm and a significant prolongation of survival in an external cohort[123]. In addition, the multilayer perceptron model for predicting lymph node metastasis in the inferior mesenteric artery (AUC = 0.873) was significantly better than expert judgment (AUC = 0.509), which may reduce unnecessary clearance[124]. Machine learning algorithms performed well in survival prediction. logistic regression models combined with clinical variables (*e.g.*, distant metastases, number of lymph nodes) predicted 1- and 5-year survival with AUCs of 0.850 and 0.872, respectively[125]. Genomic profiling identified 32 key genes by interpretable AI and predicted stage II colorectal cancer recurrence with an AUC of 0.952[126].

AI-driven innovations in hepatic oncology: From multiscale diagnostics to precision therapeutics

The degree of liver fibrosis is the most sensitive clinical warning sign for metabolic dysfunction-associated steatotic liver disease (MASLD)-associated hepatocellular carcinoma, and significant and advanced liver fibrosis not only increases the

risk of hepatic and extra-hepatic complications, but is also significantly associated with liver-related mortality[127,128]. Therefore, dynamic monitoring of liver fibrosis progression (e.g., liver stiffness value testing) has become a core strategy for early screening of hepatocellular carcinoma, and how to achieve accurate assessment of fibrosis staging remains an urgent clinical challenge. In recent years, AI technologies have significantly improved the objectivity and sensitivity of assessment through multimodal innovations: The performance of deep learning models in ultrasound steatosis grading (AUC = 0.85) is not unlike the judgment of radiologists[129]; at the histological level, an AI-based measurement tool effectively predicts the survival of patients with fibrosis through reproducible necroinflammation grading ($\kappa = 1$) and pathologists' consensus highly concordant ($\kappa = 0.62-0.74$), effectively predicted progression-free survival of fibrosis patients ($P < 0.05$), providing a highly sensitive method for clinical trial endpoint assessment[130]; in the analysis of pathomechanisms, AI-based digital pathology combined with second harmonic generation/two-photon excited fluorescence microscopy revealed the dynamics of treatment-induced regression of perisinusoidal fibrosis, breaking through the blindness of the traditional scoring for fibrosis regression[131]. For non-invasive techniques, machine learning models of imaging histology combined with diffusion-weighted imaging can accurately identify liver fibrosis (AUC = 0.973) and early cirrhosis[132], whereas multiparametric quantitative ultrasound improves the diagnostic performance of fibrosis staging to an average AUC = 0.891 through feature engineering and algorithm optimization[133]. These technologies provide high-precision tools for the full management of liver disease through standardization, quantification and dynamic tracking capabilities, promoting fibrosis monitoring from static staging towards dynamic individualized interventions.

AI has shown no less ability than human experts in diagnostic imaging of liver tumors. Ultrasound-based deep learning models significantly improve the accuracy of benign and malignant liver tumors identification by integrating patient background and blood biomarkers. For example, a multimodal deep learning model combining B-mode ultrasound images with clinical data improved the diagnostic accuracy from 68.52% to 96.30% (AUC = 0.994) in unimodal mode[134]. In addition, the application of AI in computed tomography and magnetic resonance imaging image analysis is equally prominent. A GAN-based model effectively mitigates the data imbalance problem by synthesizing high-fidelity computed tomography images of liver tumors, improving the accuracy of classification models by 21%-34%[135]. In the magnetic resonance imaging segmentation task, the 3D CNN performs well in semi-automatic segmentation of hepatocellular carcinoma tumors, and especially performs best in diffusion-weighted imaging and T1-weighted imaging, with dice similarity coefficients up to 0.778[136]. The AI-driven software also detects liver metastases missed by radiologists on contrast-enhanced computed tomography with a sensitivity of 70.8% and a false-positive rate of only 0.48/case[137]. These techniques not only improve the efficiency of the diagnosis, but also reduce human error.

AI has also demonstrated strong classification and prediction capabilities in liver cancer histopathology image analysis. Deep learning models based on the attention mechanism (e.g., SENet) achieved 95.27% accuracy in the task of classifying the degree of differentiation of hepatocellular carcinoma, which is significantly better than traditional manual reading [138]. The clustering-constrained attention multiple instance learning model predicted immunogenetic signature activation by whole slide images with AUCs of 0.78-0.91, and pathologic analysis showed that the predicted areas were enriched with lymphocytes and neutrophils[139]. Microvascular infiltration (MVI) is a major risk factor for overall postoperative mortality and recurrence in hepatocellular carcinoma. Models combining imaging histology and deep learning perform well in MVI prediction. A deep learning model based on image-pathology fusion (Swin Transformer) was effective in predicting the vessels encapsulating tumor clusters (VETC) patterns of perivascular envelope tumor clusters, and its radiological-pathological histology column-line diagrams had a C-index of 0.67 in the external test set [140]. The random forest model based on preoperative computed tomography had an accuracy of 96.8% (sensitivity 95.2%) in the test set[141], while the column-line graph model combining clinical features with deep learning features had an AUC of up to 0.940[142]. In addition, the multitask learning framework significantly improved prognostic stratification by simultaneously predicting MVI and VETC via 3D CNN with AUCs of 0.917 and 0.860, respectively[143].

AI shows potential to outperform traditional statistical methods in prognostic modeling. The machine-learning-based smart-hepatocellular carcinoma score integrates nine clinical features, including liver stiffness, and its 5-year predictive AUC is ≥ 0.89 , which is superior to existing scoring systems[144]. Deep learning column line drawings combined with magnetic resonance imaging histologic features and clinical variables had an AUC of 0.949 for predicting early recurrence after hepatocellular carcinoma[145]. The randomized survival forest model, by incorporating risk factors such as MVI and satellite nodules, predicted early recurrence with a C-index of 0.896 in the training group 0.798 in the validation group, which was significantly better than the Cox proportional risk model[146]. In addition, the knowledge-enhanced dual-style visual transformer improves the interpretability and performance of recurrence prediction by fusing multi-period computed tomography images with domain knowledge[147]. Migration learning and multimodal strategies were used to optimize hepatocellular carcinoma risk prediction in patients with MASLD, significantly alleviating the problem of data scarcity and gender bias[148]. These models provide precise tools for individualized treatment and follow-up.

AI plays a key role in mining emerging molecular markers for liver cancer and optimizing immunotherapy strategies. Based on single-cell transcriptome analysis and machine learning, S100A10 was identified as a core gene for hepatocellular carcinoma diagnosis and immunotherapy response, and its expression was positively correlated with the stem cell marker *POU5F1*[149]. Stem-related classifiers (9-gene model, *PPARGC1A*, *FTCD*, *CFHR3*, *MAGEA6*, *CXCL8*, *CABYR*, *EPO*, *HMMR*, and *UCK2*) predicted the state of the tumor immune microenvironment and the efficacy of immune checkpoint inhibitors, with a significant enrichment of Treg cells and immune-suppressing pathways in high-risk patients [150]. These findings provide new ideas for targeting and stratifying immunotherapy in hepatocellular carcinoma.

Using AI to plan radiotherapy and manage post-liver transplantation is also maturing. The hierarchical feature fusion network generated radiotherapy dose distributions close to the clinical standard (homogeneity index = 0.31, conformation index = 0.87) by integrating computed tomography images with organ contours[151]. For recurrence prediction after liver transplantation, the deep learning model had an AUC of 0.86 based on preoperative factors (e.g., tumor diameter and

alpha fetoprotein level), with a 5-year recurrence-free survival rate of 92.6% in the low-risk group[152].

Deep integration of gut microbes and machine learning: Decoding cross-disease signatures to drive precision therapies

In the study of gut microbiology in inflammatory bowel disease, machine learning techniques have systematically deconstructed the gut-type-specific pathogenicity network of UC. Cluster analysis of 16S rRNA data from 11 cohorts by a deep neural network defined for the first time the three enterotypes of *Enterobacteriaceae*, *Trichoderma*, and *Clostridiales*: Among them, patients with *Enterobacteriaceae* had abnormally elevated abundance of *Rummatococcus*, which was positively correlated with the proliferation of *Clostridium difficile* ($P < 0.01$), and the machine learning-guided metabolic pathway analysis revealed that *Odoribacter splanchnicus* and *Bacteroides uniformis* exerted a protective effect by activating the adenosine 5'-monophosphate-activated protein kinase signaling pathway[153]. A sparse partial least squares discriminant analysis was further used to construct a prediction model for active UC, which maintained more than 90% accuracy even when only 5% of the feature volume was used, and to establish *Bifidobacterium bifidum*/*Haemophilus parainfluenzae* as a negative/positive marker of disease activity[154]. Machine learning algorithm-based analysis of multicohort fecal macrogenomic data revealed that microbial gene markers in Crohn's disease patients had significantly better diagnostic performance than species and single nucleotide variants. The gene diagnostic model constructed by machine learning performed optimally in cross-geographic validation (mean AUC = 0.91) and targeted the key gene (*celB/manY*) of the phosphotransferase system, whose specificity was experimentally confirmed, revealing the potential of microbial functional genes for AI-driven precision diagnosis[155].

In terms of diagnostic technology innovation, CatBoost algorithm increased the colorectal precancer detection accuracy to 87.27% by integrating bacterial-viral two-dimensional features, identified *Prevotella sp900557255* and phage *Felixoun-avirius* as early warning markers, and the combined typing strategy enabled the prediction accuracy to exceed 98%[156]; while the iterative random forest model revealed the characteristics of pancreatic cancer metastasis-associated flora, and found that changes in the abundance of six genera, including *Anaero stipes hadrus*, were significantly correlated with the enrichment of Gram-negative bacteria (OR = 2.34, $P = 0.007$)[157]. A neural network model based on 20 characteristic microorganisms combined with nanopore sequencing technology enabled rapid detection of hepatic encephalopathy (84% specificity), which drove the optimization of diagnostic and treatment protocols in 40% of cases[158]; while hepatocellular carcinoma studies constructed a prognostic model with an AUC of 81% by integrating microbiome-transcriptome data through randomized forests, which reveals that *Mycobacterium anisopliae* spp. mediated tumor through bile acids key mechanism of immune microenvironment remodeling[159]. It is worth emphasizing that machine learning-enabled cross-disease meta-analysis identified significant overlap of flora characteristics between Crohn's disease and colorectal cancer, and between Parkinson's disease and type 2 diabetes mellitus (Jaccard's index > 0.65), which provides a new paradigm for cross-disease therapeutic target discovery[160]. This paradigm-shifting integration of gut microbiome-AI symbiosis, as exemplified in Figure 2, not only deciphers conserved microbial signatures across diseases (e.g., bile acid-immune axis remodeling in hepatocellular carcinoma) but also establishes a computational framework for translating multi-omics interactions into clinically actionable biomarkers and therapeutic blueprints.

AI-driven: An innovative antibiotic RD paradigm to crack the drug-resistant bacteria crisis

The threat to human health posed by AMR has evolved from a theoretical warning to an urgent public health crisis. The Lancet research team modeled that by 2050, 1.91 million deaths globally will be directly attributed to AMR, with another 8.22 million deaths significantly associated with it[161]. However, in the face of "key priority pathogens"[162] represented by carbapenem-resistant *Enterobacteriaceae* and third-generation cephalosporin-resistant *Enterobacteriaceae*, the antibiotic development pipeline is severe lag: Only 13 new antibiotics targeting priority pathogens have been approved globally so far in 2017[161,162], of which only 5 have demonstrated *in vitro* activity against carbapenem-resistant *Enterobacteriaceae*/third-generation cephalosporin-resistant *Enterobacteriaceae*, and some of them are difficult to be widely used due to rapidly induced resistance or dose-limiting toxicity[163,164]. This paradox highlights the need to approach the gastrointestinal ecosystem, the source of infection. The gut is not only a major colonization site for pathogenic enterobacteria, but also a key biological interface for them to acquire drug resistance, spread and initiate systemic infections.

Excitingly, driven by AI, researchers have constructed numerous ways to quickly find new and efficient antibiotics. In response to the threat of multidrug-resistant *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Enterobacter species pathogens*, traditional high-throughput screening (HTS) is becoming insufficient due to the limitations of bacterial penetration barriers and resistance mechanisms[165]. In this context, the integration of deep learning and big data technologies significantly improves the efficiency of antibiotic discovery. For example, virtual screening of 1.4 billion compounds by out-of-distribution generalization techniques in the GNEprop model identified 82 anti-microbially active molecules with a 90-fold increase in hit rate compared to conventional HTS, and most of the structures were significantly different from those of known antibiotics[166]. Similarly, the AMPSphere platform, constructed based on global microbiome data, utilized machine learning to mine 863000 non-redundant antimicrobial peptides, of which 79% of the synthetically validated peptides target drug-resistant bacteria through membrane disruption mechanisms, providing an open repository for antibiotic development[167].

It is clear that deep learning models show unique advantages in discovering novel antibiotic structures. The research team screened structurally unique halicin from Drug Repurposing Hub, which showed potent bactericidal activity against both carbapenem-resistant *Enterobacteriaceae* and *Acinetobacter baumannii*[168]. To further break through the limitations of the "black box model", interpretable graphical neural networks were used to resolve chemical substructures related to antibiotic activity, successfully targeting lead compounds from 283 candidate molecules to inhibit methicillin-resistant *Staphylococcus aureus* and *Vancomycin-Resistant Enterococcus*, which significantly reduced pathogen load in a

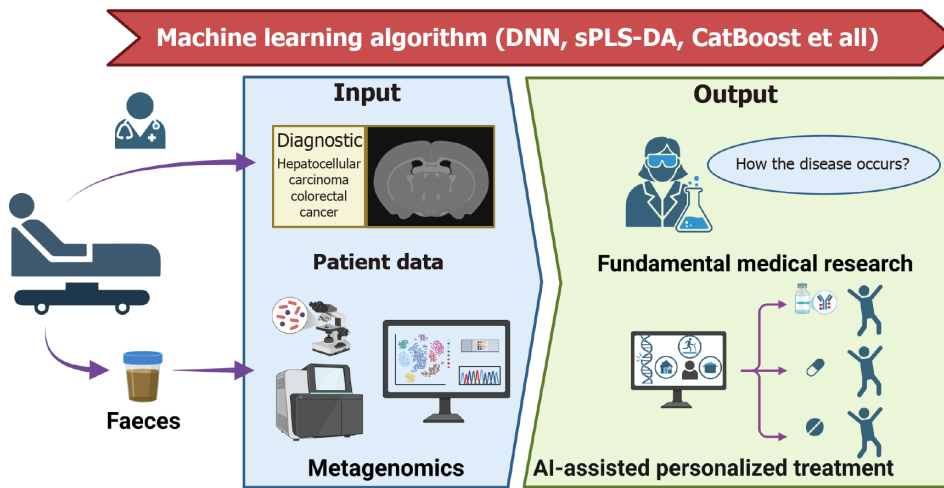


Figure 2 Schematic illustration of the deep integration between gut microbiome and machine learning for decoding cross-disease features to drive precision treatment. In the “Input” section, patient data (e.g., diagnostic information on hepatocellular carcinoma and colorectal cancer) and metagenomics data (faeces samples) are utilized. Various machine learning algorithms, such as deep neural network, sparse partial least squares-discriminant analysis, and CatBoost-process these inputs. The “Output” involves two key dimensions: One is fundamental medical research exploring “How the Disease Occurs?” through gut microbiome pattern analysis; the other is artificial intelligence-assisted personalized treatment, which leverages the integration of microbiomics and artificial intelligence to formulate tailored therapeutic strategies. This synergy between metagenomics and artificial intelligence significantly promotes in-depth disease mechanism research and personalized patient treatment. sPLS-DA: Sparse partial least squares-discriminant analysis; AI: Artificial intelligence; DNN: Deep neural network.

mouse infection model[169]. Innovative strategies such as “molecular extinction” have further expanded antibiotic sources. Ancient proteome mining techniques based on the panCleave random forest model screened stable, non-toxic antimicrobial peptides from extinct molecules and validated their efficacy in a model of *Acinetobacter baumannii* infection [170]. Against this persistent drug-resistant bacterium, machine learning has screened for the narrow-spectrum compound abaucin, which achieves precise control in a mouse wound model by interfering with the lipoprotein transport mechanism[171]. These breakthroughs not only provide a new pathway of “source blocking-precise intervention” to cope with the antimicrobial resistance crisis, but also promote the transition of medical research from single-pathogen targeting to multi-omics intelligent regulation system, and its technological framework lays a methodological foundation for the future development of structural innovative drugs and personalized flora therapy.

