ESMO - AI 2025 Clinical and AI / ML Preview

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2025 ESMO AI & DIGITAL ONCOLOGY

Annual Congress

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ESMO - AI 2025 – General Overview

- **Global AI & Digital Oncology Focus:** ESMO AI 2025 is a premier international gathering dedicated to advancing artificial intelligence and digital health in oncology, driving scientific innovation and clinical practice transformation
- **Multidisciplinary Collaboration:** The conference will bring together oncology experts, data scientists, tech innovators, and regulatory professionals to explore collaborative applications of AI in cancer care
- **Cutting-Edge AI Tools:** It will feature discussions on the latest AI models, deep learning technologies, and digital tools designed to optimize cancer detection, treatment, and patient management
- **Industry Partnerships:** The event will showcase collaborations between pharma, digital health innovators, and AI tech companies, highlighting advancements in personalized oncology
- **Innovation & Exhibitions:** A hands-on expo will demonstrate the newest AI-driven diagnostics, imaging systems, and treatment platforms for oncology
- **Flexible Access & Hybrid Participation:** Attendees will have full access to scientific content, both onsite and virtually, ensuring global engagement and comprehensive participation

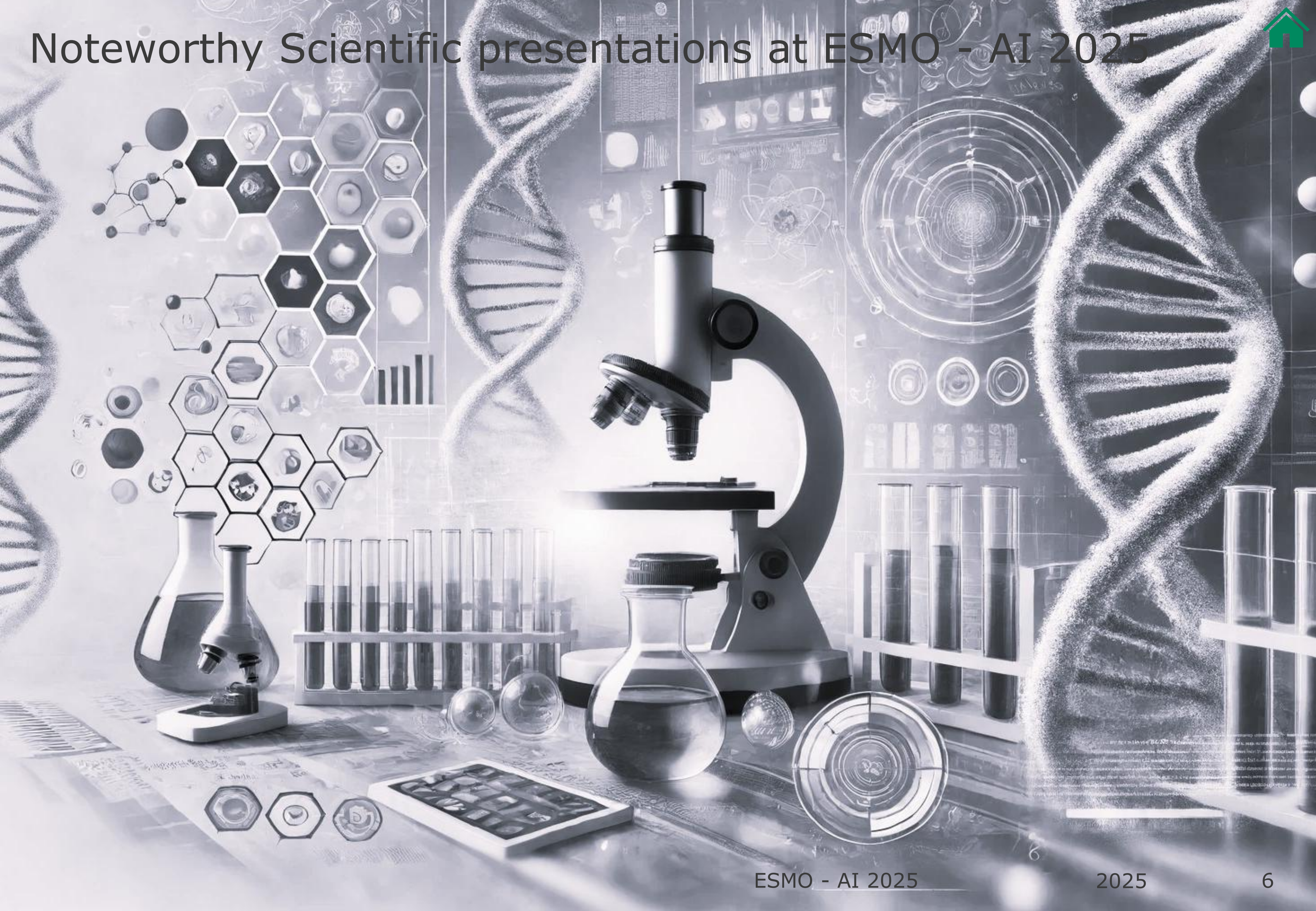
ESMO - AI 2025– Conference Themes (1/2)

- **AI in Digital Pathology:** The conference will cover how AI-driven deep learning models are transforming tissue classification, segmentation, and quantification in oncology
- **Imaging AI for Precision Oncology:** Key discussions will focus on the integration of radiomics with AI for predictive modeling, survival outcomes, and treatment response assessments
- **Multi-Omics & Genomics Integration:** AI applications in genomics and multi-omics will be explored to identify biomarkers and optimize cancer risk stratification.
- **Clinical Decision Support Systems:** Presentations will address how AI can guide treatment decision-making and predict outcomes, managing toxicities in cancer therapy
- **AI in Clinical Trials:** AI-powered systems for patient-trial matching, synthetic control arms, and accelerating drug development will be a focus

ESMO - AI 2025– Conference Themes (2/2)

- **AI for Immunotherapy Response:** The role of AI in predicting patient responses to immunotherapies, such as checkpoint inhibitors and ADCs, will be highlighted
- **Digital Health & ePROs:** The integration of telemedicine, wearables, and patient-reported outcomes (ePROs) into AI-driven cancer management will be discussed
- **AI Ethics & Regulatory Considerations:** Ethical issues surrounding AI transparency, data privacy, and its regulatory landscape in oncology will be debated
- **AI & Patient Outcomes:** The focus will be on how AI enhances patient monitoring, symptom tracking, and long-term survival prediction
- **Cross-Disciplinary AI Platforms:** AI integration across multiple domains in oncology, from diagnostics to treatment planning and patient follow-up, will be explored

Noteworthy Scientific presentations at ESMO - AI 2025



Key Topics From Notable Presentations (1/10)

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- **AI for Treatment Response, Immunotherapy & Precision Oncology:** The conference will highlight how integration of AI-driven biomarkers, machine learning models, and digital pathology will enable personalized, precision oncology treatments, improving patient outcomes by tailoring therapies and predicting responses in various cancer types

  - Personalized Biomarkers & Predictive Models: AI and multi-omic profiling in NSCLC, TNBC, and melanoma have identified key biomarkers like pTLS and immune signatures, enabling personalized treatment strategies, including immunotherapy and antibody-drug conjugates (ADCs)

  - AI in Prognosis & Survival Prediction: Machine learning models, including SVM and XGBoost, have demonstrated efficacy in predicting overall survival (OS) and long-term survival (LTS) across various cancers, including metastatic NSCLC, CRC, and aHCC

  - Innovative AI Applications in Diagnosis & Treatment Scheduling: AI-powered tools for early-stage cancer diagnosis (e.g., NSCLC) and circadian rhythm-based ICI scheduling have the potential to optimize clinical workflows and improve therapeutic efficacy, offering real-time decision support

Key Topics From Notable Presentations (2/10)

- **Cross-Domain, Multi-Agent & Integrative Platforms:** Discussions will focus on how AI-driven platforms are set to automate workflows, integrate multi-modal data for personalized oncology care, and enhance real-time global collaboration, transforming oncology decision-making and improving patient outcomes
  - AI-Driven Oncology Decision Support: Sessions are set to highlight how AI-powered platforms like ClioAssist and Konsuld® will automate clinical workflows, offer real-time decision support, and enable global peer consultations, enhancing efficiency and patient care
  - AI and Data Integration for Personalized Oncology: Experts will discuss how platforms such as OPTIMA and Lymphoma Data Hub (LDH) are set to integrate real-world, multi-modal data for AI-driven insights, advancing personalized treatment and cancer research
  - Advancements in Collaborative Oncology Tools: Presentations will showcase how Molecular Tumor Boards (MTBs) and Agentic Tumor Boards (ATBs), powered by AI and LLMs, will synthesize clinical data, improve therapeutic decision-making, and enhance collaboration among oncology specialists

Key Topics From Notable Presentations (3/10)

- **Digital Health, Patient Monitoring & ePROs:** Sessions at ESMO AI 2025 will focus on how AI-powered tools, wearable devices, and ePRO platforms are set to transform cancer care, enhancing patient monitoring, optimizing treatment plans, and improving overall clinical efficiency

- Innovative mHealth Monitoring: Sessions will highlight how mobile apps, wearables, and smart devices are enhancing patient monitoring in oncology, particularly in metastatic uveal melanoma (UM), chemotherapy, and radiotherapy

- AI-Enabled Cancer Care: Experts will discuss AI-powered solutions like Careology and Oncology Concierge, which are optimizing oncology care through proactive symptom monitoring, reducing in-person visits, and enhancing patient satisfaction

- ePROs for Symptom Monitoring: Presentations will explore the integration of ePROs with Fitbit data and digital platforms, enabling real-time symptom tracking, improving clinical workflows, and enhancing quality of life (QoL) for cancer patients

Key Topics From Notable Presentations (4/10)

- **Ethics, Regulatory & Implementation Science:** Sessions are set to address the integration of AI in oncology, focusing on its adoption, regulatory hurdles, real-world applications, and global accessibility in both high-resource and low-resource settings, guiding future ethical and regulatory frameworks
  - AI/ML Integration in Oncology: Sessions will explore how AI tools like Eyonis® LCS and AI for breast and lung cancer detection are gaining traction in oncology, focusing on challenges, regulatory barriers, and early clinical adoption
  - AI in Low-Income Settings: Discussions will focus on the AI-driven models for early detection and patient management in low- and middle-income countries (LMICs), emphasizing culturally sensitive technologies for overcoming healthcare barriers
  - Real-World AI Challenges: Experts will examine the AI adoption in oncology through the lens of workforce readiness, ethical concerns, data privacy, and training required for clinical implementation, providing insights into the current landscape and future directions

Key Topics From Notable Presentations (5/10)

- **Genomics, Multi-Omics & Biomarker Discovery:** Sessions are set to explore advancements in genomic and multi-omic technologies, with a focus on AI's potential in biomarker discovery, personalized cancer care, and precision oncology, guiding future diagnostic and therapeutic strategies
  - AI-Driven DNA Language Models for Genomic Diagnostics: Sessions will focus on the use of AI/ML-driven DNA language models (DNA-LMs) for improved cancer subtype classification and genomic diagnostics, showing promise for clinical applications
  - Integrating Genomic & Metabolic Data for Glioma Research: Genetic and metabolic profiling to enhance glioma diagnosis and risk prediction, with an emphasis on identifying new targets for precision neuro-oncology
  - Advances in Predictive Biomarkers for Cancer: Experts will discuss AI-powered biomarker discovery in pancreatic cancer, glioma, melanoma, and endometrial cancer, showcasing multi-omic integration to improve survival predictions and personalized treatment approaches

Key Topics From Notable Presentations (6/10)

- **Clinical Decision Support & Prognostic Modelling:** Experts will discuss how the integration of machine learning (ML) and AI tools in oncology significantly improves personalized decision-making and prognostic accuracy, enabling better-tailored treatment strategies and risk stratification across various cancers
  - AI-driven tools in breast cancer: Deep learning-based AI models showed high accuracy in predicting recurrence risk for HR+/HER2– breast cancer, outperforming traditional assays and offering scalable, cost-efficient solutions for personalized treatment planning
  - Improved treatment predictions in NSCLC: Machine learning models integrating biomarkers and clinical features enhanced survival prediction in metastatic NSCLC, offering more accurate risk stratification, especially in pembrolizumab-treated patients
  - ML-based prediction in liver cancer: Machine learning-guided modeling successfully improved survival prediction and treatment decision-making in hepatocellular carcinoma (HCC), demonstrating AI’s potential to guide clinical strategies in liver cancer treatment

Key Topics From Notable Presentations (7/10)

- ✓ **LLMs, NLP & Data Extraction in Oncology:** Spotlight will be on how LLMs and AI-based models are driving advancements in clinical decision support by extracting and structuring unstructured data from various oncology sources, enabling more accurate, scalable, and personalized patient care
  - AI-based Risk Stratification: LLMs generate robust survival risk scores from free-text pathology reports, enhancing personalized oncology care with strong prognostic significance for gastrointestinal cancers
  - Clinical Decision Support: Self-hosted LLM agents, integrated with a multi-dimensional confidence framework, demonstrate secure, high-performing medical reasoning for oncology workflows with improved interpretability and safety
  - Data Extraction for Therapy Matching: LLMs assist in extracting structured data from oncology EHRs, improving patient similarity retrieval for molecular tumor boards and facilitating precision decision-making

Key Topics From Notable Presentations (8/10)

- **Clinical Trial Matching & Drug Development Applications:** AI and machine learning technologies that are revolutionizing clinical trial matching by improving efficiency, accuracy, and scalability, ensuring better integration and decision support in oncology research will be discussed
  - AI in Multidisciplinary Team (MDT) Support: A study demonstrated ChatGPT's integration into MDT meetings for oncology decisions, increasing discussion breadth and supporting refined decision-making with 67.2% initial concordance and expanding diagnostic and management options
  - Adjuvant Therapy Recommendations: ChatGPT-5 showed high concordance (75.7%) with MDT decisions for breast cancer treatment, excelling in endocrine and radiotherapy recommendations while performing less well with genetic testing and surgery
  - Automated Patient–Trial Matching: LungTrial-LLMX, an AI-powered tool, achieved 83% matching accuracy for lung cancer trials, maintaining privacy and providing transparency with its dual-LLM design, supporting scalable clinical integration

Key Topics From Notable Presentations (9/10)

- ✓ **Digital Pathology & Histopathology AI:** The conference will showcase how AI models are revolutionizing digital pathology by enhancing the accuracy and efficiency of tissue analysis, biomarker detection, and prognostic predictions, offering scalable solutions for precision oncology
  - AI for Recurrence Risk Prediction: A deep learning model accurately predicted recurrence risk in breast cancer using histopathology and clinical data, achieving an AUC of 0.898 and potentially reducing unnecessary chemotherapy by reclassifying high-risk patients
  - Lung Cancer Grading with AI: Transformer-based AI improved lung adenocarcinoma (LUAD) grading and prognostic stratification by predicting subtype ratios and integrating genomic data, demonstrating high accuracy in survival predictions
  - Microsatellite Instability (MSI) Detection: Equivariant Neural Field (ENF) improved MSI prediction in gastric cancer biopsies, achieving AUC 70.0, outperforming traditional methods and reducing computational complexity

Key Topics From Notable Presentations (10/10)

- **Radiomics & Imaging AI:** AI-powered imaging and radiomics models are set to advance precision oncology by enhancing diagnostic accuracy, predicting treatment responses, and enabling noninvasive biomarkers, thus improving clinical decision-making and patient outcomes
  - Radiogenomic Fingerprinting for Glioma: AI integration of MRI radiomics and transcriptomics identifies prognostic subgroups in high-grade gliomas, facilitating personalized treatment strategies and offering potential druggable targets
  - HER2 Status Prediction in Metastatic Breast Cancer: Radiomics achieved promising results in predicting HER2 overexpression in metastatic breast cancer, showcasing a noninvasive, reproducible method for HER2 status assessment
  - AI for EGFR Mutation in NSCLC: Multimodal radiomics integrating CT and PET scans provided an accurate, noninvasive tool for predicting EGFR mutations in NSCLC, highlighting the potential of AI in molecular profiling

Focus of Key Industry-Sponsored Sessions at ESMO - AI 2025 (1/6)

- ✓ **AstraZeneca:**
  - Focus Areas: The Future of AI in Healthcare: From Promise to Practice
  - Sessions will explore the integration of AI in oncology, focusing on precision medicine and the future role of AI in transforming clinical practices
- ✓ **DoMore Diagnostics:**
  - Focus Areas: Decoding Tumour Histology with AI to Personalize Treatment
  - Discussions will focus on the application of AI in analyzing tumour histology to enable personalized treatment strategies, improving patient-specific care

Focus of Key Industry-Sponsored Sessions at ESMO - AI 2025 (2/6)

- ✓ **Pierre Fabre Laboratories:**
  - Focus Areas: Promises and Limitations of AI in Dermato-Oncology
  - Presentations will discuss the potential and current limitations of AI in diagnosing and treating dermatologic cancers, exploring AI applications in skin cancer therapies
- ✓ **Bowhead Health:**
  - Focus Areas: No Room for Hallucinations: Building AI You Can Trust for Oncology Guidelines and Trials
  - The session will address the development of reliable AI systems for oncology guidelines and clinical trial data, ensuring accurate and trustworthy AI predictions

Focus of Key Industry-Sponsored Sessions at ESMO - AI 2025 (3/6)

- ✓ **myTomorrows:**
  - Focus Areas: Practical AI for Trial Recruitment: Human-in-the-Loop Tools for Patients, Physicians, and Sites
  - Discussions will cover the role of AI in optimizing clinical trial recruitment, enhancing coordination among patients, physicians, and research sites
- ✓ **Flatiron Health:**
  - Focus Areas: The VALID Framework for LLM-Extracted Oncology Data Quality
  - Presentations will explore the VALID framework, aimed at improving data quality from large language models (LLM) for supporting oncology research and clinical decisions

Focus of Key Industry-Sponsored Sessions at ESMO - AI 2025 (4/6)

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- **Medable:**
  - Focus Areas: Harnessing AI Agents to Overcome the Complexity of Oncology Trials
  - Sessions will highlight the use of AI-driven agents in simplifying oncology trials, enhancing patient data management and reducing trial complexity

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- **Careology:**
  - Focus Areas: Empowering Patients with Connected, AI-Powered Cancer Care
  - Presentations will explore how AI-powered platforms can support continuous monitoring and personalized care, empowering patients to manage their cancer treatment effectively

Focus of Key Industry-Sponsored Sessions at ESMO - AI 2025 (5/6)

- **Johnson & Johnson:**
  - Focus Areas: Unlocking the Future of Oncology Through AI: Together for Tomorrow's Patients
  - The company will discuss how AI is transforming oncology care through collaboration, focusing on personalized treatment solutions and innovative therapeutic developments
- **Vintura:**
  - Focus Areas: Collaborative Care Meets AI: Shaping the Future of Oncology Care
  - Discussions will focus on integrating AI with collaborative care models, enhancing patient outcomes through better coordination and AI-enhanced care pathways

Focus of Key Industry-Sponsored Sessions at ESMO - AI 2025 (6/6)

- **Negedia:**

  - Focus Areas: Machine Learning Meets Transcriptomics: Negedia Pathology - An Innovative Tool Bridging Clinical Practice and Biomarker Discovery

  - Presentations will explore how Negedia is using machine learning and transcriptomic data to improve clinical practice, focusing on biomarker discovery in oncology