DISCUSSION

AI technology has shown remarkable potential in the diagnosis and treatment of gastrointestinal diseases, especially in the field of gastrointestinal and liver tumors, where several major breakthroughs have been achieved. However, technology diffusion still faces common challenges: First, the lack of interpretability caused by the black-box nature of the algorithms undermines clinical trust; Second, the lack of data and heterogeneity (including endoscopic device differences and cross-center data bias) lead to limitations in model generalization; and Third, the chain of evidence for clinical translation is still incomplete as existing studies generally lack large-scale RCTs and prospective validation[112,172-176]. In addition, the validation of molecular markers discovered by AI technology needs to expand the sample size, and the technology implementation needs to address the issue of geographic medical appropriateness[149,150]. The breakthrough of these bottlenecks will determine the process of AI technology leapfrogging from experimental results to clinical routine applications.

In response to current challenges in model interpretability, for Gradient-weighted Class Activation Mapping (Grad-CAM) and Shapley value analysis were integrated into diagnostic systems to assist clinicians in understanding the AI decision basis[177]. Grad-CAM generates a heat map to visualize the basis of model decision-making by quantifying the gradient of the target category probability relative to the final convolutional layer feature map. Its implementation is divided into three steps: First, calculate the gradient of the target category scores with respect to a specific convolutional layer feature map to obtain the importance weights of each channel; Second, perform channel-weighted summation of the feature map to generate a coarse-grained heatmap; and finally, up sample the heatmap to the input image size by bilinear interpolation to highlight the key regions. The method does not require modification of the model structure and is suitable for all types of CNNs. In biomedical research, Grad-CAM can localize molecular pathways driving classification (e.g., the *KRAS* signaling pathway in human papilloma virus status prediction) or regions of differential brain function (e.g., the default mode network of schizophrenic patients) to provide biologically plausible validation of model decisions. Its advantage lies in combining gradient information with spatial features to generate intuitive and interpretable heat maps while maintaining high resolution and class specificity, making it an important tool for connecting deep learning “black boxes” with domain knowledge[178,179]. An interpretable three-stage lightweight deep learning framework (PSE-

CNN-PCA-DELM) achieves 97.24% classification accuracy and 99.38% receiver operating characteristic-AUC metrics in a multi-level classification task of gastrointestinal diseases by integrating XAI (interpretable AI) technologies, such as Grad-CAM visualization and heat map analysis. With a model volume of only 14.88 MB and extremely fast inference performance of 59 ms, the framework breaks through the dependence of traditional AI models on high-performance arithmetic, and can be efficiently deployed in edge devices such as portable ultrasound machines and low arithmetic terminals, which is especially suitable for primary care scenarios and remote areas with a lack of resources, and can help narrow the geographic disparity of healthcare resources through the sinking of transparent and trusted AI-assisted diagnostic capabilities, contributing to promote AI-driven healthcare fairness provides a practical technical solution[19]. At the application level, AI has penetrated into multiple scenarios such as automatic ultrasound scanning, optimal classification trees retinal stratification analysis, and digital pathology nuclear fission counting, in which the EndoMind system has achieved 94.6% sensitivity in real-time cancer detection in gastrointestinal endoscopy, which significantly reduces the leakage of early lesions[180]. Interpretable AI technology fused with lightweight design is driving the transformation of smart healthcare to credible and practical with high precision and transparent decision-making, reshaping the human-machine collaborative diagnosis and treatment model.

In addressing the lack of data and heterogeneity, multi-task networks (*e.g.*, TransMT-Net) combined with active learning can maintain high accuracy with small samples (96.94% classification accuracy and 77.76% segmentation dice similarity coefficient[181]; and the course self-supervised learning framework utilizes unlabeled images to improve classification performance (73.39% F1 score)[182]. In addition, the migration learning strategy significantly alleviates the dilemma of annotated data scarcity in the medical field. In a deep migration learning study for catheter-dependent congenital heart disease (CHD) screening, the duct dependent congenital heart diseases-DenseNet model based on a two-stage migration strategy achieves the highest sensitivity for critical CHD detection by integrating the multi-center data of 6698 images and 48 videos 0.973 and specificity 0.985, and its hierarchical architectural design significantly improves cross-center generalization, providing an innovative solution for computer-aided hierarchical diagnosis of fetal heart defects in low-resource areas and model scalability[183]. And the breakthrough application of GANs is reflected in two aspects: On the one hand, it can synthesize augmented training data, and on the other hand, it can realize cross-modality image conversion (*e.g.*, magnetic resonance imaging to computed tomography) by CycleGAN, which can effectively support multi-center studies[184,185]. In one of the largest federated machine learning studies to date, researchers integrated data from 6314 patients from 71 healthcare sites across 6 continents to construct an automated tumor boundary detection model. The framework effectively integrates heterogeneous datasets from multiple sources without sharing the original data by weighting and averaging the encrypted model parameters across sites *via* a central aggregation server. Compared with the model trained only on publicly available datasets, the federated learning model achieves significant breakthroughs in surgical target area detection (33% enhancement) and overall tumor extent identification (23% enhancement), which directly corroborates the critical role of distributed data aggregation in breaking through the data size limitations of a single center. In the study, a pre-training model initialization strategy was adopted to accelerate convergence, and data diversity was gradually improved through phased training (from the initial model at 16 sites to the final consensus model at 71 sites), successfully constructing a cross-regional privacy-preserving collaborative network in rare disease scenarios, which provides a scalable technological paradigm for solving the problem of scarcity of diagnostic resources in low-resource regions[186]. In a multicenter study of prostate magnetic resonance imaging segmentation, three institutions (University of California, LA, State University of New York Upstate Medical Center, and National Cancer Institute) integrated their respective private datasets (100 cases of T2-weighted magnetic resonance imaging images each) through federated learning, and aggregated the model weights by weighted averaging without sharing the original data, so that the federated model on the external dataset (343 cases) demonstrated significantly higher performance than single-agency models[187]. Furthermore, in breast cancer diagnosis, federated learning demonstrates high diagnostic efficacy by integrating data from multiple sources and protecting privacy, enabling model accuracy of 98.9% and 95.3%[188,189]. However, no study has applied federated learning to the diagnosis and treatment of gastrointestinal diseases. For this reason, as shown in Figure 3, we design a federated learning-based collaborative framework, which relies on a central aggregation server and optimizes the encryption parameter ($\Delta\theta_i$) by using the weighted average method, in order to integrate multi-site heterogeneous datasets, and then generates a more generalized consensus model $\theta(k+1)$, which can both ensure privacy and security of gastrointestinal data and provide a scalable technology paradigm for cross-center AI collaboration. process ensures the privacy and security of gastrointestinal data while providing a scalable technical paradigm for cross-center AI collaboration. In the future, there is a need to promote multi-center collaboration, standardized data collection, and explore the deep integration of AI with multiple emerging technologies[190, 191]. These cutting-edge machine learning technologies have significantly promoted the scientific process of rare disease diagnosis and treatment by breaking through data scarcity and collaboration barriers: Migration learning adapts multi-center heterogeneous data with hierarchical architecture, GAN breaks through the double limitation of image modality and sample size, and federated learning builds a cross-regional privacy-preserving collaboration network, which jointly cracks the dilemma of the scarcity of diagnostic resources in low-resource areas.

With the clinical validation and scale deployment of AI-assisted decision-making tools (*e.g.*, the UC-SCALE standardized scoring system)[83,192], complex disease screening technologies are being embedded into different tiers of the healthcare system in an algorithmically standardized manner to promote equal coverage of diagnostic capabilities from the bottom of the technology. In resource-constrained scenarios, the technology integration strategy of "lightweight + localization + privacy protection" is especially critical: Lightweight neural network combined with edge computing architecture realizes offline inference, ensuring stable operation on terminal devices in underdeveloped regions; the federated learning framework supports the construction of cross-institutional diagnosis and treatment knowledge, avoiding the risk of leaking the original data; and the rare case data synthesized by the GAN complements the regional database. Together, the three can build an "end-side-cloud" collaborative computing architecture to provide sustainable

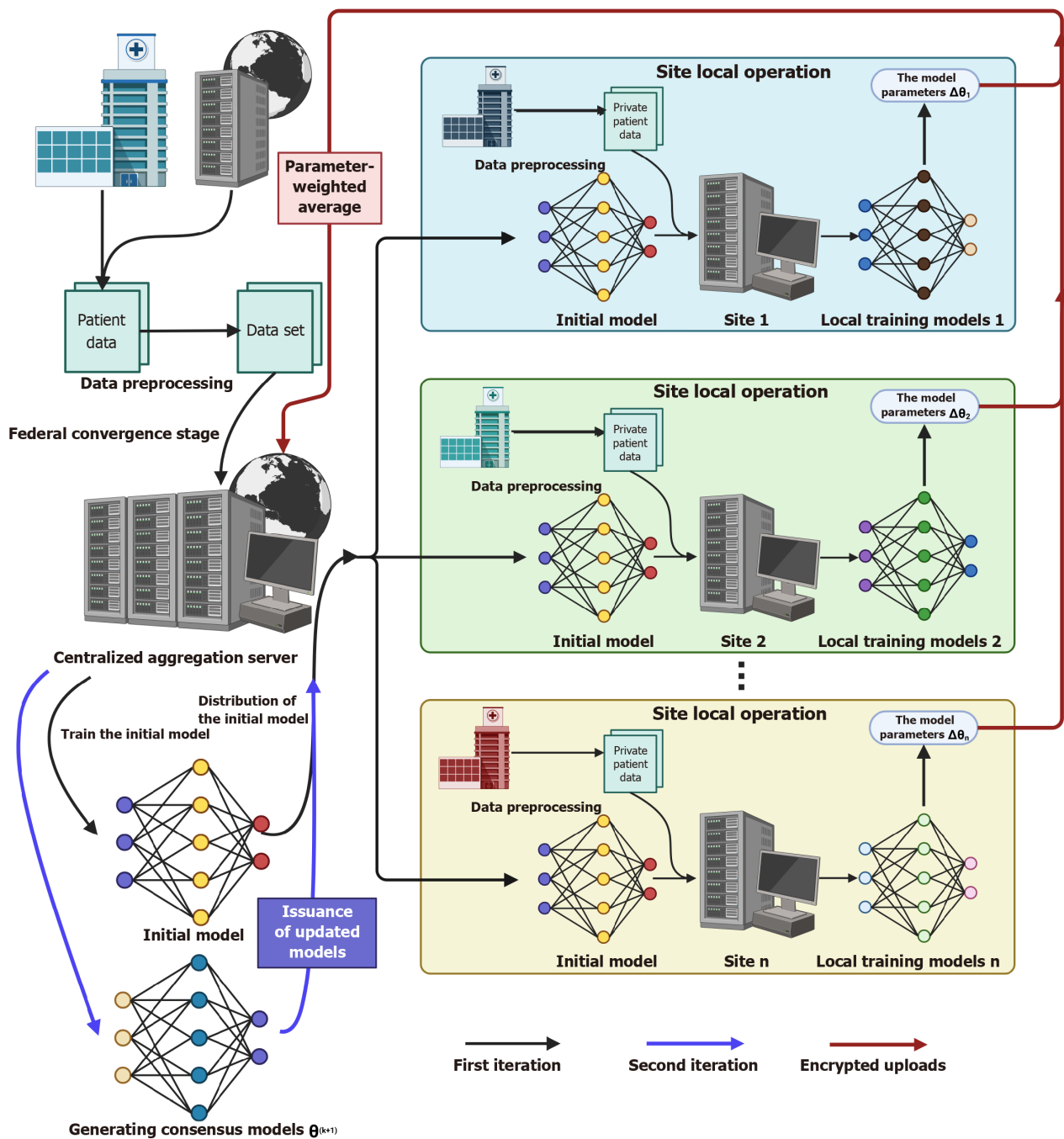


Figure 3 Schematic diagram of the envisioned federated learning architecture for gastrointestinal applications. In the federated convergence stage, the centralized aggregation server first generates an initial model, which is distributed to multiple independent sites (e.g., site 1, site 2, and site n). Each site performs data preprocessing on private gastrointestinal patient datasets and conducts local training using the initial model to produce local training models. To emphasize data privacy protection, model parameters (marked as $\Delta\theta_i$) are encrypted during upload to the centralized aggregation server. The server adopts parameter-weighted average to aggregate these parameters, issue updated models, and promote iterative training (illustrated by the first and second iterations). This architecture not only protects the privacy of gastrointestinal patient data through decentralized data processing and encryption strategies but also enhances model generalization. By integrating heterogeneous gastrointestinal datasets from multiple sites for collaborative training, the final consensus model $\theta^{(k+1)}$ can better adapt to diverse clinical scenarios. As a key framework, federated learning enables privacy-preserving collaborative model optimization, holding substantial promise for advancing artificial intelligence applications in gastrointestinal research.

technology empowerment for primary care. These technological advances not only improve the efficiency of diagnosis and treatment, but also reconstruct the medical ecology in terms of deep logic: Through algorithmic optimization of resource allocation model, innovation of medical knowledge discovery mechanism, and promotion of adaptive evolution of ethical framework, AI is upgrading from an auxiliary tool to an infrastructure for health equity. In the future, with the improvement of the technology-ethics synergy, machine learning is expected to become the core driving force to break through the plight of global health inequality, and promote the meta-goal of “health equity” from theoretical conception to practical realization.

CONCLUSION

AI has demonstrated revolutionary potential in the fields of gastroenterology and hepatology, significantly improving the diagnostic accuracy and personalized treatment of gastrointestinal diseases through image analysis, pathology, multi-modal data integration and molecular marker mining. However, the technology landing and further development still face challenges such as data heterogeneity, insufficient data volume, insufficient algorithm interpretability and ethical regulation.

FOOTNOTES

Author contributions: Chen ZL and Wang C contributed equally to this article; Chen ZL reviewed the literature and wrote the first draft of the paper; Wang C contributed to searching the literature and edited it extensively; Wang F conceived the idea and edited it; All authors have read and approved the final version.

Supported by the Natural Science Foundation of Jilin Province, No. YDZJ202401182ZYTS; Jilin Provincial Key Laboratory of Precision Infectious Diseases, No. 20200601011JC; and Jilin Provincial Engineering Laboratory of Precision Prevention and Control for Common Diseases, Jilin Province Development and Reform Commission, No. 2022C036.

Conflict-of-interest statement: The authors declare that they have no conflict of interest.

Open Access: This article is an open-access article that was selected by an in-house editor and fully peer-reviewed by external reviewers. It is distributed in accordance with the Creative Commons Attribution NonCommercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: <https://creativecommons.org/licenses/by-nc/4.0/>

Country of origin: China

ORCID number: Fang Wang [0000-0003-0871-3454](https://orcid.org/0000-0003-0871-3454).

S-Editor: Fan M

L-Editor: A

P-Editor: Wang WB

REFERENCES

- Shortliffe EH, Davis R, Axline SG, Buchanan BG, Green CC, Cohen SN. Computer-based consultations in clinical therapeutics: explanation and rule acquisition capabilities of the MYCIN system. *Comput Biomed Res* 1975; **8**: 303-320 [RCA] [PMID: 1157471] DOI: [10.1016/0010-4809\(75\)90009-9](https://doi.org/10.1016/0010-4809(75)90009-9) [FullText]
- Listgarten J, Damaraju S, Poulin B, Cook L, Dufour J, Driga A, Mackey J, Wishart D, Greiner R, Zanke B. Predictive models for breast cancer susceptibility from multiple single nucleotide polymorphisms. *Clin Cancer Res* 2004; **10**: 2725-2737 [RCA] [PMID: 15102677] DOI: [10.1158/1078-0432.ccr-1115-03](https://doi.org/10.1158/1078-0432.ccr-1115-03) [FullText]
- Lecun Y, Bottou L, Bengio Y, Haffner P. Gradient-based learning applied to document recognition. *Proc IEEE* 1998; **86**: 2278-2324 [DOI: [10.1109/5.726791](https://doi.org/10.1109/5.726791)] [FullText]
- Krizhevsky A, Sutskever I, Hinton GE. ImageNet classification with deep convolutional neural networks. *Commun ACM* 2017; **60**: 84-90 [DOI: [10.1145/3065386](https://doi.org/10.1145/3065386)] [FullText]
- Liu C, Zhao R, Pang M. A fully automatic segmentation algorithm for CT lung images based on random forest. *Med Phys* 2020; **47**: 518-529 [RCA] [PMID: 31788807] DOI: [10.1002/mp.13939](https://doi.org/10.1002/mp.13939) [FullText]
- Dosovitskiy A, Beyer L, Kolesnikov A, Weissenborn D, Zhai X, Unterthiner T, Dehghani M, Minderer M, Heigold G, Gelly S, Uszkoreit J, Houlsby N. An Image is Worth 16x16 Words: Transformers for Image Recognition at Scale. 2021 Preprint. Available from: [arXiv:2010.11929](https://arxiv.org/abs/2010.11929) [DOI: [10.48550/arXiv.2010.11929](https://doi.org/10.48550/arXiv.2010.11929)] [FullText]
- Esteva A, Kuprel B, Novoa RA, Ko J, Swetter SM, Blau HM, Thrun S. Dermatologist-level classification of skin cancer with deep neural networks. *Nature* 2017; **542**: 115-118 [RCA] [PMID: 28117445] DOI: [10.1038/nature21056](https://doi.org/10.1038/nature21056) [FullText]
- Naseem U, Khushi M, Kim J. Vision-Language Transformer for Interpretable Pathology Visual Question Answering. *IEEE J Biomed Health Inform* 2023; **27**: 1681-1690 [RCA] [PMID: 35358054] DOI: [10.1109/JBHI.2022.3163751](https://doi.org/10.1109/JBHI.2022.3163751) [FullText]
- Wu J, Hu R, Xiao Z, Chen J, Liu J. Vision Transformer-based recognition of diabetic retinopathy grade. *Med Phys* 2021; **48**: 7850-7863 [RCA] [PMID: 34693536] DOI: [10.1002/mp.15312](https://doi.org/10.1002/mp.15312) [FullText]
- Ayana G, Dese K, Dereje Y, Kebede Y, Barki H, Amdissa D, Husen N, Mulugeta F, Habtamu B, Choe SW. Vision-Transformer-Based Transfer Learning for Mammogram Classification. *Diagnostics (Basel)* 2023; **13**: 178 [RCA] [PMID: 36672988] DOI: [10.3390/diagnostics13020178](https://doi.org/10.3390/diagnostics13020178) [FullText] [Full Text(PDF)]
- Li J, Chen J, Tang Y, Wang C, Landman BA, Zhou SK. Transforming medical imaging with Transformers? A comparative review of key properties, current progresses, and future perspectives. *Med Image Anal* 2023; **85**: 102762 [RCA] [PMID: 36738650] DOI: [10.1016/j.media.2023.102762](https://doi.org/10.1016/j.media.2023.102762) [FullText]
- Zhou B, Yang G, Shi Z, Ma S. Natural Language Processing for Smart Healthcare. *IEEE Rev Biomed Eng* 2024; **17**: 4-18 [RCA] [PMID: 36170385] DOI: [10.1109/RBME.2022.3210270](https://doi.org/10.1109/RBME.2022.3210270) [FullText]

- 13 **Yim WW**, Yetisgen M, Harris WP, Kwan SW. Natural Language Processing in Oncology: A Review. *JAMA Oncol* 2016; **2**: 797-804 [RCA] [PMID: 27124593 DOI: 10.1001/jamaoncol.2016.0213] [FullText]
- 14 **Bray F**, Laversanne M, Sung H, Ferlay J, Siegel RL, Soerjomataram I, Jemal A. Global cancer statistics 2022: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. *CA Cancer J Clin* 2024; **74**: 229-263 [RCA] [PMID: 38572751 DOI: 10.3322/caac.21834] [FullText]
- 15 **Wang J**, Ni BY, Wang J, Han L, Ni X, Wang XM, Cao LC, Sun QH, Han XP, Cui HJ. Research progress of Paris polyphylla in the treatment of digestive tract cancers. *Discov Oncol* 2024; **15**: 31 [RCA] [PMID: 38324023 DOI: 10.1007/s12672-024-00882-9] [FullText]
- 16 **Kobayashi T**, Aikata H, Kobayashi T, Ohdan H, Arihiro K, Chayama K. Patients with early recurrence of hepatocellular carcinoma have poor prognosis. *Hepatobiliary Pancreat Dis Int* 2017; **16**: 279-288 [RCA] [PMID: 28603096 DOI: 10.1016/s1499-3872(16)60181-9] [FullText]
- 17 **Ramachandran R**, Grantham T, Parvataneni S, Budh D, Gollapalli S, Reddy M, Gaduputi V. Gastric Cancer: Clinical Features, Screening, Diagnosis, Treatment, and Prevention. *J Community Hosp Intern Med Perspect* 2024; **14**: 49-57 [RCA] [PMID: 38966500 DOI: 10.55729/2000-9666.1304] [FullText] [Full Text(PDF)]
- 18 **Mukherjee S**, Vagha S, Gadkari P. Navigating the Future: A Comprehensive Review of Artificial Intelligence Applications in Gastrointestinal Cancer. *Cureus* 2024; **16**: e54467 [RCA] [PMID: 38510911 DOI: 10.7759/cureus.54467] [FullText] [Full Text(PDF)]
- 19 **Luo X**, Wang J, Tan C, Dou Q, Han Z, Wang Z, Tasnim F, Wang X, Zhan Q, Li X, Zhou Q, Cheng J, Liao F, Yip HC, Jiang J, Tan RT, Liu S, Yu H. Rapid Endoscopic Diagnosis of Benign Ulcerative Colorectal Diseases With an Artificial Intelligence Contextual Framework. *Gastroenterology* 2024; **167**: 591-603.e9 [RCA] [PMID: 38583724 DOI: 10.1053/j.gastro.2024.03.039] [FullText]
- 20 **Zhou S**, Xie Y, Feng X, Li Y, Shen L, Chen Y. Artificial intelligence in gastrointestinal cancer research: Image learning advances and applications. *Cancer Lett* 2025; **614**: 217555 [RCA] [PMID: 39952597 DOI: 10.1016/j.canlet.2025.217555] [FullText]
- 21 **Li X**, Zhai Z, Ding W, Chen L, Zhao Y, Xiong W, Zhang Y, Lin D, Chen Z, Wang W, Gao Y, Cai S, Yu J, Zhang X, Liu H, Li G, Chen T. An artificial intelligence model to predict survival and chemotherapy benefits for gastric cancer patients after gastrectomy development and validation in international multicenter cohorts. *Int J Surg* 2022; **105**: 106889 [RCA] [PMID: 36084807 DOI: 10.1016/j.ijso.2022.106889] [Full Text]
- 22 **Yuan L**, Yang L, Zhang S, Xu Z, Qin J, Shi Y, Yu P, Wang Y, Bao Z, Xia Y, Sun J, He W, Chen T, Chen X, Hu C, Zhang Y, Dong C, Zhao P, Wang Y, Jiang N, Lv B, Xue Y, Jiao B, Gao H, Chai K, Li J, Wang H, Wang X, Guan X, Liu X, Zhao G, Zheng Z, Yan J, Yu H, Chen L, Ye Z, You H, Bao Y, Cheng X, Zhao P, Wang L, Zeng W, Tian Y, Chen M, You Y, Yuan G, Ruan H, Gao X, Xu J, Xu H, Du L, Zhang S, Fu H, Cheng X. Development of a tongue image-based machine learning tool for the diagnosis of gastric cancer: a prospective multicentre clinical cohort study. *EClinicalMedicine* 2023; **57**: 101834 [RCA] [PMID: 36825238 DOI: 10.1016/j.eclinm.2023.101834] [FullText] [Full Text(PDF)]
- 23 **Listopad S**, Magnan C, Asghar A, Stolz A, Tayek JA, Liu ZX, Morgan TR, Norden-Krichmar TM. Differentiating between liver diseases by applying multiclass machine learning approaches to transcriptomics of liver tissue or blood-based samples. *JHEP Rep* 2022; **4**: 100560 [RCA] [PMID: 36119721 DOI: 10.1016/j.jhepr.2022.100560] [FullText] [Full Text(PDF)]
- 24 **Liu Y**, He C, Fang W, Peng L, Shi F, Xia Y, Zhou Q, Zhang R, Li C. Prediction of Ki-67 expression in gastrointestinal stromal tumors using radiomics of plain and multiphase contrast-enhanced CT. *Eur Radiol* 2023; **33**: 7609-7617 [RCA] [PMID: 37266658 DOI: 10.1007/s00330-023-09727-5] [FullText]
- 25 **Chen T**, Wu J, Cui C, He Q, Li X, Liang W, Liu X, Liu T, Zhou X, Zhang X, Lei X, Xiong W, Yu J, Li G. CT-based radiomics nomograms for preoperative prediction of diffuse-type and signet ring cell gastric cancer: a multicenter development and validation cohort. *J Transl Med* 2022; **20**: 38 [RCA] [PMID: 35073917 DOI: 10.1186/s12967-022-03232-x] [FullText] [Full Text(PDF)]
- 26 **Bertsimas D**, Margonis GA, Sujichantararat S, Koulouras A, Ma Y, Antonescu CR, Brennan MF, Martín-Broto J, Tang S, Rutkowski P, Kreis ME, Beyer K, Wang J, Bylina E, Sobczuk P, Gutierrez A, Jadeja B, Tap WD, Chi P, Singer S. Interpretable artificial intelligence to optimise use of imatinib after resection in patients with localised gastrointestinal stromal tumours: an observational cohort study. *Lancet Oncol* 2024; **25**: 1025-1037 [RCA] [PMID: 38976997 DOI: 10.1016/S1470-2045(24)00259-6] [FullText]
- 27 **Chue KM**, Douglass BR, Ong LWL, Tan JTH, Teh JGX, Putera M, Kwan CKW, Wong WK, Yeung BPM. Maximizing oral intake tolerance in malignant gastric outlet obstruction - a Markov decision tree analysis comparing duodenal stenting, endoscopic ultrasound-guided gastroenterostomy and surgical gastrojejunostomy based on a meta-analysis of randomized controlled trials. *Int J Surg* 2025; **111**: 3006-3019 [RCA] [PMID: 39998501 DOI: 10.1097/JS9.0000000000002303] [FullText]
- 28 **Han Z**, Zhang Z, Yang X, Li Z, Sang S, Islam MT, Guo AA, Li Z, Wang X, Wang J, Zhang T, Sun Z, Yu L, Wang W, Xiong W, Li G, Jiang Y. Development and interpretation of a pathomics-driven ensemble model for predicting the response to immunotherapy in gastric cancer. *J Immunother Cancer* 2024; **12**: e008927 [RCA] [PMID: 38749538 DOI: 10.1136/jitc-2024-008927] [FullText]
- 29 **Bertsimas D**, Margonis GA, Tang S, Koulouras A, Antonescu CR, Brennan MF, Martín-Broto J, Rutkowski P, Stasinou G, Wang J, Pikoulis E, Bylina E, Sobczuk P, Gutierrez A, Jadeja B, Tap WD, Chi P, Singer S. An interpretable AI model for recurrence prediction after surgery in gastrointestinal stromal tumour: an observational cohort study. *EClinicalMedicine* 2023; **64**: 102200 [RCA] [PMID: 37731933 DOI: 10.1016/j.eclinm.2023.102200] [FullText] [Full Text(PDF)]
- 30 **Arai J**, Aoki T, Sato M, Niikura R, Suzuki N, Ishibashi R, Tsuji Y, Yamada A, Hirata Y, Ushiku T, Hayakawa Y, Fujishiro M. Machine learning-based personalized prediction of gastric cancer incidence using the endoscopic and histologic findings at the initial endoscopy. *Gastrointest Endosc* 2022; **95**: 864-872 [RCA] [PMID: 34998795 DOI: 10.1016/j.gie.2021.12.033] [FullText]
- 31 **Liu Y**, Méric G, Havulinna AS, Teo SM, Åberg F, Ruuskanen M, Sanders J, Zhu Q, Tripathi A, Verspoor K, Cheng S, Jain M, Jousilahti P, Vázquez-Baeza Y, Loomba R, Lahti L, Niiranen T, Salomaa V, Knight R, Inouye M. Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting. *Cell Metab* 2022; **34**: 719-730.e4 [RCA] [PMID: 35354069 DOI: 10.1016/j.cmet.2022.03.002] [FullText] [Full Text(PDF)]
- 32 **Wang L**, Wu X, Tian R, Ma H, Jiang Z, Zhao W, Cui G, Li M, Hu Q, Yu X, Xu W. MRI-based pre-Radiomics and delta-Radiomics models accurately predict the post-treatment response of rectal adenocarcinoma to neoadjuvant chemoradiotherapy. *Front Oncol* 2023; **13**: 1133008 [RCA] [PMID: 36925913 DOI: 10.3389/fonc.2023.1133008] [FullText]
- 33 **Facchin S**, Calgaro M, Pandolfo M, Caldari F, Ghisa M, Greco E, Sattin E, Valle G, Dellon ES, Vitolo N, Savarino EV. Salivary microbiota composition may discriminate between patients with eosinophilic oesophagitis (EoE) and non-EoE subjects. *Aliment Pharmacol Ther* 2022; **56**: 450-462 [RCA] [PMID: 35715947 DOI: 10.1111/apt.17091] [FullText]
- 34 **Cai Z**, Zhang J, He Y, Xia L, Dong X, Chen G, Zhou Y, Hu X, Zhong S, Wang Y, Chen H, Xie D, Liu X, Liu J. Liquid biopsy by combining 5-hydroxymethylcytosine signatures of plasma cell-free DNA and protein biomarkers for diagnosis and prognosis of hepatocellular carcinoma. *ESMO Open* 2021; **6**: 100021 [RCA] [PMID: 33508734 DOI: 10.1016/j.esmoop.2020.100021] [FullText] [Full Text(PDF)]