Key Noteworthy Presentations at ESMO - AI 2025

Notable Presentations At ESMO - AI 2025

AI for Treatment Response, Immunotherapy & Precision Oncology (1/7)

Date	Title	Author	Summary
12 Nov 2025	An ensemble multi-omics framework to select NSCLC patients for chemo-de-escalation, PEOPLE phase II trial	Luca M. Invernizzi	• **Introduction**:The PEOPLE (NCT03447678) trial explored multi-omic biomarkers predictive of pembrolizumab response in PD-L1–low/negative advanced NSCLC, addressing immune heterogeneity overlooked by single-omic analyses. • **Methodology:** Samples from 65 evaluable patients underwent circulating immune profiling (CIP), tumor gene expression (GEP), and gut metagenomics. Data were log$_2$-normalized and analyzed using MOFA2 (unsupervised factorization), DIABLO (supervised survival classification), and Similarity Network Fusion (SNF) for subtype clustering. • **Results:** DIABLO identified survival-linked multi-omic components: poor survival correlated with atypical monocytes, pmn-MDSCs, and neutrophils, while long survival associated with T/NK activation genes and Phocaeicola massiliensis. SNF and MOFA confirmed concordant immune-microbial signatures across modalities. • **Conclusions:** Integrated multi-omic profiling stratified PD-L1–low NSCLC, distinguishing immunoresistant myeloid-dominant and T/NK-enriched responders, supporting pembrolizumab monotherapy de-escalation and informing precision immunotherapy strategies.
12 Nov 2025	AI-driven immune biomarker classifier predicts clinical benefit from neoadjuvant immunotherapy in triple-negative breast cancer	Davit Kvaratskhelia	• **Introduction**: Triple-negative breast cancer (TNBC) is associated with high recurrence rates, and predictive biomarkers for treatment benefit are lacking. This study explores the integration of artificial intelligence (AI) and transcriptomics to identify biomarkers for TNBC patient stratification. • **Methodology:** RNA sequencing data from TNBC tumors (TCGA-BRCA, METABRIC) were analyzed, filtering for immune-related gene signatures. Surrogate pCR labels were derived using established gene expression scores (ImPredict, Tumor Inflammation Signature) and 5-year relapse-free survival. Machine learning models (XGBoost, logistic regression) were trained with stratified cross-validation, and feature importance was assessed via SHAP values. • **Results:** The XGBoost model achieved an AUC of 0.83 and precision-recall AUC of 0.79 for predicting pCR, with sensitivity and specificity of 76% and 80%. Key predictive features included CXCL13, CD8A, and GZMB. Predicted responders had significantly longer relapse-free survival ($p < 0.01$). • **Conclusions:** Immune gene signatures can accurately predict pCR to neoadjuvant immunotherapy in TNBC, supporting AI-based patient stratification. Prospective validation in clinical trials is needed to confirm clinical applicability.

Notable Presentations At ESMO - AI 2025

AI for Treatment Response, Immunotherapy & Precision Oncology (2/7)

Date	Title	Author	Summary
12 Nov 2025	Machine learning refines predictive tertiary lymphoid structures (pTLS) in non-small cell lung cancer (NSCLC) immunotherapy	Lucile Vanhersecke	• **Introduction**: Immunotherapy response in Non-Small Cell Lung Cancer (NSCLC) remains suboptimal, highlighting the need for reliable biomarkers. Tertiary lymphoid structures (TLS) have been identified as potential predictors, but their characteristics linked to response require further investigation. • **Methodology:** A multicenter cohort of 141 NSCLC patients treated with immune checkpoint inhibitors (ICI) or ICI–chemotherapy (ICI-CT) had pre-therapy samples analyzed via multiplex immunofluorescence and PD-L1 immunohistochemistry. Machine learning models, including GLMnet, XGBoost, and Random Forest, were employed to identify predictive TLS features (pTLS), which were validated by expert pathologists. • **Results:** pTLS, characterized by CD8+ T-cell enrichment and intratumoral location, predicted a 70% response rate and better progression-free survival (HR=0.59, p=0.028), independent of PD-L1 and CD8+ TILs. These features were translated into practical histopathological criteria (≥20% CD8+ T-cell enrichment). • **Conclusions:** xpTLS, defined as CD8+-enriched TLS, are independent prognostic biomarkers for immunotherapy response in NSCLC. These findings support the integration of ML-derived criteria into routine histopathology for patient stratification in precision oncology.
12 Nov 2025	In development: Fully automatic treatment benefit prediction in advanced colorectal cancer patients	Jesse H. Wolters	• **Introduction**: Cancer treatment decision-making has become more complex due to new therapies and increasing options. The ACTIN project develops cascading algorithms to identify the best treatment and predict benefits, focusing on treatment-naïve metastatic colorectal cancer (CRC). • **Methodology:** ACTIN includes a data extraction algorithm to annotate patient records, combining unstructured data annotated by a large language model and structured data mapped to a prediction algorithm. The prediction model is trained using Netherlands Cancer Registry data. Eight models, including attention and multitask variants, were evaluated using metrics like C-index and Integrated Brier Score. • **Results:** Data from 15,618 patients were used, with 96 parameters including first-line treatment. The Multitask Deepsurv with attention model performed best (C-index 0.76; CFB 0.59). Key negative predictors of survival included intrahepatic metastases, high WHO performance status, and RAS mutations. • **Conclusions:** ACTIN has developed a promising tool for supporting clinical decisions in CRC, with further optimization and expansion to other cancer types planned.

Notable Presentations At ESMO - AI 2025

AI for Treatment Response, Immunotherapy & Precision Oncology (3/7)

Date	Title	Author	Summary
12 Nov 2025	The added clinical value of AI-assisted histopathology analyses in ICI response prediction in patients with advanced melanoma	Mark Schuiveling	- **Introduction**: Predictive biomarkers for immune checkpoint inhibitor (ICI) response in melanoma are limited. This study evaluates whether AI-based histopathology models can improve prediction of ICI response when combined with a clinical model. - **Methodology:** Data from 1,941 patients with advanced melanoma treated with ICI were analyzed. AI models using features from pretreatment H&E-stained metastatic specimens were trained on tumor-only regions using CLAM and attention-based MIL. The model's predicted response likelihood was added to a clinical model with variables like age, sex, ECOG, and BRAF mutation. - **Results:** The AI model with tumor-only features achieved an AUC of 0.63. The clinical model achieved an AUC of 0.61, and adding AI features improved the AUC to 0.66, with better calibration. - **Conclusions:** AI-assisted histopathology improved calibration and discrimination in predicting ICI response in melanoma, though further refinement is needed for clinical use.
12 Nov 2025	Decoding circadian immune coherence using fourier analysis and AI: Towards personalized ICI scheduling	Ivan Bivolarski	- **Introduction**: Circadian rhythms regulate immune surveillance and therapeutic responses to immune checkpoint inhibitors (ICIs). Despite biological evidence, their integration into clinical decision-making remains limited. AI, combined with Fourier-based spectral analysis, offers a novel framework to identify patient-specific timing windows for optimal ICI administration. - **Methodology:** We analyzed immune-related blood markers (e.g., NLR) from 51 cancer patients treated with ICIs. Fourier transform was applied to longitudinal data to extract periodic spectral features. Machine learning models classified circadian immune coherence and estimated personalized therapy delivery timings. Cross-validation ensured robustness and reduced overfitting. - **Results:** Fourier analysis identified recurring immune rhythm patterns, with machine learning achieving >80% accuracy in classifying immune coherence. The framework suggested that optimal ICI windows are dynamic, not fixed, with "morning" and "evening" as conditional windows. This individualized approach may enhance efficacy while minimizing toxicity. - **Conclusions:** This study introduces a Fourier–AI framework for personalized ICI scheduling, paving the way for precision chrono-immunotherapy and AI-guided cancer care.

Notable Presentations At ESMO - AI 2025

AI for Treatment Response, Immunotherapy & Precision Oncology (4/7)

Date	Title	Author	Summary
12 Nov 2025	AI-enhanced prediction of diagnostic failure in early-stage lung cancer: Preprocedural score for ION robotic bronchoscopy	Claudia Bardoni	• **Introduction**: Diagnosing early-stage non-small cell lung cancer (NSCLC) often relies on bronchoscopic sampling of small peripheral nodules. Despite improvements with ION bronchoscopy, non-diagnostic outcomes remain common. This study developed and validated an AI model to predict diagnostic failure and derive a clinically applicable risk score. • **Methodology:** A retrospective cohort of 189 ION procedures was analyzed. Diagnostic failure was defined as non-diagnostic histology later confirmed or presumed malignant. A gradient boosting model (XGBoost) was trained with 5-fold cross-validation. SHAP analysis guided feature selection for a logistic regression-based clinical score. • **Results:** The AI model achieved an ROC-AUC of 0.90, with precision = 0.76, recall = 0.78, and specificity = 0.83. Feature importance identified five predictors, which were used to create a simplified 10-point clinical score. The score stratified risk into low, intermediate, and high failure categories with corresponding failure rates of 8.3%, 20.9%, and 42.3%, respectively. • **Conclusions:** AI-based modeling accurately predicts diagnostic failure in ION procedures. The derived clinical score offers a valuable decision-support tool to improve diagnostic yield and workflow efficiency, with prospective validation underway.
12 Nov 2025	Deep learning prediction of response to antibody-drug conjugates in patients with metastatic breast cancer using digital pathology	Elena Fountzilas	• **Introduction**: Antibody-drug conjugates (ADCs) have transformed treatment for metastatic breast cancer (mBC), but predictive biomarkers remain inadequate. This study aimed to utilize digital pathology and machine learning (ML) to assess tumor heterogeneity and develop a predictive model for ADC response in mBC patients. • **Methodology:** In this multicenter study, H&E-stained tissue slides from 177 mBC patients treated with trastuzumab deruxtecan (T-DXd) or sacituzumab govitecan (SG) were analyzed. Image features from Whole Slide Images (WSIs) were extracted using the UNI foundation model and applied to a Vision Transformer (ViT) for ADC response prediction, with progression-free survival (PFS) used as the primary endpoint. • **Results:** The ViT model achieved AUCs of 0.82 and 0.80 for response prediction in validation and external test sets. Feature analysis identified five key predictors of diagnostic failure, including inadequate ultrasound visualization and apical/posterior segment location. Heterogeneity differences were observed between metastatic and primary tumors ($p<0.05$). • **Conclusions:** AI and ML-based digital pathology models show potential in predicting ADC response in mBC, highlighting the role of tumor heterogeneity. These models could contribute to personalized treatment strategies and biomarker discovery.