- 35 **Khrom M**, Long M, Dube S, Robbins L, Botwin GJ, Yang S, Mengesha E, Li D, Naito T, Bonthala NN, Ha C, Melmed G, Rabizadeh S, Syal G, Vasiliauskas E, Ziring D, Brant SR, Cho J, Duerr RH, Rioux J, Schumm P, Silverberg M, Ananthakrishnan AN, Faubion WA, Jabri B, Lira SA, Newberry RD, Sandler RS, Xavier RJ, Kugathasan S, Hercules D, Targan SR, Sartor RB, Haritunians T, McGovern DPB. Comprehensive Association Analyses of Extraintestinal Manifestations in Inflammatory Bowel Disease. *Gastroenterology* 2024; **167**: 315-332 [RCA] [PMID: 38490347 DOI: 10.1053/j.gastro.2024.02.026] [FullText]
- 36 **Jung JO**, Pisula JI, Bozek K, Popp F, Fuchs HF, Schröder W, Bruns CJ, Schmidt T. Prediction of postoperative complications after oesophagectomy using machine-learning methods. *Br J Surg* 2023; **110**: 1361-1366 [RCA] [PMID: 37343072 DOI: 10.1093/bjs/znad181] [FullText]
- 37 **Pera M**, Gibert J, Gimeno M, Garsot E, Eizaguirre E, Miró M, Castro S, Miranda C, Reka L, Leturio S, González-Duaigües M, Codony C, Gobbi Y, Luna A, Fernández-Ananin S, Sarriugarte A, Olona C, Rodríguez-Santiago J, Osorio J, Grande L; Spanish EURECCA Esophagogastric Cancer Group. Machine Learning Risk Prediction Model of 90-day Mortality After Gastrectomy for Cancer. *Ann Surg* 2022; **276**: 776-783 [RCA] [PMID: 35866643 DOI: 10.1097/SLA.0000000000005616] [FullText]
- 38 **Zou L**, Jiang Q, Guo T, Wu X, Wang Q, Feng Y, Zhang S, Fang W, Zhou W, Yang A. Endoscopic characteristics in predicting prognosis of biopsy-diagnosed gastric low-grade intraepithelial neoplasia. *Chin Med J (Engl)* 2022; **135**: 26-35 [RCA] [PMID: 34873080 DOI: 10.1097/CM9.0000000000001637] [FullText] [FullText(PDF)]
- 39 **Yu S**, Jiang H, Xia J, Gu J, Chen M, Wang Y, Zhao X, Liao Z, Zeng P, Xie T, Sui X. Construction of machine learning-based models for screening the high-risk patients with gastric precancerous lesions. *Chin Med* 2025; **20**: 7 [RCA] [PMID: 39773492 DOI: 10.1186/s13020-025-01059-4] [FullText]
- 40 **Zeng Y**, Li J, Zheng Y, Zhang D, Zhong N, Zuo X, Li Y, Yu W, Lu J. Development and validation of a predictive model for submucosal fibrosis in patients with early gastric cancer undergoing endoscopic submucosal dissection: experience from a large tertiary center. *Ann Med* 2024; **56**: 2391536 [RCA] [PMID: 39149760 DOI: 10.1080/07853890.2024.2391536] [FullText]
- 41 **Reddy KR**, McLerran D, Marsh T, Parikh N, Roberts LR, Schwartz M, Nguyen MH, Befeler A, Page-Lester S, Tang R, Srivastava S, Rinaudo JA, Feng Z, Marrero JA. Incidence and Risk Factors for Hepatocellular Carcinoma in Cirrhosis: The Multicenter Hepatocellular Carcinoma Early Detection Strategy (HEDS) Study. *Gastroenterology* 2023; **165**: 1053-1063.e6 [RCA] [PMID: 37429366 DOI: 10.1053/j.gastro.2023.06.027] [FullText]
- 42 **Ma L**, Zhang C, Wen Y, Xing K, Li S, Geng Z, Liao S, Yuan S, Li X, Zhong C, Hou J, Zhang J, Gao M, Xu B, Guo R, Wei W, Xie C, Lu L. Imaging-based surrogate classification for risk stratification of hepatocellular carcinoma with microvascular invasion to adjuvant hepatic arterial infusion chemotherapy: a multicenter retrospective study. *Int J Surg* 2025; **111**: 872-883 [RCA] [PMID: 39051653 DOI: 10.1097/JS9.0000000000001903] [FullText]
- 43 **Xia TY**, Zhou ZH, Meng XP, Zha JH, Yu Q, Wang WL, Song Y, Wang YC, Tang TY, Xu J, Zhang T, Long XY, Liang Y, Xiao WB, Ju SH. Predicting Microvascular Invasion in Hepatocellular Carcinoma Using CT-based Radiomics Model. *Radiology* 2023; **307**: e222729 [RCA] [PMID: 37097141 DOI: 10.1148/radiol.222729] [FullText]
- 44 **Schoenberger H**, Chong N, Fetzer DT, Rich NE, Yokoo T, Khatri G, Olivares J, Parikh ND, Yopp AC, Marrero JA, Singal AG. Dynamic Changes in Ultrasound Quality for Hepatocellular Carcinoma Screening in Patients With Cirrhosis. *Clin Gastroenterol Hepatol* 2022; **20**: 1561-1569.e4 [RCA] [PMID: 34119640 DOI: 10.1016/j.cgh.2021.06.012] [FullText]
- 45 **Singal AG**, Chen Y, Sridhar S, Mittal V, Fullington H, Shaik M, Waljee AK, Tiro J. Novel Application of Predictive Modeling: A Tailored Approach to Promoting HCC Surveillance in Patients With Cirrhosis. *Clin Gastroenterol Hepatol* 2022; **20**: 1795-1802.e2 [RCA] [PMID: 33662594 DOI: 10.1016/j.cgh.2021.02.038] [FullText]
- 46 **Wang JJ**, Feng J, Gomes C, Calthorpe L, Ashraf Ganjouei A, Romero-Hernandez F, Benedetti Cacciaguerra A, Hibi T, Adam MA, Alseidi A, Abu Hilal M, Rashidian N; International Post-Hepatectomy Liver Failure Study Group. Development and Validation of Prediction Models and Risk Calculators for Posthepatectomy Liver Failure and Postoperative Complications Using a Diverse International Cohort of Major Hepatectomies. *Ann Surg* 2023; **278**: 976-984 [RCA] [PMID: 37226846 DOI: 10.1097/SLA.0000000000005916] [FullText]
- 47 **Briggs SEW**, Law P, East JE, Wordsworth S, Dunlop M, Houlston R, Hippisley-Cox J, Tomlinson I. Integrating genome-wide polygenic risk scores and non-genetic risk to predict colorectal cancer diagnosis using UK Biobank data: population based cohort study. *BMJ* 2022; **379**: e071707 [RCA] [PMID: 36351667 DOI: 10.1136/bmj-2022-071707] [FullText]
- 48 **Cross AJ**, Robbins EC, Saunders BP, Duffy SW, Wooldrage K. Higher Adenoma Detection Rates at Screening Associated With Lower Long-Term Colorectal Cancer Incidence and Mortality. *Clin Gastroenterol Hepatol* 2022; **20**: e148-e167 [RCA] [PMID: 32931959 DOI: 10.1016/j.cgh.2020.09.020] [FullText]
- 49 **Bever AM**, Hang D, Lee DH, Tabung FK, Ugai T, Ogino S, Meyerhardt JA, Chan AT, Eliassen AH, Liang L, Stampfer MJ, Song M. Metabolomic signatures of inflammation and metabolic dysregulation in relation to colorectal cancer risk. *J Natl Cancer Inst* 2024; **116**: 1126-1136 [RCA] [PMID: 38430005 DOI: 10.1093/jnci/djae047] [FullText]
- 50 **Yang X**, Qiu H, Wang L, Wang X. Predicting Colorectal Cancer Survival Using Time-to-Event Machine Learning: Retrospective Cohort Study. *J Med Internet Res* 2023; **25**: e44417 [RCA] [PMID: 37883174 DOI: 10.2196/44417] [FullText]
- 51 **Meyer YM**, Wilting SM, Kraan J, Olthof P, Vermeulen P, Martens J, Grünhagen DJ, Sleijfer S, Verhoef C. Circulating tumour cells are associated with histopathological growth patterns of colorectal cancer liver metastases. *Clin Exp Metastasis* 2023; **40**: 69-77 [RCA] [PMID: 36326981 DOI: 10.1007/s10585-022-10191-6] [FullText]
- 52 **Tian S**, Shi H, Chen W, Li S, Han C, Du F, Wang W, Wen H, Lei Y, Deng L, Tang J, Zhang J, Lin J, Shi L, Ning B, Zhao K, Miao J, Wang G, Hou H, Huang X, Kong W, Jin X, Ding Z, Lin R. Artificial intelligence-based diagnosis of standard endoscopic ultrasonography scanning sites in the biliopancreatic system: a multicenter retrospective study. *Int J Surg* 2024; **110**: 1637-1644 [RCA] [PMID: 38079604 DOI: 10.1097/JS9.0000000000000995] [FullText]
- 53 **Nguyen TH**, Doan NNT, Tran TH, Huynh LAK, Doan PL, Nguyen THH, Nguyen VTC, Nguyen GTH, Nguyen HN, Giang H, Tran LS, Phan MD. Tissue of origin detection for cancer tumor using low-depth cfDNA samples through combination of tumor-specific methylation atlas and genome-wide methylation density in graph convolutional neural networks. *J Transl Med* 2024; **22**: 618 [RCA] [PMID: 38961476 DOI: 10.1186/s12967-024-05416-z] [FullText]
- 54 **Hao D**, Li Q, Feng QX, Qi L, Liu XS, Arefan D, Zhang YD, Wu S. SurvivalCNN: A deep learning-based method for gastric cancer survival prediction using radiological imaging data and clinicopathological variables. *Artif Intell Med* 2022; **134**: 102424 [RCA] [PMID: 36462894 DOI: 10.1016/j.artmed.2022.102424] [FullText]
- 55 **Wu Z**, Wang T, Lan J, Wang J, Chen G, Tong T, Zhang H. Deep learning-based prediction of HER2 status and trastuzumab treatment efficacy of gastric adenocarcinoma based on morphological features. *J Transl Med* 2025; **23**: 13 [RCA] [PMID: 39762854 DOI: 10.1186/s13020-025-01059-4] [FullText]

- 10.1186/s12967-024-06034-5] [FullText] [Full Text(PDF)]
- 56 **Nakatsuka T**, Tateishi R, Sato M, Hashizume N, Kamada A, Nakano H, Kabeya Y, Yonezawa S, Irie R, Tsujikawa H, Sumida Y, Yoneda M, Akuta N, Kawaguchi T, Takahashi H, Eguchi Y, Seko Y, Itoh Y, Murakami E, Chayama K, Taniai M, Tokushige K, Okanou T, Sakamoto M, Fujishiro M, Koike K. Deep learning and digital pathology powers prediction of HCC development in steatotic liver disease. *Hepatology* 2025; **81**: 976-989 [RCA] [PMID: 38768142 DOI: 10.1097/HEP.0000000000000904] [FullText]
- 57 **Liu B**, Li J, Yang X, Chen F, Zhang Y, Li H. Diagnosis of primary clear cell carcinoma of the liver based on Faster region-based convolutional neural network. *Chin Med J (Engl)* 2023; **136**: 2706-2711 [RCA] [PMID: 37882066 DOI: 10.1097/CM9.0000000000002853] [FullText]
- 58 **Wagner SJ**, Reisenbüchler D, West NP, Niehues JM, Zhu J, Foersch S, Veldhuizen GP, Quirke P, Grabsch HL, van den Brandt PA, Hutchins GGA, Richman SD, Yuan T, Langer R, Jenniskens JCA, Offermans K, Mueller W, Gray R, Gruber SB, Greenson JK, Rennert G, Bonner JD, Schmolze D, Jonnagaddala J, Hawkins NJ, Ward RL, Morton D, Seymour M, Magill L, Nowak M, Hay J, Koelzer VH, Church DN; TransSCOT consortium, Matek C, Geppert C, Peng C, Zhi C, Ouyang X, James JA, Loughrey MB, Salto-Tellez M, Brenner H, Hoffmeister M, Truhn D, Schnabel JA, Boxberg M, Peng T, Kather JN. Transformer-based biomarker prediction from colorectal cancer histology: A large-scale multicentric study. *Cancer Cell* 2023; **41**: 1650-1661.e4 [RCA] [PMID: 37652006 DOI: 10.1016/j.ccell.2023.08.002] [FullText] [Full Text(PDF)]
- 59 **Wang R**, Dai W, Gong J, Huang M, Hu T, Li H, Lin K, Tan C, Hu H, Tong T, Cai G. Development of a novel combined nomogram model integrating deep learning-pathomics, radiomics and immunoscore to predict postoperative outcome of colorectal cancer lung metastasis patients. *J Hematol Oncol* 2022; **15**: 11 [RCA] [PMID: 35073937 DOI: 10.1186/s13045-022-01225-3] [FullText] [Full Text(PDF)]
- 60 **Chang X**, Wang J, Zhang G, Yang M, Xi Y, Xi C, Chen G, Nie X, Meng B, Quan X. Predicting colorectal cancer microsatellite instability with a self-attention-enabled convolutional neural network. *Cell Rep Med* 2023; **4**: 100914 [RCA] [PMID: 36720223 DOI: 10.1016/j.xcrm.2022.100914] [FullText] [Full Text(PDF)]
- 61 **Sinonquel P**, Eelbode T, Pech O, De Wulf D, Dewint P, Neumann H, Antonelli G, Iacopini F, Tate D, Lemmers A, Pilonis ND, Kaminski MF, Roelandt P, Hassan C, Ingrid D, Maes F, Bisschops R. Clinical consequences of computer-aided colorectal polyp detection. *Gut* 2024; **73**: 1974-1983 [RCA] [PMID: 38876773 DOI: 10.1136/gutjnl-2024-331943] [FullText]
- 62 **Su J**, Liu Z, Li H, Kang L, Huang K, Wu J, Huang H, Ling F, Yao X, Huang C. Artificial intelligence-based model to predict recurrence after local excision in T1 rectal cancer. *Eur J Surg Oncol* 2025; **51**: 109717 [RCA] [PMID: 40043596 DOI: 10.1016/j.ejso.2025.109717] [FullText]
- 63 **Wang F**, Zhan G, Chen QQ, Xu HY, Cao D, Zhang YY, Li YH, Zhang CJ, Jin Y, Ji WB, Ma JB, Yang YJ, Zhou W, Peng ZY, Liang X, Deng LP, Lin LF, Chen YW, Hu HJ. Multitask deep learning for prediction of microvascular invasion and recurrence-free survival in hepatocellular carcinoma based on MRI images. *Liver Int* 2024; **44**: 1351-1362 [RCA] [PMID: 38436551 DOI: 10.1111/liv.15870] [FullText]
- 64 **Kong Q**, Li K. Predicting early recurrence of hepatocellular carcinoma after thermal ablation based on longitudinal MRI with a deep learning approach. *Oncologist* 2025; **30**: oyaf013 [RCA] [PMID: 40110765 DOI: 10.1093/oncolo/oyaf013] [FullText] [Full Text(PDF)]
- 65 **Iseke S**, Zeevi T, Kucukkaya AS, Raju R, Gross M, Haider SP, Petukhova-Greenstein A, Kuhn TN, Lin M, Nowak M, Cooper K, Thomas E, Weber MA, Madoff DC, Staib L, Batra R, Chapiro J. Machine Learning Models for Prediction of Posttreatment Recurrence in Early-Stage Hepatocellular Carcinoma Using Pretreatment Clinical and MRI Features: A Proof-of-Concept Study. *AJR Am J Roentgenol* 2023; **220**: 245-255 [RCA] [PMID: 35975886 DOI: 10.2214/AJR.22.28077] [FullText]
- 66 **Zhang Y**, Shi K, Feng Y, Wang XB. Machine learning model using immune indicators to predict outcomes in early liver cancer. *World J Gastroenterol* 2025; **31**: 101722 [RCA] [PMID: 39926221 DOI: 10.3748/wjg.v31.i5.101722] [FullText] [Full Text(PDF)]
- 67 **Qu H**, Zhang S, Guo M, Miao Y, Han Y, Ju R, Cui X, Li Y. Deep Learning Model for Predicting Proliferative Hepatocellular Carcinoma Using Dynamic Contrast-Enhanced MRI: Implications for Early Recurrence Prediction Following Radical Resection. *Acad Radiol* 2024; **31**: 4445-4455 [RCA] [PMID: 38749868 DOI: 10.1016/j.acra.2024.04.028] [FullText]
- 68 **Guo X**, Chen M, Zhou L, Zhu L, Liu S, Zheng L, Chen Y, Li Q, Xia S, Lu C, Chen M, Chen F, Ji J. Predicting early recurrence in locally advanced gastric cancer after gastrectomy using CT-based deep learning model: a multicenter study. *Int J Surg* 2025; **111**: 2089-2100 [RCA] [PMID: 39715142 DOI: 10.1097/JS9.0000000000002184] [FullText]
- 69 **Lin CH**, Hsu PI, Tseng CD, Chao PJ, Wu IT, Ghose S, Shih CA, Lee SH, Ren JH, Shie CB, Lee TF. Application of artificial intelligence in endoscopic image analysis for the diagnosis of a gastric cancer pathogen-Helicobacter pylori infection. *Sci Rep* 2023; **13**: 13380 [RCA] [PMID: 37592004 DOI: 10.1038/s41598-023-40179-5] [FullText]
- 70 **Wang CW**, Liu TC, Lai PJ, Muzakky H, Wang YC, Yu MH, Wu CH, Chao TK. Ensemble transformer-based multiple instance learning to predict pathological subtypes and tumor mutational burden from histopathological whole slide images of endometrial and colorectal cancer. *Med Image Anal* 2025; **99**: 103372 [RCA] [PMID: 39461079 DOI: 10.1016/j.media.2024.103372] [FullText]
- 71 **Elforaici MEA**, Montagnon E, Romero FP, Le WT, Azzi F, Trudel D, Nguyen B, Turcotte S, Tang A, Kadoury S. Semi-supervised ViT knowledge distillation network with style transfer normalization for colorectal liver metastases survival prediction. *Med Image Anal* 2025; **99**: 103346 [RCA] [PMID: 39423564 DOI: 10.1016/j.media.2024.103346] [FullText]
- 72 **Khan A**, Brouwer N, Blank A, Müller F, Soldini D, Noske A, Gaus E, Brandt S, Nagtegaal I, Dawson H, Thiran JP, Perren A, Lugli A, Zlobec I. Computer-Assisted Diagnosis of Lymph Node Metastases in Colorectal Cancers Using Transfer Learning With an Ensemble Model. *Mod Pathol* 2023; **36**: 100118 [RCA] [PMID: 36805793 DOI: 10.1016/j.modpat.2023.100118] [FullText]
- 73 **Zhang W**, Lu F, Su H, Hu Y. Dual-branch multi-information aggregation network with transformer and convolution for polyp segmentation. *Comput Biol Med* 2024; **168**: 107760 [RCA] [PMID: 38064849 DOI: 10.1016/j.compbimed.2023.107760] [FullText]
- 74 **Qi J**, Ruan G, Ping Y, Xiao Z, Liu K, Cheng Y, Liu R, Zhang B, Zhi M, Chen J, Xiao F, Zhao T, Li J, Zhang Z, Zou Y, Cao Q, Nian Y, Wei Y. Development and validation of a deep learning-based approach to predict the Mayo endoscopic score of ulcerative colitis. *Therap Adv Gastroenterol* 2023; **16**: 17562848231170945 [RCA] [PMID: 37251086 DOI: 10.1177/17562848231170945] [FullText] [Full Text(PDF)]
- 75 **Cai H**, Feng X, Yin R, Zhao Y, Guo L, Fan X, Liao J. MIST: multiple instance learning network based on Swin Transformer for whole slide image classification of colorectal adenomas. *J Pathol* 2023; **259**: 125-135 [RCA] [PMID: 36318158 DOI: 10.1002/path.6027] [FullText]
- 76 **Ou J**, Jiang L, Bai T, Zhan P, Liu R, Xiao H. ResTransUnet: An effective network combined with Transformer and U-Net for liver segmentation in CT scans. *Comput Biol Med* 2024; **177**: 108625 [RCA] [PMID: 38823365 DOI: 10.1016/j.compbimed.2024.108625] [Full Text]
- 77 **Deng B**, Tian Y, Zhang Q, Wang Y, Chai Z, Ye Q, Yao S, Liang T, Li J. NecroGlobalGCN: Integrating micronecrosis information in HCC prognosis prediction via graph convolutional neural networks. *Comput Methods Programs Biomed* 2024; **257**: 108435 [RCA] [PMID: 39357091 DOI: 10.1016/j.cmpb.2024.108435] [FullText]
- 78 **Gui X**, Bazarova A, Del Amor R, Vieth M, de Hertogh G, Villanacci V, Zardo D, Parigi TL, Røyset ES, Shivaji UN, Monica MAT, Mandelli

- G, Bhandari P, Danese S, Ferraz JG, Hayee B, Lazarev M, Parra-Blanco A, Pastorelli L, Panaccione R, Rath T, Tontini GE, Kiesslich R, Bisschops R, Grisan E, Naranjo V, Ghosh S, Iacucci M. PICaSSO Histologic Remission Index (PHRI) in ulcerative colitis: development of a novel simplified histological score for monitoring mucosal healing and predicting clinical outcomes and its applicability in an artificial intelligence system. *Gut* 2022; **71**: 889-898 [RCA] [PMID: 35173041 DOI: 10.1136/gutjnl-2021-326376] [FullText] [Full Text(PDF)]
- 79 **Peyrin-Biroulet L**, Adsul S, Stancati A, Dehmeshki J, Kubassova O. An artificial intelligence-driven scoring system to measure histological disease activity in ulcerative colitis. *United European Gastroenterol J* 2024; **12**: 1028-1033 [RCA] [PMID: 38590110 DOI: 10.1002/ueg2.12562] [FullText]
- 80 **Turan M**, Durmus F. UC-NfNet: Deep learning-enabled assessment of ulcerative colitis from colonoscopy images. *Med Image Anal* 2022; **82**: 102587 [RCA] [PMID: 36058054 DOI: 10.1016/j.media.2022.102587] [FullText]
- 81 **Kuroki T**, Maeda Y, Kudo SE, Ogata N, Iacucci M, Takishima K, Ide Y, Shibuya T, Semba S, Kawashima J, Kato S, Ogawa Y, Ichimasa K, Nakamura H, Hayashi T, Wakamura K, Miyachi H, Baba T, Nemoto T, Ohtsuka K, Misawa M. A novel artificial intelligence-assisted "vascular healing" diagnosis for prediction of future clinical relapse in patients with ulcerative colitis: a prospective cohort study (with video). *Gastrointest Endosc* 2024; **100**: 97-108 [RCA] [PMID: 38215859 DOI: 10.1016/j.gie.2024.01.010] [FullText]
- 82 **Ohara J**, Nemoto T, Maeda Y, Ogata N, Kudo SE, Yamochi T. Deep learning-based automated quantification of goblet cell mucus using histological images as a predictor of clinical relapse of ulcerative colitis with endoscopic remission. *J Gastroenterol* 2022; **57**: 962-970 [RCA] [PMID: 36184701 DOI: 10.1007/s00535-022-01924-1] [FullText]
- 83 **Gutierrez-Becker B**, Fraessle S, Yao H, Luscher J, Girycki R, Machura B, Czornik J, Goslinsky J, Pitura M, Levitte S, Arús-Pous J, Fisher E, Bojic D, Richmond D, Bigorgne AE, Prunotto M. Ulcerative Colitis Severity Classification and Localized Extent (UC-SCALE): An Artificial Intelligence Scoring System for a Spatial Assessment of Disease Severity in Ulcerative Colitis. *J Crohns Colitis* 2025; **19**: jjae187 [RCA] [PMID: 39657580 DOI: 10.1093/ecco-jcc/jjae187] [FullText]
- 84 **Guez I**, Focht G, Greer MC, Cytter-Kuint R, Pratt LT, Castro DA, Turner D, Griffiths AM, Freiman M. Development of a multimodal machine-learning fusion model to non-invasively assess ileal Crohn's disease endoscopic activity. *Comput Methods Programs Biomed* 2022; **227**: 107207 [RCA] [PMID: 36375417 DOI: 10.1016/j.cmpb.2022.107207] [FullText]
- 85 **Rymarczyk D**, Schultz W, Borowa A, Friedman JR, Danel T, Branigan P, Chalupczak M, Bracha A, Krawiec T, Warchol M, Li K, De Hertogh G, Zieliński B, Ghanem LR, Stojmirovic A. Deep Learning Models Capture Histological Disease Activity in Crohn's Disease and Ulcerative Colitis with High Fidelity. *J Crohns Colitis* 2024; **18**: 604-614 [RCA] [PMID: 37814351 DOI: 10.1093/ecco-jcc/jjad171] [FullText] [Full Text(PDF)]
- 86 **Kiyokawa H**, Abe M, Matsui T, Kurashige M, Ohshima K, Tahara S, Nojima S, Ogino T, Sekido Y, Mizushima T, Morii E. Deep Learning Analysis of Histologic Images from Intestinal Specimen Reveals Adipocyte Shrinkage and Mast Cell Infiltration to Predict Postoperative Crohn Disease. *Am J Pathol* 2022; **192**: 904-916 [RCA] [PMID: 35358474 DOI: 10.1016/j.ajpath.2022.03.006] [FullText]
- 87 **Ribeiro T**, Mascarenhas M, Afonso J, Cardoso H, Andrade P, Lopes S, Ferreira J, Mascarenhas Saraiva M, Macedo G. Artificial intelligence and colon capsule endoscopy: Automatic detection of ulcers and erosions using a convolutional neural network. *J Gastroenterol Hepatol* 2022; **37**: 2282-2288 [RCA] [PMID: 36181257 DOI: 10.1111/jgh.16011] [FullText]
- 88 **Mascarenhas Saraiva MJ**, Afonso J, Ribeiro T, Ferreira J, Cardoso H, Andrade AP, Parente M, Natal R, Mascarenhas Saraiva M, Macedo G. Deep learning and capsule endoscopy: automatic identification and differentiation of small bowel lesions with distinct haemorrhagic potential using a convolutional neural network. *BMJ Open Gastroenterol* 2021; **8**: e000753 [RCA] [PMID: 34580155 DOI: 10.1136/bmjgast-2021-000753] [FullText] [Full Text(PDF)]
- 89 **Barash Y**, Azaria L, Soffer S, Margalit Yehuda R, Shlomi O, Ben-Horin S, Eliakim R, Klang E, Kopylov U. Ulcer severity grading in video capsule images of patients with Crohn's disease: an ordinal neural network solution. *Gastrointest Endosc* 2021; **93**: 187-192 [RCA] [PMID: 32535191 DOI: 10.1016/j.gie.2020.05.066] [FullText]
- 90 **Gong R**, He S, Tian T, Chen J, Hao Y, Qiao C. FRCNN-AA-CIF: An automatic detection model of colon polyps based on attention awareness and context information fusion. *Comput Biol Med* 2023; **158**: 106787 [RCA] [PMID: 37044051 DOI: 10.1016/j.compbiomed.2023.106787] [FullText]
- 91 **Sharma A**, Kumar R, Garg P. Deep learning-based prediction model for diagnosing gastrointestinal diseases using endoscopy images. *Int J Med Inform* 2023; **177**: 105142 [RCA] [PMID: 37422969 DOI: 10.1016/j.ijmedinf.2023.105142] [FullText]
- 92 **Tang CP**, Chen KH, Lin TL. Computer-Aided Colon Polyp Detection on High Resolution Colonoscopy Using Transfer Learning Techniques. *Sensors (Basel)* 2021; **21**: 5315 [RCA] [PMID: 34450756 DOI: 10.3390/s21165315] [FullText] [Full Text(PDF)]
- 93 **Ziegelmayr S**, Reischl S, Havrda H, Gawlitza J, Graf M, Lenhart N, Nehls N, Lemke T, Wilhelm D, Lohöfer F, Burian E, Neumann PA, Makowski M, Braren R. Development and Validation of a Deep Learning Algorithm to Differentiate Colon Carcinoma From Acute Diverticulitis in Computed Tomography Images. *JAMA Netw Open* 2023; **6**: e2253370 [RCA] [PMID: 36705919 DOI: 10.1001/jamanetworkopen.2022.53370] [FullText]
- 94 **Harb SF**, Ali A, Yousuf M, Elshazly S, Farag A. G-SET-DCL: a guided sequential episodic training with dual contrastive learning approach for colon segmentation. *Int J Comput Assist Radiol Surg* 2025; **20**: 279-287 [RCA] [PMID: 39789205 DOI: 10.1007/s11548-024-03319-4] [FullText]
- 95 **Enchakalody BE**, Wasnik AP, Al-Hawary MM, Wang SC, Su GL, Ross B, Stidham RW. Local Assessment and Small Bowel Crohn's Disease Severity Scoring using AI. *Acad Radiol* 2024; **31**: 4045-4056 [RCA] [PMID: 38702212 DOI: 10.1016/j.acra.2024.03.044] [FullText]
- 96 **Abe H**, Kurose Y, Takahama S, Kume A, Nishida S, Fukasawa M, Yasunaga Y, Ushiku T, Ninomiya Y, Yoshizawa A, Murao K, Sato S, Kitsuregawa M, Harada T, Kitagawa M, Fukayama M; Japan Pathology AI Diagnostics/National Institution of Informatics (JP-AID/NII) Study Group for Gastric Biopsy Pathology. Development and multi-institutional validation of an artificial intelligence-based diagnostic system for gastric biopsy. *Cancer Sci* 2022; **113**: 3608-3617 [RCA] [PMID: 36068652 DOI: 10.1111/cas.15514] [FullText] [Full Text(PDF)]
- 97 **Franklin MM**, Schultz FA, Tafoya MA, Kerwin AA, Broehm CJ, Fischer EG, Gullapalli RR, Clark DP, Hanson JA, Martin DR. A Deep Learning Convolutional Neural Network Can Differentiate Between Helicobacter Pylori Gastritis and Autoimmune Gastritis With Results Comparable to Gastrointestinal Pathologists. *Arch Pathol Lab Med* 2022; **146**: 117-122 [RCA] [PMID: 33861314 DOI: 10.5858/arpa.2020-0520-OA] [FullText]
- 98 **Faust O**, De Michele S, Koh JE, Jahmunah V, Lih OS, Kamath AP, Barua PD, Ciaccio EJ, Lewis SK, Green PH, Bhagat G, Acharya UR. Automated analysis of small intestinal lamina propria to distinguish normal, Celiac Disease, and Non-Celiac Duodenitis biopsy images. *Comput Methods Programs Biomed* 2023; **230**: 107320 [RCA] [PMID: 36608429 DOI: 10.1016/j.cmpb.2022.107320] [FullText]
- 99 **Luo H**, Xu G, Li C, He L, Luo L, Wang Z, Jing B, Deng Y, Jin Y, Li Y, Li B, Tan W, He C, Seeruttan SR, Wu Q, Huang J, Huang DW, Chen B, Lin SB, Chen QM, Yuan CM, Chen HX, Pu HY, Zhou F, He Y, Xu RH. Real-time artificial intelligence for detection of upper