Notable Presentations At ESMO - AI 2025

AI for Treatment Response, Immunotherapy & Precision Oncology (5/7)

Date	Title	Author	Summary
12 Nov 2025	Development of a machine-learning model on pre-treatment characteristics to predict long-term survivorship to atezolizumab plus bevacizumab in advanced hepatocellular carcinoma	Falah J. Rahim	- **Introduction**: Combination immunotherapy with atezolizumab and bevacizumab (A+B) is a first-line treatment for advanced hepatocellular carcinoma (aHCC), but only a subset of patients benefit long-term. This study aimed to develop machine learning models to predict overall survival (OS), and long-term and short-term survivorship (LTS and STS) in patients receiving A+B. - **Methodology:** Data from 695 aHCC patients treated with A+B were retrospectively analyzed using the AB-Real registry. Two machine learning models were trained: a Support Vector Machine (SVM) for LTS and STS prediction, and a Random Survival Forest (RSF) for OS prediction, based on 43 pre-treatment clinical features. - **Results:** The SVM model achieved strong performance for LTS (AUC: 0.82) and STS (AUC: 0.83). The RSF model stratified patients into high- and low-risk groups for OS with significant survival differences (median OS: 17.08 vs 9.49 months, p < 0.001). - **Conclusions:** Machine learning models provide robust predictions for OS and LTS in aHCC patients treated with A+B, aiding in personalized risk stratification and clinical decision-making.
12 Nov 2025	Dual AI models for perioperative decision support in resectable NSCLC: A real-world cohort analysis	Cristina Diotti	- **Introduction**: Accurate perioperative assessment is essential in early-stage non-small cell lung cancer (NSCLC), but current staging and prognostic tools remain limited. This study developed and validated two machine learning models using the IBM XGBoost algorithm: one for predicting pathological upstaging (≥ stage II) and another for estimating the likelihood of achieving a favorable postoperative outcome (no evidence of disease, NED). - **Methodology:** A retrospective analysis of 197 NSCLC patients undergoing curative resection (2023-2025) was conducted. Data from demographics, clinical, pathological, and treatment variables were used. Model performance was evaluated using ROC-AUC, precision, recall, and F1-score, with SHAP for feature interpretation. - **Results:** Model 1 predicted advanced pathological stage with 86.7% accuracy (ROC-AUC 0.95), while Model 2 predicted NED status with 93.9% accuracy (ROC-AUC 0.90). Both models showed promising results for predicting outcomes, with SHAP supporting clinically relevant features. - **Conclusions:** These AI-driven models offer scalable, interpretable tools for improving preoperative staging and postoperative prognostication in NSCLC. External validation is needed to assess generalizability and clinical readiness.

Notable Presentations At ESMO - AI 2025

AI for Treatment Response, Immunotherapy & Precision Oncology (6/7)

Date	Title	Author	Summary
12 Nov 2025	External validation of the LORIS score for predicting immunotherapy response in a Asian patient cohort	Jerold Loh	• **Introduction**: The LORIS (Lymphocyte, Organ, Renal, Inflammation Score) has shown promise as a predictive biomarker for immune checkpoint blockade (ICB) response. This study aimed to externally validate the LORIS score in a cohort of Singaporean patients with advanced cancers. • **Methodology:** Data from 72 Singaporean patients treated with ICB were retrospectively analyzed. LORIS scores were calculated, and its performance was compared with models like GBoost, HGBoost, TMB, and dMMR using AUC and F1 score. • **Results:** The LORIS score had an AUC of 0.693 and an F1 score of 0.731, showing superior balance between precision and recall. LORIS-High outperformed TMB and dMMR for predicting response, with better median OS for LORIS-H patients (820 days vs 448 days). • **Conclusions:** External validation supports the LORIS score as a practical predictive biomarker for ICB response, showing strong clinical relevance despite a lower AUC compared to other models.
12 Nov 2025	A multimodal deep learning framework for predicting platinum sensitivity from ovarian cancer histopathology	Enyu Tang	• **Introduction**: Platinum resistance significantly impacts ovarian cancer prognosis. This study developed a multimodal AI model integrating pathology and clinical data to predict platinum sensitivity, guiding personalized treatment. • **Methodology:** The study included 431 patients and 1,182 pathological slides. A weakly-supervised multiple instance learning framework was used, combining whole-slide image features with clinical and pathological variables. The model was tested on both internal (376 patients) and external (55 TCGA patients) datasets. • **Results:** The baseline model achieved an AUC of 0.896 in the internal test group and 0.876 externally. Integration of metastatic pathology and clinical data improved the AUC to 0.914. • **Conclusions:** This multimodal AI model accurately predicts platinum sensitivity, supporting personalized ovarian cancer therapy decisions.

Notable Presentations At ESMO - AI 2025

AI for Treatment Response, Immunotherapy & Precision Oncology (7/7)

Date	Title	Author	Summary
12 Nov 2025	Prediction of response to immunotherapy from digital pathology in the TANGERINE study	Victor Moreno Aguado	• **Introduction**: Immune checkpoint inhibitors (ICIs) have revolutionized cancer treatment, but predicting response remains challenging. The TANGERINE study aims to develop AI-based histology image analysis and radiomics to predict ICI responses in metastatic cancer patients. • **Methodology:** The study analyzed diagnostic tumor histopathology slides from patients treated with ICIs in three hospitals. AI models were trained using the STAMP framework to predict ICI response through image embeddings and a vision transformer model. • **Results:** The pancancer-multidrug model for predicting complete response (CR) achieved an average AUC of 0.68 and 0.70 in test sets. The model showed limited performance for predicting progressive disease (PD), with AUC values of 0.59 (CV) and 0.68 (test). • **Conclusions:** While the AI model shows moderate success in predicting CR, it has limitations for PD prediction. Digital pathology holds promise as a biomarker for ICI response.
12 Nov 2025	A multimodal deep learning model for prediction of early progression in patients with advanced hepatocellular carcinoma treated with atezolizumab-bevacizumab	Ciro Celsa	• **Introduction**: Atezolizumab-Bevacizumab is a first-line treatment for advanced/unresectable hepatocellular carcinoma (HCC), but there is no validated system to predict early treatment response or identify non-responders. This study developed an AI model to predict 6-month progression-free survival (PFS) in HCC patients. • **Methodology:** 51 patients were included, and a multimodal AI model was created, combining convolutional neural networks (CNN) for CT image feature extraction and multilayer perceptron (MLP) for clinical-laboratory data. The final classifier predicted 6-month PFS using these integrated features. • **Results:** The AI model achieved excellent performance, with accuracy of 96.25%, precision of 97.82%, recall of 70.66%, F1-score of 82.05%, and AUC of 0.95. • **Conclusions:** The multimodal AI model successfully predicts early treatment failure in HCC patients, offering a reliable decision-support tool for personalized therapy.

Notable Presentations At ESMO - AI 2025

Cross-Domain, Multi-Agent & Integrative Platforms (1/8)

Date	Title	Author	Summary
12 Nov 2025	Edge-native artificial intelligence for automated anamnesis, real-time documentation, and multilingual communication in oncology practice	Linghui Luo	• **Introduction**: In Germany, repetitive anamnesis and clinical documentation are significant time burdens for physicians in oncology, hematology, and internal medicine, consuming more than half of their workday. This reduces time for patient care, increases diagnostic errors, and contributes to physician burnout, exacerbated by language barriers between clinicians and patients, particularly in oncology. • **Methodology:** ClioAssist, an edge-native AI platform, was developed to automate anamnesis, reduce documentation workload, and bridge language barriers. The platform conducts structured anamnesis interviews, generates pre-reports, and produces real-time transcriptions during consultations. It also includes a live translation module and runs on consumer-grade devices while ensuring GDPR compliance. • **Results:** Preliminary evaluations indicate time savings of up to 10 minutes per patient. A prospective clinical study is underway to assess ClioAssist's feasibility, usability, and its impact on physician workload, documentation quality, and patient satisfaction. • **Conclusions:** ClioAssist shows promise as a scalable solution to streamline clinical workflows, reduce physician burnout, and enhance patient care, particularly in oncology settings.
12 Nov 2025	A fully-automated integrative workflow to support clinical decisions in molecular tumour boards	Maria Giulia Carta	• **Introduction**: Molecular Tumor Boards (MTBs) rely on next-generation sequencing (NGS)-based tumor molecular profiling to inform actionable clinical decisions. However, the complexity of bioinformatics tools and continuous human intervention required for variant interpretation creates delays and inefficiencies. This study develops a fully automated integrative workflow to enhance NGS-based decision-making in MTBs. • **Methodology:** The workflow was developed in Erlangen's pathology department and adapted to Caltagirone's fully digitized department. Triggered by new NGS data or initiated by molecular biologists via the AP-LIS interface, the workflow automates key bioinformatics steps, including variant annotation, oncogenicity classification via OncoVI, HRD score computation, and report generation. • **Results:** The workflow minimizes delays and manual interventions, automating tasks such as generating sequencing quality metrics, annotating variants, classifying oncogenicity, and calculating HRD scores. Results are displayed in a PDF report with variant distribution and genomic instability plots, accessible via the AP-LIS. • **Conclusions:** This fully automated strategy accelerates NGS data analysis and interpretation, streamlining the decision-making process in MTBs and supporting faster, more efficient cancer patient care.