- gastrointestinal cancer by endoscopy: a multicentre, case-control, diagnostic study. *Lancet Oncol* 2019; **20**: 1645-1654 [RCA] [PMID: 31591062 DOI: 10.1016/S1470-2045(19)30637-0] [FullText]
- 100 Goto A, Kubota N, Nishikawa J, Ogawa R, Hamabe K, Hashimoto S, Ogihara H, Hamamoto Y, Yanai H, Miura O, Takami T. Cooperation between artificial intelligence and endoscopists for diagnosing invasion depth of early gastric cancer. *Gastric Cancer* 2023; **26**: 116-122 [RCA] [PMID: 36040575 DOI: 10.1007/s10120-022-01330-9] [FullText]
- 101 Wu L, Shang R, Sharma P, Zhou W, Liu J, Yao L, Dong Z, Yuan J, Zeng Z, Yu Y, He C, Xiong Q, Li Y, Deng Y, Cao Z, Huang C, Zhou R, Li H, Hu G, Chen Y, Wang Y, He X, Zhu Y, Yu H. Effect of a deep learning-based system on the miss rate of gastric neoplasms during upper gastrointestinal endoscopy: a single-centre, tandem, randomised controlled trial. *Lancet Gastroenterol Hepatol* 2021; **6**: 700-708 [RCA] [PMID: 34297944 DOI: 10.1016/S2468-1253(21)00216-8] [FullText]
- 102 Botros M, de Boer OJ, Cardenas B, Bekkers EJ, Jansen M, van der Wel MJ, Sánchez CI, Meijer SL. Deep Learning for Histopathological Assessment of Esophageal Adenocarcinoma Precursor Lesions. *Mod Pathol* 2024; **37**: 100531 [RCA] [PMID: 38830407 DOI: 10.1016/j.modpat.2024.100531] [FullText]
- 103 Jiang Y, Zhang Z, Yuan Q, Wang W, Wang H, Li T, Huang W, Xie J, Chen C, Sun Z, Yu J, Xu Y, Poultsides GA, Xing L, Zhou Z, Li G, Li R. Predicting peritoneal recurrence and disease-free survival from CT images in gastric cancer with multitask deep learning: a retrospective study. *Lancet Digit Health* 2022; **4**: e340-e350 [RCA] [PMID: 35461691 DOI: 10.1016/S2589-7500(22)00040-1] [FullText]
- 104 Liu L, Zhang R, Shi Y, Sun J, Xu X. Automated machine learning for predicting liver metastasis in patients with gastrointestinal stromal tumor: a SEER-based analysis. *Sci Rep* 2024; **14**: 12415 [RCA] [PMID: 38816560 DOI: 10.1038/s41598-024-62311-9] [FullText]
- 105 Ma Y, Jin J, Xue Z, Zhao J, Cai W, Zhang W. Integrated multi-omics analysis and machine learning developed a prognostic model based on mitochondrial function in a large multicenter cohort for Gastric Cancer. *J Transl Med* 2024; **22**: 381 [RCA] [PMID: 38654380 DOI: 10.1186/s12967-024-05109-7] [FullText]
- 106 Che G, Yin J, Wang W, Luo Y, Chen Y, Yu X, Wang H, Liu X, Chen Z, Wang X, Chen Y, Wang X, Tang K, Tang J, Shao W, Wu C, Sheng J, Li Q, Liu J. Circumventing drug resistance in gastric cancer: A spatial multi-omics exploration of chemo and immuno-therapeutic response dynamics. *Drug Resist Updat* 2024; **74**: 101080 [RCA] [PMID: 38579635 DOI: 10.1016/j.drug.2024.101080] [FullText]
- 107 Wang H, Yin Y, Zhu ZJ. Encoding LC-MS-Based Untargeted Metabolomics Data into Images toward AI-Based Clinical Diagnosis. *Anal Chem* 2023; **95**: 6533-6541 [RCA] [PMID: 37042095 DOI: 10.1021/acs.analchem.2c05079] [FullText]
- 108 Liu L, Yu Z, Chen H, Gong Z, Huang X, Chen L, Fan Z, Zhang J, Yan J, Tian H, Zeng X, Chen Z, Zhang P, Zhou H. Imatinib adherence prediction using machine learning approach in patients with gastrointestinal stromal tumor. *Cancer* 2025; **131**: e35548 [RCA] [PMID: 39238433 DOI: 10.1002/encr.35548] [FullText]
- 109 Wallace MB, Sharma P, Bhandari P, East J, Antonelli G, Lorenzetti R, Vieth M, Speranza I, Spadaccini M, Desai M, Lukens FJ, Babameto G, Batista D, Singh D, Palmer W, Ramirez F, Palmer R, Lunsford T, Ruff K, Bird-Liebermann E, Ciofoaia V, Arndt S, Cangemi D, Puddick K, Derfus G, Johal AS, Barawi M, Longo L, Moro L, Repici A, Hassan C. Impact of Artificial Intelligence on Miss Rate of Colorectal Neoplasia. *Gastroenterology* 2022; **163**: 295-304.e5 [RCA] [PMID: 35304117 DOI: 10.1053/j.gastro.2022.03.007] [FullText]
- 110 Glissen Brown JR, Mansour NM, Wang P, Chuchuca MA, Minchenberg SB, Chandnani M, Liu L, Gross SA, Sengupta N, Berzin TM. Deep Learning Computer-aided Polyp Detection Reduces Adenoma Miss Rate: A United States Multi-center Randomized Tandem Colonoscopy Study (CADET-CS Trial). *Clin Gastroenterol Hepatol* 2022; **20**: 1499-1507.e4 [RCA] [PMID: 34530161 DOI: 10.1016/j.cgh.2021.09.009] [FullText]
- 111 Seager A, Sharp L, Neilson LJ, Brand A, Hampton JS, Lee TJW, Evans R, Vale L, Whelpton J, Bestwick N, Rees CJ; COLO-DETECT trial team. Polyp detection with colonoscopy assisted by the GI Genius artificial intelligence endoscopy module compared with standard colonoscopy in routine colonoscopy practice (COLO-DETECT): a multicentre, open-label, parallel-arm, pragmatic randomised controlled trial. *Lancet Gastroenterol Hepatol* 2024; **9**: 911-923 [RCA] [PMID: 39153491 DOI: 10.1016/S2468-1253(24)00161-4] [FullText]
- 112 Griem J, Eich ML, Schallenberg S, Pryalukhin A, Bychok A, Fukuoaka J, Zayats V, Hulla W, Munkhdelger J, Seper A, Tsvetkov T, Mukhopadhyay A, Sanner A, Stieber J, Fuchs M, Babendererde N, Schömig-Markiefka B, Klein S, Buettner R, Quaaas A, Tolkach Y. Artificial Intelligence-Based Tool for Tumor Detection and Quantitative Tissue Analysis in Colorectal Specimens. *Mod Pathol* 2023; **36**: 100327 [RCA] [PMID: 37683932 DOI: 10.1016/j.modpat.2023.100327] [FullText]
- 113 Song JH, Hong Y, Kim ER, Kim SH, Sohn I. Utility of artificial intelligence with deep learning of hematoxylin and eosin-stained whole slide images to predict lymph node metastasis in T1 colorectal cancer using endoscopically resected specimens; prediction of lymph node metastasis in T1 colorectal cancer. *J Gastroenterol* 2022; **57**: 654-666 [RCA] [PMID: 35802259 DOI: 10.1007/s00535-022-01894-4] [FullText]
- 114 Yang J, Ye H, Fan X, Li Y, Wu X, Zhao M, Hu Q, Ye Y, Wu L, Li Z, Zhang X, Liang C, Wang Y, Xu Y, Li Q, Yao S, You D, Zhao K, Liu Z. Artificial intelligence for quantifying immune infiltrates interacting with stroma in colorectal cancer. *J Transl Med* 2022; **20**: 451 [RCA] [PMID: 36195956 DOI: 10.1186/s12967-022-03666-3] [FullText] [Full Text(PDF)]
- 115 Saillard C, Dubois R, Tchita O, Loiseau N, Garcia T, Adriansen A, Carpentier S, Reyre J, Enea D, von Loga K, Kamoun A, Rossat S, Wiscart C, Sefta M, Auffret M, Guillou L, Fouillet A, Kather JN, Svrcek M. Validation of MSIntuit as an AI-based pre-screening tool for MSI detection from colorectal cancer histology slides. *Nat Commun* 2023; **14**: 6695 [RCA] [PMID: 37932267 DOI: 10.1038/s41467-023-42453-6] [FullText]
- 116 Gerwert K, Schörner S, Großerueschkamp F, Kraeft AL, Schuhmacher D, Sternemann C, Feder IS, Wissner S, Lugnier C, Arnold D, Teschendorf C, Mueller L, Timmesfeld N, Mosig A, Reinacher-Schick A, Tannapfel A. Fast and label-free automated detection of microsatellite status in early colon cancer using artificial intelligence integrated infrared imaging. *Eur J Cancer* 2023; **182**: 122-131 [RCA] [PMID: 36773401 DOI: 10.1016/j.ejca.2022.12.026] [FullText]
- 117 Wang FA, Zhuang Y, Gao F, He R, Zhang S, Wang L, Liu J, Li Y. TMO-Net: an explainable pretrained multi-omics model for multi-task learning in oncology. *Genome Biol* 2024; **25**: 149 [RCA] [PMID: 38845006 DOI: 10.1186/s13059-024-03293-9] [FullText]
- 118 Liu Y, Ji Y, Chen J, Zhang Y, Li X, Li X. Pioneering noninvasive colorectal cancer detection with an AI-enhanced breath volatiles platform. *Theranostics* 2024; **14**: 4240-4255 [RCA] [PMID: 39113791 DOI: 10.7150/thno.94950] [FullText]
- 119 Feng L, Liu Z, Li C, Li Z, Lou X, Shao L, Wang Y, Huang Y, Chen H, Pang X, Liu S, He F, Zheng J, Meng X, Xie P, Yang G, Ding Y, Wei M, Yun J, Hung MC, Zhou W, Wahl DR, Lan P, Tian J, Wan X. Development and validation of a radiopathomics model to predict pathological complete response to neoadjuvant chemoradiotherapy in locally advanced rectal cancer: a multicentre observational study. *Lancet Digit Health* 2022; **4**: e8-e17 [RCA] [PMID: 34952679 DOI: 10.1016/S2589-7500(21)00215-6] [FullText]
- 120 Bahrambanan F, Alizamir M, Moradveisi K, Heddam S, Kim S, Kim S, Soleimani M, Afshar S, Taherkhani A. The development of an efficient artificial intelligence-based classification approach for colorectal cancer response to radiochemotherapy: deep learning vs. machine learning. *Sci Rep* 2025; **15**: 62 [RCA] [PMID: 39748016 DOI: 10.1038/s41598-024-84023-w] [FullText]

- 121 **Bao X**, Li Q, Chen D, Dai X, Liu C, Tian W, Zhang H, Jin Y, Wang Y, Cheng J, Lai C, Ye C, Xin S, Li X, Su G, Ding Y, Xiong Y, Xie J, Tano V, Wang Y, Fu W, Deng S, Fang W, Sheng J, Ruan J, Zhao P. A multiomics analysis-assisted deep learning model identifies a macrophage-oriented module as a potential therapeutic target in colorectal cancer. *Cell Rep Med* 2024; **5**: 101399 [RCA] [PMID: 38307032] DOI: 10.1016/j.xcrm.2024.101399 [FullText]
- 122 **Wesdorp NJ**, Zeeuw JM, Postma SCJ, Roor J, van Waesberghe JHTM, van den Bergh JE, Nota IM, Moos S, Kemna R, Vadakkumpadan F, Ambrozic C, van Dieren S, van Amerongen MJ, Chapelle T, Engelbrecht MRW, Gerhards MF, Grunhagen D, van Gulik TM, Hermans JJ, de Jong KP, Klaase JM, Liem MSL, van Lienden KP, Molenaar IQ, Patijn GA, Rijken AM, Ruers TM, Verhoef C, de Wilt JHW, Marquering HA, Stoker J, Swijnenburg RJ, Punt CJA, Huiskens J, Kazemier G. Deep learning models for automatic tumor segmentation and total tumor volume assessment in patients with colorectal liver metastases. *Eur Radiol Exp* 2023; **7**: 75 [RCA] [PMID: 38038829] DOI: 10.1186/s41747-023-00383-4 [FullText]
- 123 **Bertsimas D**, Margonis GA, Sujichantararat S, Boerner T, Ma Y, Wang J, Kamphues C, Sasaki K, Tang S, Gagniere J, Dupré A, Løes IM, Wagner D, Stasinou G, Macher-Beer A, Burkhardt R, Morioka D, Imai K, Ardiles V, O'Connor JM, Pawlik TM, Poultides G, Seeliger H, Beyer K, Kaczirek K, Kornprat P, Aucejo FN, de Santibañes E, Baba H, Endo I, Lønning PE, Kreis ME, Weiss MJ, Wolfgang CL, D'Angelica M. Using Artificial Intelligence to Find the Optimal Margin Width in Hepatectomy for Colorectal Cancer Liver Metastases. *JAMA Surg* 2022; **157**: e221819 [RCA] [PMID: 35648428] DOI: 10.1001/jamasurg.2022.1819 [FullText]
- 124 **Wang X**, Zheng Z, Xie Z, Yu Q, Lu X, Zhao Z, Huang S, Huang Y, Chi P. Development and validation of artificial intelligence models for preoperative prediction of inferior mesenteric artery lymph nodes metastasis in left colon and rectal cancer. *Eur J Surg Oncol* 2022; **48**: 2475-2486 [RCA] [PMID: 35864013] DOI: 10.1016/j.ejso.2022.06.009 [FullText]
- 125 **Susič D**, Syed-Abdul S, Dovgan E, Jonnagaddala J, Gradišek A. Artificial intelligence based personalized predictive survival among colorectal cancer patients. *Comput Methods Programs Biomed* 2023; **231**: 107435 [RCA] [PMID: 36842345] DOI: 10.1016/j.cmpb.2023.107435 [FullText]
- 126 **Hummel JJ**, Liu D, Tallon E, Snyder J, Warren W, Shyu CR, Mitchem J, Cortese R. Identification of Genomic Signatures for Colorectal Cancer Survival Using Exploratory Data Mining. *Int J Mol Sci* 2024; **25**: 3220 [RCA] [PMID: 38542194] DOI: 10.3390/ijms25063220 [FullText]
- 127 **Taylor RS**, Taylor RJ, Bayliss S, Hagström H, Nasr P, Schattenberg JM, Ishigami M, Toyoda H, Wai-Sun Wong V, Peleg N, Shlomai A, Sebastiani G, Seko Y, Bhala N, Younossi ZM, Anstee QM, McPherson S, Newsome PN. Association Between Fibrosis Stage and Outcomes of Patients With Nonalcoholic Fatty Liver Disease: A Systematic Review and Meta-Analysis. *Gastroenterology* 2020; **158**: 1611-1625.e12 [RCA] [PMID: 32027911] DOI: 10.1053/j.gastro.2020.01.043 [FullText]
- 128 **Kanwal F**, Shubrook RH, Adams LA, Pfothenauer K, Wai-Sun Wong V, Wright E, Abdelmalek MF, Harrison SA, Loomba R, Mantzoros CS, Bugianesi E, Eckel RH, Kaplan LM, El-Serag HB, Cusi K. Clinical Care Pathway for the Risk Stratification and Management of Patients With Nonalcoholic Fatty Liver Disease. *Gastroenterology* 2021; **161**: 1657-1669 [RCA] [PMID: 34602251] DOI: 10.1053/j.gastro.2021.07.049 [FullText]
- 129 **Vianna P**, Calce SI, Boustros P, Larocque-Rigney C, Patry-Beaudoin L, Luo YH, Aslan E, Marinos J, Alamri TM, Vu KN, Murphy-Lavallée J, Billiard JS, Montagnon E, Li H, Kadoury S, Nguyen BN, Gauthier S, Therien B, Rish I, Belilovsky E, Wolf G, Chassé M, Cloutier G, Tang A. Comparison of Radiologists and Deep Learning for US Grading of Hepatic Steatosis. *Radiology* 2023; **309**: e230659 [RCA] [PMID: 37787678] DOI: 10.1148/radiol.230659 [FullText]
- 130 **Iyer JS**, Juyal D, Le Q, Shanis Z, Pokkalla H, Pouryahya M, Pedawi A, Stanford-Moore SA, Biddle-Snead C, Carrasco-Zevallos O, Lin M, Egger R, Hoffman S, Elliott H, Leidal K, Myers RP, Chung C, Billin AN, Watkins TR, Patterson SD, Resnick M, Wack K, Glickman J, Burt AD, Loomba R, Sanyal AJ, Glass B, Montalto MC, Taylor-Weiner A, Wapinski I, Beck AH. AI-based automation of enrollment criteria and endpoint assessment in clinical trials in liver diseases. *Nat Med* 2024; **30**: 2914-2923 [RCA] [PMID: 39112795] DOI: 10.1038/s41591-024-03172-7 [FullText]
- 131 **Naoumov NV**, Brees D, Loeffler J, Chng E, Ren Y, Lopez P, Tai D, Lamle S, Sanyal AJ. Digital pathology with artificial intelligence analyses provides greater insights into treatment-induced fibrosis regression in NASH. *J Hepatol* 2022; **77**: 1399-1409 [RCA] [PMID: 35779659] DOI: 10.1016/j.jhep.2022.06.018 [FullText]
- 132 **Qiu QT**, Zhang J, Duan JH, Wu SZ, Ding JL, Yin Y. Development and validation of radiomics model built by incorporating machine learning for identifying liver fibrosis and early-stage cirrhosis. *Chin Med J (Engl)* 2020; **133**: 2653-2659 [RCA] [PMID: 33009025] DOI: 10.1097/CM9.0000000000001113 [FullText] [FullText(PDF)]
- 133 **Wen H**, Zheng W, Li M, Li Q, Liu Q, Zhou J, Liu Z, Chen X. Multiparametric Quantitative US Examination of Liver Fibrosis: A Feature-Engineering and Machine-Learning Based Analysis. *IEEE J Biomed Health Inform* 2022; **26**: 715-726 [RCA] [PMID: 34329172] DOI: 10.1109/JBHI.2021.3100319 [FullText]
- 134 **Sato M**, Kobayashi T, Soroida Y, Tanaka T, Nakatsuka T, Nakagawa H, Nakamura A, Kurihara M, Endo M, Hikita H, Sato M, Gotoh H, Iwai T, Tateishi R, Koike K, Yatomi Y. Development of novel deep multimodal representation learning-based model for the differentiation of liver tumors on B-mode ultrasound images. *J Gastroenterol Hepatol* 2022; **37**: 678-684 [RCA] [PMID: 34911147] DOI: 10.1111/jgh.15763 [FullText]
- 135 **Zheng Z**, Wang M, Fan C, Wang C, He X, He X. Light&fast generative adversarial network for high-fidelity CT image synthesis of liver tumor. *Comput Methods Programs Biomed* 2024; **254**: 108252 [RCA] [PMID: 38843572] DOI: 10.1016/j.cmpb.2024.108252 [FullText]
- 136 **Said D**, Carbonell G, Stocker D, Hectors S, Vietti-Violi N, Bane O, Chin X, Schwartz M, Tabrizian P, Lewis S, Greenspan H, Jégou S, Schiratti JB, Jehanno P, Taouli B. Semiautomated segmentation of hepatocellular carcinoma tumors with MRI using convolutional neural networks. *Eur Radiol* 2023; **33**: 6020-6032 [RCA] [PMID: 37071167] DOI: 10.1007/s00330-023-09613-0 [FullText]
- 137 **Nakai H**, Sakamoto R, Kakigi T, Coeur C, Isoda H, Nakamoto Y. Artificial intelligence-powered software detected more than half of the liver metastases overlooked by radiologists on contrast-enhanced CT. *Eur J Radiol* 2023; **163**: 110823 [RCA] [PMID: 37059006] DOI: 10.1016/j.ejrad.2023.110823 [FullText]
- 138 **Chen C**, Chen C, Ma M, Ma X, Lv X, Dong X, Yan Z, Zhu M, Chen J. Classification of multi-differentiated liver cancer pathological images based on deep learning attention mechanism. *BMC Med Inform Decis Mak* 2022; **22**: 176 [RCA] [PMID: 35787805] DOI: 10.1186/s12911-022-01919-1 [FullText] [FullText(PDF)]
- 139 **Zeng Q**, Klein C, Caruso S, Maille P, Laleh NG, Sommacale D, Laurent A, Amaddeo G, Gentien D, Rapinat A, Regnault H, Charpy C, Nguyen CT, Tournigand C, Brustia R, Pawlowsky JM, Kather JN, Maiuri MC, Loménie N, Calderaro J. Artificial intelligence predicts immune and inflammatory gene signatures directly from hepatocellular carcinoma histology. *J Hepatol* 2022; **77**: 116-127 [RCA] [PMID: 35143898] DOI: 10.1016/j.jhep.2022.01.018 [FullText]

- 140 **Yu Y**, Cao L, Shen B, Du M, Gu W, Gu C, Fan Y, Shi C, Wu Q, Zhang T, Zhu M, Wang X, Hu C. Deep Learning Radiopathomics Models Based on Contrast-enhanced MRI and Pathologic Imaging for Predicting Vessels Encapsulating Tumor Clusters and Prognosis in Hepatocellular Carcinoma. *Radiol Imaging Cancer* 2025; **7**: e240213 [RCA] [PMID: 40084948 DOI: 10.1148/rycan.240213] [FullText]
- 141 **Famularo S**, Penzo C, Maino C, Milana F, Oliva R, Marescaux J, Diana M, Romano F, Giulante F, Ardito F, Grazi GL, Donadon M, Torzilli G. Preoperative detection of hepatocellular carcinoma's microvascular invasion on CT-scan by machine learning and radiomics: A preliminary analysis. *Eur J Surg Oncol* 2025; **51**: 108274 [RCA] [PMID: 38538504 DOI: 10.1016/j.ejso.2024.108274] [FullText]
- 142 **Li X**, Qi Z, Du H, Geng Z, Li Z, Qin S, Zhang X, Liang J, Zhang X, Liang W, Yang W, Xie C, Quan X. Deep convolutional neural network for preoperative prediction of microvascular invasion and clinical outcomes in patients with HCCs. *Eur Radiol* 2022; **32**: 771-782 [RCA] [PMID: 34347160 DOI: 10.1007/s00330-021-08198-w] [FullText]
- 143 **Chu T**, Zhao C, Zhang J, Duan K, Li M, Zhang T, Lv S, Liu H, Wei F. Application of a Convolutional Neural Network for Multitask Learning to Simultaneously Predict Microvascular Invasion and Vessels that Encapsulate Tumor Clusters in Hepatocellular Carcinoma. *Ann Surg Oncol* 2022; **29**: 6774-6783 [RCA] [PMID: 35754067 DOI: 10.1245/s10434-022-12000-6] [FullText] [Full Text(PDF)]
- 144 **Lin H**, Li G, Delamarre A, Ahn SH, Zhang X, Kim BK, Liang LY, Lee HW, Wong GL, Yuen PC, Chan HL, Chan SL, Wong VW, de Lédinghen V, Kim SU, Yip TC. A Liver Stiffness-Based Etiology-Independent Machine Learning Algorithm to Predict Hepatocellular Carcinoma. *Clin Gastroenterol Hepatol* 2024; **22**: 602-610.e7 [RCA] [PMID: 37993034 DOI: 10.1016/j.cgh.2023.11.005] [FullText]
- 145 **Yan M**, Zhang X, Zhang B, Geng Z, Xie C, Yang W, Zhang S, Qi Z, Lin T, Ke Q, Li X, Wang S, Quan X. Deep learning nomogram based on Gd-EOB-DTPA MRI for predicting early recurrence in hepatocellular carcinoma after hepatectomy. *Eur Radiol* 2023; **33**: 4949-4961 [RCA] [PMID: 36786905 DOI: 10.1007/s00330-023-09419-0] [FullText]
- 146 **Zhang J**, Chen Q, Zhang Y, Zhou J. Construction of a random survival forest model based on a machine learning algorithm to predict early recurrence after hepatectomy for adult hepatocellular carcinoma. *BMC Cancer* 2024; **24**: 1575 [RCA] [PMID: 39722042 DOI: 10.1186/s12885-024-13366-4] [FullText]
- 147 **Gao Y**, Yang X, Li H, Ding DW. A knowledge-enhanced interpretable network for early recurrence prediction of hepatocellular carcinoma via multi-phase CT imaging. *Int J Med Inform* 2024; **189**: 105509 [RCA] [PMID: 38851131 DOI: 10.1016/j.ijmedinf.2024.105509] [FullText]
- 148 **Li Z**, Lan L, Zhou Y, Li R, Chavin KD, Xu H, Li L, Shih DJH, Jim Zheng W. Developing deep learning-based strategies to predict the risk of hepatocellular carcinoma among patients with nonalcoholic fatty liver disease from electronic health records. *J Biomed Inform* 2024; **152**: 104626 [RCA] [PMID: 38521180 DOI: 10.1016/j.jbi.2024.104626] [FullText]
- 149 **Huang S**, Tu T. Integrating single cell analysis and machine learning methods reveals stem cell-related gene S100A10 as an important target for prediction of liver cancer diagnosis and immunotherapy. *Front Immunol* 2024; **15**: 1534723 [RCA] [PMID: 39840058 DOI: 10.3389/fimmu.2024.1534723] [FullText]
- 150 **Chen E**, Zou Z, Wang R, Liu J, Peng Z, Gan Z, Lin Z, Liu J. Predictive value of a stemness-based classifier for prognosis and immunotherapy response of hepatocellular carcinoma based on bioinformatics and machine-learning strategies. *Front Immunol* 2024; **15**: 1244392 [RCA] [PMID: 38694506 DOI: 10.3389/fimmu.2024.1244392] [FullText] [Full Text(PDF)]
- 151 **Liao M**, Di S, Zhao Y, Liang W, Yang Z. FA-Net: A hierarchical feature fusion and interactive attention-based network for dose prediction in liver cancer patients. *Artif Intell Med* 2024; **156**: 102961 [RCA] [PMID: 39180923 DOI: 10.1016/j.artmed.2024.102961] [FullText]
- 152 **Altaf A**, Mustafa A, Dar A, Nazer R, Riyaz S, Rana A, Bhatti ABH. Artificial intelligence-based model for the recurrence of hepatocellular carcinoma after liver transplantation. *Surgery* 2024; **176**: 1500-1506 [RCA] [PMID: 39181726 DOI: 10.1016/j.surg.2024.07.039] [FullText]
- 153 **Wu X**, Zhang T, Zhang T, Park S. The impact of gut microbiome enterotypes on ulcerative colitis: identifying key bacterial species and revealing species co-occurrence networks using machine learning. *Gut Microbes* 2024; **16**: 2292254 [RCA] [PMID: 38117560 DOI: 10.1080/19490976.2023.2292254] [FullText] [Full Text(PDF)]
- 154 **Barberio B**, Facchin S, Patuzzi I, Ford AC, Massimi D, Valle G, Sattin E, Simionati B, Bertazzo E, Zingone F, Savarino EV. A specific microbiota signature is associated to various degrees of ulcerative colitis as assessed by a machine learning approach. *Gut Microbes* 2022; **14**: 2028366 [RCA] [PMID: 35129058 DOI: 10.1080/19490976.2022.2028366] [FullText] [Full Text(PDF)]
- 155 **Gao S**, Gao X, Zhu R, Wu D, Feng Z, Jiao N, Sun R, Gao W, He Q, Liu Z, Zhu L. Microbial genes outperform species and SNVs as diagnostic markers for Crohn's disease on multicohort fecal metagenomes empowered by artificial intelligence. *Gut Microbes* 2023; **15**: 2221428 [RCA] [PMID: 37278203 DOI: 10.1080/19490976.2023.2221428] [FullText]
- 156 **Jing Z**, Zheng W, Jianwen S, Hong S, Xiaojian Y, Qiang W, Yunfeng Y, Xinyue W, Shuwen H, Feimin Z. Gut microbes on the risk of advanced adenomas. *BMC Microbiol* 2024; **24**: 264 [RCA] [PMID: 39026166 DOI: 10.1186/s12866-024-03416-z] [FullText]
- 157 **Villani A**, Fontana A, Panebianco C, Ferro C, Copetti M, Pavlovic R, Drago D, Fiorentini C, Terracciano F, Bazzocchi F, Canistro G, Pisati F, Maiello E, Latiano TP, Perri F, Paziienza V. A powerful machine learning approach to identify interactions of differentially abundant gut microbial subsets in patients with metastatic and non-metastatic pancreatic cancer. *Gut Microbes* 2024; **16**: 2375483 [RCA] [PMID: 38972056 DOI: 10.1080/19490976.2024.2375483] [FullText]
- 158 **Bajaj JS**, O'Leary JG, Jakab SS, Fagan A, Sikaroodi M, Gillevet PM. Gut microbiome profiles to exclude the diagnosis of hepatic encephalopathy in patients with cirrhosis. *Gut Microbes* 2024; **16**: 2392880 [RCA] [PMID: 39189586 DOI: 10.1080/19490976.2024.2392880] [FullText]
- 159 **Huang H**, Ren Z, Gao X, Hu X, Zhou Y, Jiang J, Lu H, Yin S, Ji J, Zhou L, Zheng S. Integrated analysis of microbiome and host transcriptome reveals correlations between gut microbiota and clinical outcomes in HBV-related hepatocellular carcinoma. *Genome Med* 2020; **12**: 102 [RCA] [PMID: 33225985 DOI: 10.1186/s13073-020-00796-5] [FullText] [Full Text(PDF)]
- 160 **Jin D-M**, Morton JT, Bonneau R. Meta-analysis of the human gut microbiome uncovers shared and distinct microbial signatures between diseases. *mSystems* 2024; **9**: e0029524 [RCA] [PMID: 39078158 DOI: 10.1128/msystems.00295-24] [FullText]
- 161 **GBD 2021 Antimicrobial Resistance Collaborators**. Global burden of bacterial antimicrobial resistance 1990-2021: a systematic analysis with forecasts to 2050. *Lancet* 2024; **404**: 1199-1226 [RCA] [PMID: 39299261 DOI: 10.1016/S0140-6736(24)01867-1] [FullText] [Full Text (PDF)]
- 162 **Melchiorri D**, Rocke T, Alm RA, Cameron AM, Gigante V. Addressing urgent priorities in antibiotic development: insights from WHO 2023 antibacterial clinical pipeline analyses. *Lancet Microbe* 2025; **6**: 100992 [RCA] [PMID: 39454608 DOI: 10.1016/j.lanmic.2024.100992] [FullText]
- 163 **Solomkin JS**, Gardovskis J, Lawrence K, Montravers P, Sway A, Evans D, Tsai L. IGNITE4: Results of a Phase 3, Randomized, Multicenter, Prospective Trial of Eravacycline vs Meropenem in the Treatment of Complicated Intraabdominal Infections. *Clin Infect Dis* 2019; **69**: 921-929 [RCA] [PMID: 30561562 DOI: 10.1093/cid/ciy1029] [FullText] [Full Text(PDF)]
- 164 **Wagenlehner FME**, Cloutier DJ, Komirenko AS, Cebrik DS, Krause KM, Keepers TR, Connolly LE, Miller LG, Friedland I, Dwyer JP, EPIC