Notable Presentations At ESMO - AI 2025

Cross-Domain, Multi-Agent & Integrative Platforms (2/8)

Date	Title	Author	Summary
12 Nov 2025	Consultation with Konsuld: a new AI collaboration platform.	Stefan Gluck	• **Introduction**: Oncology decision-making is hindered by information overload, lack of real-time peer consultation, and non-compliant AI tools. Konsuld® combines AI with HIPAA-compliant infrastructure to address these challenges. • **Methodology:** Konsuld® offers AI-powered access to publications, guidelines, clinical trials, and secure collaboration tools for tumor boards and specialty forums. Key features include natural language processing, curated content integration, and real-time global case consultation. • **Results:** Konsuld® facilitates AI-driven treatment recommendations ("Konsuldations") and enables secure, peer-reviewed case discussions, improving decision-making and patient care. • **Conclusions:** Konsuld® combines AI with HIPAA-compliant collaboration, transforming oncology practice by enabling secure, global peer consultation.
12 Nov 2025	Development of on-premises small language models (SLMs) for cancer clinical practice via retrieval-augmented generation (RAG) prompt compression	Shunsuke Hidaka	• **Introduction**: Generative language models (SLMs) are pivotal in cancer care, but high memory requirements hinder their deployment. This study evaluates the impact of prompt compression via summarization to reduce GPU memory usage and enhance efficiency in RAG for cancer clinical applications. • **Methodology:** A knowledge base of oncology guidelines and PubMed abstracts was created for retrieval. Retrieved documents were summarized to compress prompts. Accuracy was tested on 147 oncology MCQs using three methods: chain-of-thought (CoT), naïve RAG, and compressed RAG. • **Results:** Prompt compression reduced token count from 22,603 to 3,871, enabling deployment of a 14B model. Compressed RAG achieved 75.1% accuracy, outperforming CoT (72.1%). • **Conclusions:** Summarizing retrieved texts reduces GPU memory needs, enabling high-performance, on-premises SLMs for clinical decision support while maintaining privacy and performance.

Notable Presentations At ESMO - AI 2025

Cross-Domain, Multi-Agent & Integrative Platforms (3/8)

Date	Title	Author	Summary
12 Nov 2025	A responsible AI assistant for instant, source-verified access to NCCN guidelines using retrieval-augmented generation (RAG)	Adar Yaacov	• **Introduction**: The National Comprehensive Cancer Network (NCCN) guidelines are critical resources for oncologists but are extensive and difficult to navigate. We developed an AI system to provide instant, citation-backed access to these guidelines. • **Methodology:** We processed 41 NCCN guideline PDFs (2025 versions) into 23,508 searchable segments. The AI system utilized a multi-step workflow to understand medical queries, retrieve relevant information, and validate safety, citing the NCCN source for each response. • **Results:** The system achieved a 100% functional success rate across 28 clinical queries with an average response time of 13 seconds. All responses were accurately cited, and 35.7% of responses were deemed high-confidence. • **Conclusions:** This AI assistant effectively supports oncologists by providing fast, accurate, and safe access to NCCN guidelines, with strong potential for clinical adoption.
12 Nov 2025	Lymphoma Data Hub: A collaborative and secure cloud platform for AI-driven hematology research	Léa Marlot	• **Introduction**: The Carnot Calym Institute consortium aims to support AI research in lymphoid malignancies by collecting, enriching, organizing, sharing, and analyzing health data across geographic regions. The Lymphoma Data Hub (LDH) platform was developed as a cloud-based solution to address these challenges while ensuring data security and governance. • **Methodology:** The LDH platform uses certified cloud services to ingest and transform raw data into a structured environment, ensuring interoperability. Purpose-designed workspaces provide controlled access for advanced analysis within AI research projects, particularly in lymphoid malignancies. Data governance ensures secure collaboration among physicians, researchers, and data providers. • **Results:** The LDH hosts over 30 terabytes of data, including clinical, imaging, and omics data. AI research aims to identify patient subgroups for personalized care and discover novel biomarkers by integrating diverse data types. Dedicated workspaces and shared exploratory environments enable interdisciplinary collaboration. • **Conclusions:** The LDH platform enables AI-driven research in hematology, facilitating personalized care and biomarker discovery. It also holds potential for expansion into other therapeutic areas by engaging domain-specific experts, broadening its translational applications

Notable Presentations At ESMO - AI 2025

Cross-Domain, Multi-Agent & Integrative Platforms (4/8)

Date	Title	Author	Summary
12 Nov 2025	Agentic tumor boards: the use of large language model orchestration for therapeutic recommendations in breast cancer patients	Lucas Emanuel Silva e Oliveira	- **Introduction**: The increasing complexity of breast cancer care has made multidisciplinary tumor boards (MTBs) essential, but the constant updates to clinical guidelines and growing evidence make consistent decision-making challenging. Agentic tumor boards (ATBs), powered by large language model (LLM) orchestration, offer a novel solution to synthesize evidence and support real-time therapeutic recommendations while preserving clinical judgment. - **Methodology:** Data from 80 patients with invasive breast cancer, discussed in MTBs from 2023 to 2025, were analyzed. The ATB workflow used GPT-5 as the orchestrator, aggregating recommendations from various LLMs (e.g., Gemini 2.5 Pro) to generate therapeutic recommendations. Agreement with MTB decisions was measured using Cohen's kappa. - **Results:** The ATB showed strong agreement with MTB recommendations for systemic therapy ($\kappa = 0.80$), moderate agreement for radiotherapy ($\kappa = 0.49$), and weak agreement for surgical treatment ($\kappa = 0.22$). - **Conclusions:** ATBs demonstrate potential in improving MTB efficiency, particularly for systemic therapy. Future research should integrate specialized tools to enhance recommendation generation.
12 Nov 2025	Distributed Foundation Models for Digital Pathology: Privacy-Preserving Cross-Institutional Fine-Tuning via Swarm Learning	Jie Fu Zhu	- **Introduction**: Foundation models in digital pathology face adoption challenges due to non-IID data distributions, limited annotated data, and privacy constraints. Decentralized swarm learning enables cross-institutional training without the need for raw data exchange, addressing these barriers. - **Methodology:** A three-stage distributed fine-tuning workflow was implemented across multiple European academic hospitals using over 7,000 whole-slide images (WSIs). The workflow involved domain adaptation, federated slide-level aggregation with secure aggregation, and global harmonization of model checkpoints using differential privacy. - **Results:** The decentralized pipeline achieved state-of-the-art performance: MSI prediction in colorectal cancer (AUROC 0.92) and tumor detection in lung cancer (AUROC 0.96), outperforming benchmarks. The system also improved efficiency, reducing communication overhead by 30% and compute demand by 25%. - **Conclusions:** This decentralized, privacy-preserving fine-tuning approach enhances foundation model performance across institutions, surpassing centralized training. The framework reduces technical barriers and is scalable for real-world deployment. Future work will expand to additional cancer types and clinical validation.

Notable Presentations At ESMO - AI 2025

Cross-Domain, Multi-Agent & Integrative Platforms (5/8)

Date	Title	Author	Summary
12 Nov 2025	PHENO-RAG: A modular ensemble large language model framework for hepatocellular carcinoma with patient phenotyping and retrieval augmented generation-guided management	Ciro Celsa	• **Introduction**: Managing hepatocellular carcinoma (HCC) is challenging due to its association with chronic liver disease and multiple treatment options. Multidisciplinary team (MDT) discussions improve outcomes, but are resource-intensive. This study developed a Large Language Model (LLM) framework integrating HCC management guidelines with patient-specific clinical data for better patient stratification. • **Methodology:** 489 clinical reports from 424 patients were analyzed. Various LLMs (LLAMA-8B, LLAMA-70B) were tested with Natural Language Processing (NLP) techniques like Regular Expression (REGEX) and prompting strategies (zero-shot, few-shot, and RAG). The model's ability to predict treatment decisions, clinical complexity, and MDT evaluations was evaluated. • **Results:** The combined REGEX and LLAMA-70B approach achieved high accuracy in clinical parameter extraction (F1-scores 74.9%-90.9%) and treatment decisions (80.8% exact match). • **Conclusions:** The LLM framework accurately predicts HCC treatment decisions and clinical complexity, providing a valuable tool for optimizing MDT resource allocation.
12 Nov 2025	Co-creation and iterative needs assessment with patients and research stakeholders to develop a decentralized oncology research infrastructure: the WeShare platform	Sibille Everhard	• **Introduction**: WeShare is a French government–funded program designed to streamline oncology research through a co-created, patient-centered e-research platform, enhancing clinical workflows and promoting inclusivity. • **Methodology:** WeShare's platform was developed through co-design with clinicians, researchers, social scientists, and patient representatives using the Exploration, Preparation, Implementation, and Sustainment (EPIS) framework. Usability was assessed with the French System Usability Scale (F-SUS) and Net Promoter Score (NPS). • **Results:** Co-creation included 100 users, 50 verification sessions, and 30 testing sessions. First version deployment (2022–2023) included 2 studies across 19 centers with 599 patients. The second version, tested in 3 studies (817 patients), added new modules. • **Conclusions:** WeShare's iterative, user-driven development ensures usability and sustainability, with broader integration planned for end-2025 adoption.

Notable Presentations At ESMO - AI 2025

Cross-Domain, Multi-Agent & Integrative Platforms (6/8)

Date	Title	Author	Summary
12 Nov 2025	A novel target discovery platform: Uncovering targets linked to long-term cancer survival	Nick Riddiford	- **Introduction**: Studying long-term survivors of aggressive cancers offers valuable insights into treatment response and disease control. The ROSALIND study explores multi-omic and clinical profiles of long-term cancer survivors to uncover mechanisms of exceptional survival. - **Methodology:** The retrospective, multi-centric case-control study analyzed data from three aggressive cancer cohorts (mPDAC, GBM-IDHwt, ES-SCLC). Tumor samples underwent multi-omic sequencing, and data were analyzed with machine learning to identify key genetic events and clinically-relevant subgroups. - **Results:** Analysis of 50 patients identified 90 targets with significant multi-omic differences, 6 of which have progressed to clinical trials. 35 identified targets are known to be druggable. - **Conclusions:** The integration of multi-omic profiling and clinical data enabled the identification of novel therapeutic targets, advancing potential treatments for aggressive cancers.
12 Nov 2025	PosterLens: An AI-powered tool for rapid summarisation of oncology congress posters	Nick J. Lamb	- **Introduction**: Major oncology congresses present vast amounts of poster content, leading to information overload for attendees. PosterLens is an AI-powered mobile application designed to generate concise summaries of oncology posters, improving efficiency and accessibility for researchers and clinicians. - **Methodology:** PosterLens uses optical character recognition (OCR) to extract text from poster images, followed by large language model (LLM) processing to create structured summaries. The outputs are organized into sections such as background, methods, results, and conclusions. Planned evaluation will assess content fidelity, word count reduction, and user-perceived efficiency. - **Results:** Pilot testing suggests that PosterLens effectively generates concise summaries while retaining essential content. Early feedback highlights its potential for rapid poster screening and prioritization. - **Conclusions:** PosterLens offers a promising tool to address information overload at oncology congresses, enabling faster access to key findings. Further evaluation will confirm its role in enhancing the efficiency of oncology researchers, clinicians, and trainees.

Notable Presentations At ESMO - AI 2025

Cross-Domain, Multi-Agent & Integrative Platforms (7/8)

Date	Title	Author	Summary
12 Nov 2025	Instantly research-ready: A strategy towards hospital-wide data representation at a tertiary hospital	Annelies T. Verbiest	**Introduction**: Hospital data is often fragmented, requiring repeated data cleaning for each research project. The Data Innovation Lab of Antwerp University Hospital developed a data lake to provide unified patient profiles, supporting retrospective studies, quality monitoring, and AI development. **Methodology:** The hospital's data lake consists of four layers: Layer 1 captures raw data; Layer 2 models each source independently; Layer 3 integrates data across sources; and Layer 4 provides tailored insights for use cases. The OMOP Common Data Model enables standardized, federated network studies across disease domains. **Results:** The OMOP instance passed the European Medicines Agency quality assessment as a DARWIN EU® partner. The infrastructure supports oncology research with international consortia and enables scalable, rapid longitudinal outcomes research and pharmacovigilance. **Conclusions:** The integrated data strategy accelerates oncology research by ensuring auditable, research-grade datasets are readily available, enabling timely real-world evidence generation and AI training.
12 Nov 2025	Live validation of a generative AI platform for multilevel clinical simulation and decision support in oncology	Diogo R. Ribas Silveira	**Introduction**: Artificial Intelligence (AI) is revolutionizing oncology, enhancing clinical decisions and medical training. Despite increasing interest in large language models (LLMs), their integration into structured clinical reasoning remains limited. We developed a generative AI platform to simulate multilevel oncology scenarios, enabling real-time diagnostic reasoning, staging, and treatment planning. **Methodology:** The platform is a web-based tool that processes structured clinical data (e.g., history, exams, lab results, imaging) to simulate diagnostic reasoning and suggest treatments. Users can modify case parameters, and the platform updates outputs in real time, facilitating dynamic exploration. Accuracy and consistency were validated with complex cases. **Results:** Preliminary validation with ten cases showed 87% concordance with expert tumor board assessments. The platform will be tested live at the ESMO AI & Digital Oncology Congress 2025, where participants will interact with it and provide feedback. **Conclusions:** This platform demonstrates AI's potential in real-time diagnostic reasoning for oncology. It supports reproducibility, transparency, and collaborative learning, with significant applications in medical education and clinical workflows.

Notable Presentations At ESMO - AI 2025

Cross-Domain, Multi-Agent & Integrative Platforms (8/8)

Date	Title	Author	Summary
12 Nov 2025	OPTIMA: European real-world oncology data and evidence generation platform for improving oncology care in prostate, lung, and breast cancer	Nadezhda Knauer	• **Introduction**: The growing volume of oncology data presents both opportunities and challenges in research and patient decision-making. OPTIMA, a European consortium, addresses these by developing the first GDPR-compliant real-world oncology data platform, providing decision support tools for breast, lung, and prostate cancers. • **Methodology:** OPTIMA collaborates with major medical societies, data-driven initiatives, patient groups, academic units, and industry partners to integrate expertise. The platform uses datasets covering over 200 million individuals and employs federated learning to develop AI/ML models. Research questions are prioritized by multi-stakeholder groups to generate evidence in breast, lung, and prostate cancers. • **Results:** Prototyping has begun, integrating data from European cancer registries. Early analyses highlight variations in treatment pathways, demonstrating the platform's potential to generate actionable real-world evidence. • **Conclusions:** OPTIMA enhances decision-making and aims to transform oncology care in Europe, with potential applications in other therapeutic areas, supported by AI-driven tools and broad data access.

Notable Presentations At ESMO - AI 2025

Digital Health, Patient Monitoring & ePROs (1/9)

Date	Title	Author	Summary
12 Nov 2025	Digital remote monitoring and patient-reported quality of life in a phase II trial combining melphalan percutaneous hepatic perfusion with ipilimumab and nivolumab in metastatic uveal melanoma (CHOPIN): Insights from mHealth endpoints	Dominique G. Stuijt	• **Introduction**: Uveal melanoma (UM) can develop hepatic metastases despite local treatment, leading to poor prognosis. The CHOPIN trial (NCT04283890) assessed the safety and efficacy of melphalan percutaneous hepatic perfusion (M-PHP) with or without ipilimumab/nivolumab (M-PHP+I/N). This study also integrated mHealth monitoring to assess quality of life (QoL) and recovery time. • **Methodology:** Patients used a mobile app for QoL, a smartwatch for physical activity, and a smart scale for weight monitoring. The trial lasted 6 months, with follow-up for 1 year, collecting both clinical and digital outcomes. • **Results:** 19 patients participated, with 10 completing the mHealth study. The M-PHP+I/N group had significantly more grade 2-4 adverse events. QoL scores were higher in the M-PHP-only group but showed no significant changes over time. • **Conclusions:** mHealth monitoring was feasible for metastatic UM patients undergoing treatment. No significant QoL changes were observed over time, though the M-PHP+I/N group had lower baseline QoL.
12 Nov 2025	Telemedicine integration of oncology and home hospice care: A mixed-methods study of feasibility, acceptability, and caregiver experience	Tony Kin Wai Hung	• **Introduction**: Patients with cancer and their caregivers face significant unmet needs at the end of life, often experiencing distress during the transition to hospice care. Maintaining continuity with oncologists may ease this adjustment, but current models rarely integrate oncologists with hospice providers. Telemedicine may offer a solution, but its feasibility and value remain unclear. • **Methodology:** This prospective, single-arm study (May 2021–Sep 2024) evaluated a telemedicine-enabled synchronous oncology–hospice model. Adults with a Hartford HealthCare oncologist and initiating home hospice were enrolled. Video visits connected oncologists with hospice nurse home visits. Feasibility, acceptability, and communication were assessed using 5-point Likert surveys and bereavement interviews with caregivers. • **Results:** Forty patient-caregiver dyads participated. Communication improved across all groups (oncologists, nurses, patients, caregivers). The therapeutic alliance remained stable for patients and caregivers but improved for oncologists and nurses. Caregivers reported reframing hospice perceptions and greater support in their roles. • **Conclusions:** The model was feasible and acceptable. It improved communication, maintained therapeutic alliances, and reassured caregivers by preserving oncologist continuity. This model warrants further evaluation to improve person-centered care.

Notable Presentations At ESMO - AI 2025

Digital Health, Patient Monitoring & ePROs (2/9)

Date	Title	Author	Summary
12 Nov 2025	Integrating ePROs with EQ-5D quality-of-life measures to enable digital oncology monitoring	Andreas Trojan	• **Introduction**: ePROs in oncology offer real-time symptom monitoring, yet their relationship with standardized QoL tools like the EQ-5D is underexplored. Establishing these links is essential for integrating ePROs into clinical decision-making. • **Methodology:** We collected ePRO data from 53 breast cancer patients undergoing systemic treatment, generating ~14,000 entries. These were matched with EQ-5D-5L questionnaires. Pearson correlation and LASSO regression were used to examine associations between ePROs and EQ-5D outcomes. • **Results:** ePROs showed meaningful alignment with EQ-5D-5L, particularly in pain, mood, and mobility. Pain and mobility correlated at r=0.35. • **Conclusions:** Linking ePROs with EQ-5D-5L enables continuous symptom monitoring, improving QoL detection and symptom management in digital oncology care.
12 Nov 2025	Designing the acute oncology service (AOS) of the future: Integrating digital platforms with traditional models to deliver smarter, connected, and patient-centric cancer care	Paul Landau	• **Introduction**: Proactive management of chemotherapy-associated toxicities is essential for patient safety, treatment adherence, and quality of life during Systemic Anti-Cancer Therapy (SACT). Airedale NHS Foundation Trust uses a 24-hour Acute Oncology Service (AOS) to triage symptoms, but this model often leads to unnecessary face-to-face (F2F) assessments, straining oncology units. In February 2025, the Careology digital cancer care platform was introduced to complement the AOS service for more efficient triage and care delivery. • **Methodology:** Between February and March 2025, all new SACT patients were introduced to Careology. Patient-reported outcomes (PROs) from Careology users were analyzed and compared with non-users, focusing on F2F reviews and service utilization. • **Results:** In the non-digital group, 50% of green and 58% of amber symptoms resulted in F2F assessments. In contrast, only 8% of amber cases in Careology users required F2F review, a reduction of >80%. Early evidence shows improved service efficiency and patient experience. • **Conclusions:** Integrating Careology with traditional AOS reduced unnecessary F2F assessments by 50%, improving efficiency and clinical safety. Future integration of AI could further optimize care by shifting to predictive, rather than reactive, management.