- Study Group. Once-Daily Plazomicin for Complicated Urinary Tract Infections. *N Engl J Med* 2019; **380**: 729-740 [RCA] [PMID: 30786187 DOI: 10.1056/NEJMoa1801467] [FullText]
- 165 **Tommasi R**, Brown DG, Walkup GK, Manchester JL, Miller AA. ESKAPEing the labyrinth of antibacterial discovery. *Nat Rev Drug Discov* 2015; **14**: 529-542 [RCA] [PMID: 26139286 DOI: 10.1038/nrd4572] [FullText]
- 166 **Scalia G**, Rutherford ST, Lu Z, Buchholz KR, Skelton N, Chuang K, Diamant N, Hütter J, Luescher J, Miu A, Blaney J, Gendelev L, Skippington E, Zynda G, Dickson N, Koziarski M, Bengio Y, Regev A, Tan M, Biancalani T. A high-throughput phenotypic screen combined with an ultra-large-scale deep learning-based virtual screening reveals novel scaffolds of antibacterial compounds. 2024 Preprint [DOI: 10.1101/2024.09.11.612340] [FullText]
- 167 **Santos-Júnior CD**, Torres MDT, Duan Y, Rodríguez Del Río Á, Schmidt TSB, Chong H, Fullam A, Kuhn M, Zhu C, Houseman A, Somborski J, Vines A, Zhao XM, Bork P, Huerta-Cepas J, de la Fuente-Nunez C, Coelho LP. Discovery of antimicrobial peptides in the global microbiome with machine learning. *Cell* 2024; **187**: 3761-3778.e16 [RCA] [PMID: 38843834 DOI: 10.1016/j.cell.2024.05.013] [FullText]
- 168 **Stokes JM**, Yang K, Swanson K, Jin W, Cubillos-Ruiz A, Donghia NM, MacNair CR, French S, Carfrae LA, Bloom-Ackermann Z, Tran VM, Chiappino-Pepe A, Badran AH, Andrews IW, Chory EJ, Church GM, Brown ED, Jaakkola TS, Barzilay R, Collins JJ. A Deep Learning Approach to Antibiotic Discovery. *Cell* 2020; **180**: 688-702.e13 [RCA] [PMID: 32084340 DOI: 10.1016/j.cell.2020.01.021] [FullText]
- 169 **Wong F**, Zheng EJ, Valeri JA, Donghia NM, Anahtar MN, Omori S, Li A, Cubillos-Ruiz A, Krishnan A, Jin W, Manson AL, Friedrichs J, Helbig R, Hajian B, Fiejtek DK, Wagner FF, Soutter HH, Earl AM, Stokes JM, Renner LD, Collins JJ. Discovery of a structural class of antibiotics with explainable deep learning. *Nature* 2024; **626**: 177-185 [RCA] [PMID: 38123686 DOI: 10.1038/s41586-023-06887-8] [FullText]
- 170 **Maasch JRMA**, Torres MDT, Melo MCR, de la Fuente-Nunez C. Molecular de-extinction of ancient antimicrobial peptides enabled by machine learning. *Cell Host Microbe* 2023; **31**: 1260-1274.e6 [RCA] [PMID: 37516110 DOI: 10.1016/j.chom.2023.07.001] [FullText]
- 171 **Liu G**, Catacutan DB, Rathod K, Swanson K, Jin W, Mohammed JK, Chiappino-Pepe A, Syed SA, Fragas M, Rachwalski K, Magolan J, Surette MG, Coombes BK, Jaakkola T, Barzilay R, Collins JJ, Stokes JM. Deep learning-guided discovery of an antibiotic targeting *Acinetobacter baumannii*. *Nat Chem Biol* 2023; **19**: 1342-1350 [RCA] [PMID: 37231267 DOI: 10.1038/s41589-023-01349-8] [FullText]
- 172 **Dilaghi E**, Lahner E, Annibale B, Esposito G. Systematic review and meta-analysis: Artificial intelligence for the diagnosis of gastric precancerous lesions and *Helicobacter pylori* infection. *Dig Liver Dis* 2022; **54**: 1630-1638 [RCA] [PMID: 35382973 DOI: 10.1016/j.dld.2022.03.007] [FullText]
- 173 **Gao P**, Xiao Q, Tan H, Song J, Fu Y, Xu J, Zhao J, Miao Y, Li X, Jing Y, Feng Y, Wang Z, Zhang Y, Yao E, Xu T, Mei J, Chen H, Jiang X, Yang Y, Wang Z, Gao X, Zheng M, Zhang L, Jiang M, Long Y, He L, Sun J, Deng Y, Wang B, Zhao Y, Ba Y, Wang G, Zhang Y, Deng T, Shen D, Wang Z. Interpretable multi-modal artificial intelligence model for predicting gastric cancer response to neoadjuvant chemotherapy. *Cell Rep Med* 2024; **5**: 101848 [RCA] [PMID: 39637859 DOI: 10.1016/j.xcrm.2024.101848] [FullText]
- 174 **Uema R**, Hayashi Y, Kizu T, Igura T, Ogiyama H, Yamada T, Takeda R, Nagai K, Inoue T, Yamamoto M, Yamaguchi S, Kanesaka T, Yoshihara T, Kato M, Yoshii S, Tsujii Y, Shinzaki S, Takehara T. A novel artificial intelligence-based endoscopic ultrasonography diagnostic system for diagnosing the invasion depth of early gastric cancer. *J Gastroenterol* 2024; **59**: 543-555 [RCA] [PMID: 38713263 DOI: 10.1007/s00535-024-02102-1] [FullText]
- 175 **Guo B**, Li X, Yang M, Jonnagaddala J, Zhang H, Xu XS. Predicting microsatellite instability and key biomarkers in colorectal cancer from H&E-stained images: achieving state-of-the-art predictive performance with fewer data using Swin Transformer. *J Pathol Clin Res* 2023; **9**: 223-235 [RCA] [PMID: 36723384 DOI: 10.1002/cjp.2.312] [FullText]
- 176 **van der Zander QEW**, Roumans R, Kusters CHJ, Dehghani N, Masclee AAM, de With PHN, van der Sommen F, Sniijders CCP, Schoon EJ. Appropriate trust in artificial intelligence for the optical diagnosis of colorectal polyps: the role of human/artificial intelligence interaction. *Gastrointest Endosc* 2024; **100**: 1070-1078.e10 [RCA] [PMID: 38942330 DOI: 10.1016/j.gie.2024.06.029] [FullText]
- 177 **Allgaier J**, Mulansky L, Draelos RL, Pryss R. How does the model make predictions? A systematic literature review on the explainability power of machine learning in healthcare. *Artif Intell Med* 2023; **143**: 102616 [RCA] [PMID: 37673561 DOI: 10.1016/j.artmed.2023.102616] [FullText]
- 178 **Ghassemi N**, Shoeibi A, Khodatars M, Heras J, Rahimi A, Zare A, Zhang YD, Pachori RB, Gorriz JM. Automatic diagnosis of COVID-19 from CT images using CycleGAN and transfer learning. *Appl Soft Comput* 2023; **144**: 110511 [RCA] [PMID: 37346824 DOI: 10.1016/j.asoc.2023.110511] [FullText]
- 179 **Lin QH**, Niu YW, Sui J, Zhao WD, Zhuo C, Calhoun VD. SSPNet: An interpretable 3D-CNN for classification of schizophrenia using phase maps of resting-state complex-valued fMRI data. *Med Image Anal* 2022; **79**: 102430 [RCA] [PMID: 35397470 DOI: 10.1016/j.media.2022.102430] [FullText]
- 180 **Troya J**, Sudarevic B, Krenzer A, Banck M, Brand M, Walter BM, Puppe F, Zoller WG, Meining A, Hann A. Direct comparison of multiple computer-aided polyp detection systems. *Endoscopy* 2024; **56**: 63-69 [RCA] [PMID: 37532115 DOI: 10.1055/a-2147-0571] [FullText]
- 181 **Tang S**, Yu X, Cheang CF, Liang Y, Zhao P, Yu HH, Choi IC. Transformer-based multi-task learning for classification and segmentation of gastrointestinal tract endoscopic images. *Comput Biol Med* 2023; **157**: 106723 [RCA] [PMID: 36907035 DOI: 10.1016/j.combiomed.2023.106723] [FullText]
- 182 **Kim JE**, Choi YH, Lee YC, Seong G, Song JH, Kim TJ, Kim ER, Hong SN, Chang DK, Kim YH, Shin SY. Deep learning model for distinguishing Mayo endoscopic subscore 0 and 1 in patients with ulcerative colitis. *Sci Rep* 2023; **13**: 11351 [RCA] [PMID: 37443370 DOI: 10.1038/s41598-023-38206-6] [FullText]
- 183 **Tang J**, Liang Y, Jiang Y, Liu J, Zhang R, Huang D, Pang C, Huang C, Luo D, Zhou X, Li R, Zhang K, Xie B, Hu L, Zhu F, Xia H, Lu L, Wang H. A multicenter study on two-stage transfer learning model for duct-dependent CHDs screening in fetal echocardiography. *NPJ Digit Med* 2023; **6**: 143 [RCA] [PMID: 37573426 DOI: 10.1038/s41746-023-00883-y] [FullText]
- 184 **You C**, Li G, Zhang Y, Zhang X, Shan H, Li M, Ju S, Zhao Z, Zhang Z, Cong W, Vannier MW, Saha PK, Hoffman EA, Wang G. CT Super-Resolution GAN Constrained by the Identical, Residual, and Cycle Learning Ensemble (GAN-CIRCLE). *IEEE Trans Med Imaging* 2020; **39**: 188-203 [RCA] [PMID: 31217097 DOI: 10.1109/TMI.2019.2922960] [FullText]
- 185 **Chartsias A**, Joyce T, Papanastasiou G, Semple S, Williams M, Newby DE, Dharmakumar R, Tsafaris SA. Disentangled representation learning in cardiac image analysis. *Med Image Anal* 2019; **58**: 101535 [RCA] [PMID: 31351230 DOI: 10.1016/j.media.2019.101535] [FullText]
- 186 **Pati S**, Baid U, Edwards B, Sheller M, Wang SH, Reina GA, Foley P, Gruzdev A, Karkada D, Davatzikos C, Sako C, Ghodasara S, Bilello M, Mohan S, Vollmuth P, Brugnara G, Preetha CJ, Sahm F, Maier-Hein K, Zenk M, Bendszus M, Wick W, Calabrese E, Rudie J, Villanueva-Meyer J, Cha S, Ingahlhalikar M, Jadhav M, Pandey U, Saini J, Garrett J, Larson M, Jeraj R, Currie S, Frood R, Fatania K, Huang RY, Chang K,

- Balaña C, Capellades J, Puig J, Trenkler J, Pichler J, Necker G, Haunschmidt A, Meckel S, Shukla G, Liem S, Alexander GS, Lombardo J, Palmer JD, Flanders AE, Dicker AP, Sair HI, Jones CK, Venkataraman A, Jiang M, So TY, Chen C, Heng PA, Dou Q, Kozubek M, Lux F, Michálek J, Matula P, Keřkovský M, Kopřivová T, Dostál M, Vybíhal V, Vogelbaum MA, Mitchell JR, Farinhas J, Maldjian JA, Yogananda CGB, Pinho MC, Reddy D, Holcomb J, Wagner BC, Ellingson BM, Cloughesy TF, Raymond C, Oughourlian T, Hagiwara A, Wang C, To MS, Bhardwaj S, Chong C, Agzarian M, Falcão AX, Martins SB, Teixeira BCA, Sprenger F, Menotti D, Lucio DR, LaMontagne P, Marcus D, Wiestler B, Kofler F, Ezhov I, Metz M, Jain R, Lee M, Lui YW, McKinley R, Slotboom J, Radojewski P, Meier R, Wiest R, Murcia D, Fu E, Haas R, Thompson J, Ormond DR, Badve C, Sloan AE, Vadmal V, Waite K, Colen RR, Pei L, Ak M, Srinivasan A, Bapuraj JR, Rao A, Wang N, Yoshiaki O, Moritani T, Turk S, Lee J, Prabhudesai S, Morón F, Mandel J, Kamnitsas K, Glocker B, Dixon LVM, Williams M, Zampakis P, Panagiotopoulos V, Tsiganos P, Alexiou S, Haliassos I, Zacharakis EI, Moustakas K, Kalogeropoulou C, Kardamakis DM, Choi YS, Lee SK, Chang JH, Ahn SS, Luo B, Poisson L, Wen N, Tiwari P, Verma R, Bareja R, Yadav I, Chen J, Kumar N, Smits M, van der Voort SR, Alafandi A, Incekar F, Wijnenga MMJ, Kapsas G, Gahrman R, Schouten JW, Dubbink HJ, Vincent AJPE, van den Bent MJ, French PJ, Klein S, Yuan Y, Sharma S, Tseng TC, Adabi S, Niclou SP, Keunen O, Hau AC, Vallières M, Fortin D, Lepage M, Landman B, Ramadass K, Xu K, Chotai S, Chambless LB, Mistry A, Thompson RC, Gusev Y, Bhuvaneshwar K, Sayah A, Bencheqroun C, Belouali A, Madhavan S, Booth TC, Chelliah A, Modat M, Shuaib H, Dragos C, Abayazeed A, Kolodziej K, Hill M, Abbassy A, Gamal S, Mekhaimar M, Qayati M, Reyes M, Park JE, Yun J, Kim HS, Mahajan A, Muzi M, Benson S, Beets-Tan RGH, Teuwen J, Herrera-Trujillo A, Trujillo M, Escobar W, Abello A, Bernal J, Gómez J, Choi J, Baek S, Kim Y, Ismael H, Allen B, Buatti JM, Kotrotsou A, Li H, Weiss T, Weller M, Bink A, Pouymayou B, Shaykh HF, Saltz J, Prasanna P, Shrestha S, Mani KM, Payne D, Kurc T, Pelaez E, Franco-Maldonado H, Loayza F, Quevedo S, Guevara P, Torche E, Mendoza C, Vera F, Ríos E, López E, Velastin SA, Ogbole G, Soneye M, Oyekunle D, Odafe-Oyibotho O, Osobu B, Shu'aibu M, Dorcas A, Dako F, Simpson AL, Hamghalam M, Peoples JJ, Hu R, Tran A, Cutler D, Moraes FY, Boss MA, Gimpel J, Veettil DK, Schmidt K, Bialecki B, Marella S, Price C, Cimino L, Apgar C, Shah P, Menze B, Barnholtz-Sloan JS, Martin J, Bakas S. Federated learning enables big data for rare cancer boundary detection. *Nat Commun* 2022; **13**: 7346 [RCA] [PMID: 36470898 DOI: 10.1038/s41467-022-33407-5] [FullText] [Full Text(PDF)]
- 187 **Sarma KV**, Harmon S, Sanford T, Roth HR, Xu Z, Tetreault J, Xu D, Flores MG, Raman AG, Kulkarni R, Wood BJ, Choyke PL, Priester AM, Marks LS, Raman SS, Enzmann D, Turkbey B, Speier W, Arnold CW. Federated learning improves site performance in multicenter deep learning without data sharing. *J Am Med Inform Assoc* 2021; **28**: 1259-1264 [RCA] [PMID: 33537772 DOI: 10.1093/jamia/ocaa341] [FullText] [Full Text(PDF)]
- 188 **Sharma J**, Kumar D, Verma R. Secure and Collaborative Breast Cancer Detection Using Federated Learning. 2024 2nd World Conference on Communication & Computing (WCONF); 2024 July 12-14; RAIPUR, India. IEEE, 2024 [DOI: 10.1109/wconf61366.2024.10692318] [Full Text]
- 189 **Alsalmán H**, Al-rakhami MS, Alfakih T, Hassan MM. Federated Learning Approach for Breast Cancer Detection Based on DCNN. *IEEE Access* 2024; **12**: 40114-40138 [DOI: 10.1109/access.2024.3374650] [FullText]
- 190 **Varkalaite G**, Forster M, Franke A, Kupcinkas J, Skieceviciene J. Liquid Biopsy in Gastric Cancer: Analysis of Somatic Cancer Tissue Mutations in Plasma Cell-Free DNA for Predicting Disease State and Patient Survival. *Clin Transl Gastroenterol* 2021; **12**: e00403 [RCA] [PMID: 34644276 DOI: 10.14309/ctg.0000000000000403] [FullText] [Full Text(PDF)]
- 191 **Dai SL**, Pan JQ, Su ZR. Multi-omics features of immunogenic cell death in gastric cancer identified by combining single-cell sequencing analysis and machine learning. *Sci Rep* 2024; **14**: 21751 [RCA] [PMID: 39294296 DOI: 10.1038/s41598-024-73071-x] [FullText]
- 192 **Maeda Y**, Kudo SE, Ogata N, Misawa M, Iacucci M, Homma M, Nemoto T, Takishima K, Mochida K, Miyachi H, Baba T, Mori K, Ohtsuka K, Mori Y. Evaluation in real-time use of artificial intelligence during colonoscopy to predict relapse of ulcerative colitis: a prospective study. *Gastrointest Endosc* 2022; **95**: 747-756.e2 [RCA] [PMID: 34695422 DOI: 10.1016/j.gie.2021.10.019] [FullText]



Published by **Baishideng Publishing Group Inc**
7041 Koll Center Parkway, Suite 160, Pleasanton, CA 94566, USA

Telephone: +1-925-3991568

E-mail: office@baishideng.com

Help Desk: <https://www.f6publishing.com/helpdesk>

<https://www.wjgnet.com>