Notable Presentations At ESMO - AI 2025

Digital Health, Patient Monitoring & ePROs (3/9)

Date	Title	Author	Summary
12 Nov 2025	A Digital Platform for Psycho-Cognitive Assessment and Support in Oncology	Ilaria Durosini	• **Introduction**: Cancer patients often experience psycho-cognitive impairments, with caregivers facing emotional burdens. Digital systems are emerging in healthcare, offering a potential solution for mental health assessment and support. This study, part of the ALTHEA project, explores attitudes and preferences regarding a digital platform for psycho-cognitive support. • **Methodology:** Online surveys and four focus groups were conducted with Italian cancer patients (n=8), caregivers (n=7), oncologists, nurses, surgeons (n=8), and psycho-oncologists (n=5). Quantitative data were analyzed descriptively, while qualitative data were analyzed using content analysis. • **Results:** 75% of patients and 57.2% of caregivers expressed interest in a digital platform for psycho-cognitive support. Patients particularly valued monitoring emotional changes (87.5%) and accessing mental health information (75%). Professionals agreed that the platform could enhance workflow and support communication. • **Conclusions:** Findings support the development of a web-based platform for mental health screening and psychological support, addressing the psycho-cognitive needs of patients and caregivers. Further refinement needed to incorporate user concerns and optimize functionality
12 Nov 2025	ROSETTA-BC: A digital training tool to strengthen breast cancer MDT decision-making through guideline-based case simulation	Man Li	• **Introduction**: Breast cancer (BC) is the most common cancer in women in China, with increasing incidence and care complexity. While multidisciplinary team (MDT) care is central to BC management, discrepancies in pre- and post-MDT decisions highlight the need for guideline-based training to improve decision consistency and care quality. • **Methodology:** ROSETTA (Multidisciplinary Oncology Strategies for Enhanced Team-based Treatment Approaches) is a cloud-based platform designed to improve MDT decision concordance. It presents simulated patient cases with clinical history, imaging, and diagnostics, asking participants to make decisions based on guidelines. The platform was adapted for BC using 67 real-world cases from a remote MDT platform. • **Results:** ROSETTA-BC showed strong potential to enhance MDT decision-making and guideline adherence. It addressed key knowledge gaps with a diverse range of cases, covering early and metastatic stages, and various treatment plans, including targeted therapy, immunotherapy, and chemotherapy. • **Conclusions:** ROSETTA-BC is a scalable solution to enhance MDT decision-making in BC care, offering interactive learning, expert feedback, and guideline-conformant care.

Notable Presentations At ESMO - AI 2025

Digital Health, Patient Monitoring & ePROs (4/9)

Date	Title	Author	Summary
12 Nov 2025	Digital and AI-assisted multimodal supportive care for advanced pancreatic cancer patients: Combining physical activity, nutrition, and pain management during chemotherapy	Gabrielle Oestreicher	• **Introduction**: The European RELEVIUM project aims to assess the impact of a digitally-assisted multimodal supportive care intervention on health-related quality of life (QoL) in patients with pancreatic cancer. The goal is to improve early access to multidisciplinary and cost-effective palliative care. • **Methodology:** In cancer centers across Estonia, Israel, and Germany, 132 patients are randomly assigned to either the control group (usual care) or the intervention group (digitally-assisted multimodal support). The intervention includes monitoring of pain, nutrition, fatigue, sarcopenia, and physical activity, with real-time data displayed on a clinician dashboard and tailored recommendations provided via the RELEVIUM app. • **Results:** The study, which began in the second quarter of 2025, will assess the intervention's impact on QoL, with results expected in 2026. Secondary endpoints include pain, physical function, and socioeconomic factors. • **Conclusions:** The study will provide insights into the efficacy of digitally-assisted supportive care in pancreatic cancer, highlighting the potential of digital health tools in enhancing clinical decision-making and improving care quality in Europe.
12 Nov 2025	Implementation and evaluation of an artificial intelligence-based query resolution tool in oncology clinical trials	Michele Moschetta	• **Introduction**: Timely resolution of investigator and site queries in oncology trials is essential for protocol adherence, patient safety, and efficiency. Traditional methods of resolving these queries—such as manual document searches and expert consultations—are time-consuming and prone to delays. AI, particularly when integrated into Retrieval-Augmented Generation (RAG) frameworks, offers a faster, more accurate solution. • **Methodology:** This study developed and evaluated the Study Document Assistant (SDA), a RAG-based tool designed to provide real-time, context-aware responses to trial queries. SDA compiles trial documents into a digital repository and uses semantic search and LLM reasoning to generate coherent, context-specific answers. • **Results:** In a controlled experiment, SDA reduced the mean response time by 43.8% (14.9 minutes vs. 26.5 minutes, $p < 0.04$) compared to manual review. SDA maintained accuracy and user satisfaction, achieving similar results to traditional methods. • **Conclusions:** SDA significantly reduces response times in oncology trials while preserving answer quality and user satisfaction. RAG-based tools like SDA can enhance operational effectiveness in clinical research.

Notable Presentations At ESMO - AI 2025

Digital Health, Patient Monitoring & ePROs (5/9)

Date	Title	Author	Summary
12 Nov 2025	Nutrition and digital oncology: Telemedicine strategies for expanding access and nutrition and digital oncology - Telemedicine strategies for expanding access and improving quality of care	Thiago Jorge	• **Introduction**: Early nutritional care in cancer patients is crucial for improving prognosis, treatment tolerance, and quality of life. Digital platforms and telemedicine have transformative potential in providing equitable, remote nutritional support, particularly for vulnerable populations. • **Methodology:** This study used data from a digital platform providing nutritional care to cancer patients from 2021 to 2025. Nutritional risk was assessed using the Patient-Generated Subjective Global Assessment (PG-SGA SF). Descriptive analysis of demographic, clinical, and nutritional indicators was performed. • **Results:** Among 270 patients, 58.9% were treated in the Brazilian Public Health System. Before telemedicine follow-up, 85.2% lacked access to a nutritionist. After initiating follow-up, 61.3% required oral nutritional supplements (ONS), and nutritional risk decreased from 50.4% to 31.9%. • **Conclusions:** Digital health strategies improved nutritional care identification and reduced nutritional risk, demonstrating their potential to enhance equity and access to oncology care.
12 Nov 2025	Implementation of an ePRO-driven digital navigation and telemonitoring model in oncology: A HEOR-oriented pilot study in Brazil	Matheus S. Rocha	• **Introduction**: Oncology treatment often faces clinical and economic burdens. Traditional patient navigation lacks real-time monitoring, limiting timely interventions. Digital Health Interventions (DHIs) using electronic Patient-Reported Outcomes (ePROs) offer a promising solution, but their use in Brazil remains limited. This study evaluates a DHI ePRO-based navigation model's impact on clinical outcomes and cost in Brazilian oncology care. • **Methodology:** A pilot study (July–October 2024) enrolled 23 oncology patients in a DHI ePRO navigation program and compared outcomes with a control group (n=15). Outcomes included clinical stability, activation and engagement rates, team satisfaction and cost avoidance • **Results:** The intervention group showed improved clinical stability, with more patients classified as low-risk (74% vs. 70%). The model achieved 69% activation and 65% engagement rates. The navigation team achieved a 100% Net Promoter Score. The estimated cost avoidance was R$ 942,165.00 (± USD 175,000.00). • **Conclusions:** The DHI ePRO-driven navigation model effectively improved clinical stability and generated significant short-term cost savings, demonstrating its potential for broader implementation in oncology care.

Notable Presentations At ESMO - AI 2025

Digital Health, Patient Monitoring & ePROs (6/9)

Date	Title	Author	Summary
12 Nov 2025	AI-based dual-interface mobile application for remote monitoring and risk stratification of post-chemotherapy and radiotherapy toxicities	Ahmed N. Mahmoud	• **Introduction**: Patients undergoing chemotherapy and radiotherapy often experience toxicities that may require urgent intervention. Current hospital-based follow-up models can delay recognition of these toxicities and add burden to both patients and healthcare systems. AI-powered mobile applications present an opportunity for personalized, home-based toxicity monitoring. • **Methodology:** This conceptual framework proposes an AI-powered mobile application with two interfaces: a clinician interface for entering patient data and a patient interface for self-reporting symptoms and physiological parameters. The AI engine integrates both data streams to assess toxicity risk and provide real-time recommendations based on severity. • **Results:** No clinical or technical results are available yet. A feasibility study will evaluate usability, adherence, and accuracy of the AI-driven monitoring system. • **Conclusions:** This AI application offers an innovative approach to continuous toxicity monitoring, potentially improving early detection, reducing hospital admissions, and enhancing patient satisfaction.
12 Nov 2025	Oncology concierge: A digital solution to optimize access, continuity, and patient experience in high-demand specialties	Claudio Salas	• **Introduction**: In Chile, unrestricted access to oncology specialists has led to excessive workload, diagnostic delays, and dissatisfaction. To address this, Clínica Alemana de Santiago implemented the Oncology Concierge, a guided digital scheduling tool that directs patients based on their diagnostic or therapeutic stage. • **Methodology:** A descriptive study was conducted with adults seeking oncology consultation. Patients were guided through the digital tool, which categorized them based on diagnosis, active treatment, or family history. • **Results:** In the first month, 638 users accessed the oncology webpage, with 470 redirected to other specialties. 140 patients scheduled oncology consultations, and 70% of appointments became accessible online, reducing administrative workload. • **Conclusions:** The Oncology Concierge optimizes resources, improves care timeliness, and enhances patient experience, offering a scalable model for other high-demand specialties.

Notable Presentations At ESMO - AI 2025

Digital Health, Patient Monitoring & ePROs (7/9)

Date	Title	Author	Summary
12 Nov 2025	Preliminary findings from a six-months feasibility study of AYABytes: An eHealth mobile application supporting adolescents and young adults with cancer	Brian Shao Tian Woon	• **Introduction**: Adolescents and young adults (AYAs) with cancer face significant distress due to treatment burden and disrupted life milestones. AYABytes is a co-created mobile app designed to provide reliable cancer information, self-monitoring tools, and peer experiences. This study reports preliminary data on its feasibility and acceptability. • **Methodology:** Participants were given access to AYABytes for six months. Feasibility was based on usage frequency (≥2 log-ins). Acceptability was assessed using the mHealth App Usability Questionnaire (MAUQ) and exit interviews. • **Results:** 37 participants enrolled, with 48.5% meeting the feasibility threshold. MAUQ scores indicated good usability (mean 4.9/7). Frequent users valued peer narratives and symptom tracking. • **Conclusions:** AYABytes is a relevant and acceptable digital tool for AYAs, with potential to reduce distress in engaged users. Future efforts will focus on improving accessibility and content updates.
12 Nov 2025	Intelligent follow-up platform: An AI-driven breast cancer-specific model for long-term patient management in China	Fei Ma	• **Introduction**: Global cancer incidence is rising, underscoring the need for scalable long-term care. In breast cancer, delays in follow-up and poor adherence monitoring worsen outcomes. This study presents China's leading AI-powered follow-up platform for breast cancer, integrating national guidelines, real-world data, and ChatGLM for automated patient interaction and follow-up. • **Methodology:** Two clinical studies were conducted: early-stage breast cancer (adherence and quality of life) and advanced-stage patients on ADC therapy (adherence and adverse event monitoring). Platform functions included emotional support, Q&A, risk assessments, reminders, and follow-up protocols, operational across 60 hospitals in 24 provinces. • **Results:** The AI platform reduced counseling time by 60%, cut consultation volume by 50%, and increased patient education reach by 45%. Proactive adverse event monitoring improved satisfaction by 35%, and real-time symptom capture boosted follow-up efficiency. • **Conclusions:** This AI-powered platform enhances patient satisfaction, operational efficiency, and decentralized research, offering a scalable model for AI-assisted oncology care globally.

Notable Presentations At ESMO - AI 2025

Digital Health, Patient Monitoring & ePROs (8/9)

Date	Title	Author	Summary
12 Nov 2025	Early detection of symptoms during chemo(immune)therapy treatment of metastatic breast cancer using ePRO and Fitbits: The SYMPHA trial	Lars Woudstra	- **Introduction**: Chemotherapy for metastatic breast cancer (mBC) often leads to symptoms that affect health-related quality of life (HRQoL). While electronic patient-reported outcomes (ePRO) have shown promise in symptom monitoring, this study aims to explore the potential of multimodal Fitbit data to predict early symptoms during chemotherapy, reducing the need for active patient input. - **Methodology:** This prospective study recruits 448 mBC patients across 28 hospitals in the Netherlands. Patients are randomized to receive either an ePRO app or not. Fitbit devices will continuously collect heart rate, activity, and sleep data. These data will be used to train a machine learning model to predict symptoms related to chemotherapy. Feature selection and temporal sensitivity analysis will be applied. - **Results:** xWe aim to use Fitbit data to predict treatment-related symptoms, complementing HRQoL assessments and reducing reliance on ePRO responses. - **Conclusions:** This study could provide new insights into predicting symptoms using passive wearable data, enhancing symptom monitoring and improving HRQoL in mBC patients
12 Nov 2025	Oral health management in patients with solid tumors undergoing chemotherapy: Quality of life assessment – Use of e-Health applications	Pinelopi Petropoulou	- **Introduction**: Oral complications during and after anticancer therapy are common and significantly impact quality of life and treatment adherence. Integration of dentists into multidisciplinary oncology teams and the use of e-health applications can help manage these complications and improve patient outcomes. - **Methodology:** This randomized interventional study involved 102 patients with solid tumors receiving chemotherapy or combined treatments. The control group received standard oral health instructions, while the intervention group received both in-person and electronic dental support. - **Results:** E-health tools led to a significant reduction in oral complications such as mucositis, xerostomia, and swallowing difficulties, preventing therapy interruptions. Patients demonstrated improved oral hygiene and better quality of life, with active participation in treatment decisions. - **Conclusions:** Early detection and management of oral complications through e-health tools are critical for treatment completion, optimal outcomes, and improved quality of life in oncology patients.

Notable Presentations At ESMO - AI 2025

Digital Health, Patient Monitoring & ePROs (9/9)

Date	Title	Author	Summary
12 Nov 2025	Implementing and sustaining digital symptom monitoring as standard cancer care in Northern Norway: Barriers and facilitators	Siv G. Aanes	• **Introduction**: Patient-reported outcomes (PROs) are essential in cancer care for tracking symptoms, adverse events, and quality of life. Nordland Hospital Trust in Northern Norway implemented Elekta Kaiku for digital symptom monitoring across six rural hospitals, aiming to integrate PROs into routine clinical practice. • **Methodology:** The IHI Model for Improvement guided the implementation, which involved redesigning workflows, rapid cycle testing, and continuous adaptations. Modules were introduced for immunotherapy, targeted therapies, and hormonal prostate treatment, with outcome measures focused on clinical effectiveness and process efficiency. • **Results:** 458 patients were enrolled, with steady annual growth. Over 80% of immunotherapy patients and 100% of CDK4/6 inhibitor patients used the platform, generating 600 symptom reports and 325 clinical values monthly. Key facilitators included leadership support and multidisciplinary collaboration. • **Conclusions:** A structured implementation framework ensured efficient and sustainable integration of digital symptom monitoring into cancer care.

Notable Presentations At ESMO - AI 2025

Ethics, Regulatory & Implementation Science (1/8)

Date	Title	Author	Summary
12 Nov 2025	Radiologists perception on AI/ML software as a medical device (SaMD) unveiled via post-study usability survey: Key assets to redefine lung cancer screening practice	Francesco Grossi	• **Introduction**: Eyonis® LCS is an AI/ML-based computer-aided detection/diagnosis (CADe/CADx) tool that aids radiologists in detecting, localizing, and characterizing lung nodules in Low-Dose Computed Tomography (LDCT) images. This study evaluates its user experience and clinical utility through a survey of North American radiologists. • **Methodology:** A post-study survey was conducted with 16 radiologists (mean experience 13.3 years) following a Multi-Reader Multi-Case (MRMC) pivotal study. The survey, consisting of 17 Likert scale and free-text questions, assessed diagnostic support, clinical decision-making, workflow, and user feedback on the malignancy score. • **Results:** 94% of radiologists responded, with 82% of questions receiving positive feedback. Key findings include improved productivity (80%), enhanced accuracy (80%), reduced review time (73%), and aid in clinical decisions (73%). The malignancy score was well-understood by most respondents. • **Conclusions:** Eyonis® LCS is perceived as useful and ready for clinical adoption. Its design aligns with user needs, suggesting its potential for effective integration into radiology workflows. Further experience and data will enhance its clinical trustworthiness
12 Nov 2025	Breaking cultural barriers with artificial intelligence: A systematic review of AI driven solutions in cervical and breast cancer care across low income countries	Snigdha Baddepudi	• **Introduction**: Cervical and breast cancer remain leading causes of death in women in low and middle-income countries (LMICs), largely due to late presentation driven by cultural, stigma, and gendered barriers. AI, especially in mobile and low-cost technologies, presents a solution to overcome these barriers, enabling early detection and decentralizing care. • **Methodology:** A systematic search was conducted across PubMed, Scopus, and Web of Science from 2012 to 2025 using keywords like "AI," "deep learning," "breast/cervical cancer," and "cultural barriers." Studies focusing on AI for screening, follow-up, or surveillance in LMICs addressing socio-cultural delays were included. PRISMA guidelines were applied to screen 3,020 records, resulting in 137 studies for review. • **Results:** xAI tools, including smartphone-based visual inspection, deep-learning cytology, and handheld breast scanners, showed diagnostic accuracies exceeding 90%. Studies incorporating culturally sensitive interfaces and female-led health delivery reported higher uptake and lower refusal rates. Challenges included infrastructure limitations, trust-building, and dataset diversity • **Conclusions:** This review proposes a 5-step framework integrating community co-design, AI education, and ethical oversight to enhance cultural accessibility in oncology, emphasizing AI’s potential to close the survival gap for women in LMICs.

Notable Presentations At ESMO - AI 2025

Ethics, Regulatory & Implementation Science (2/8)

Date	Title	Author	Summary
12 Nov 2025	From skepticism to optimism: A human-centered analysis of radiologists' trust in AI	Kalina Chupetlovska	• **Introduction**: While AI in radiology has gained attention, the human aspects—particularly radiologists' trust—are underexplored. Trust is crucial for the adoption of AI, yet little research has focused on understanding what influences radiologists' acceptance. • **Methodology:** Semi-structured interviews with 15 radiologists from two hospitals were conducted using a guideline based on five domains: user, system, developer, ethical, and patient factors. Interviews were thematically analyzed to identify key themes and nuances in radiologists' perspectives. • **Results:** Most radiologists (11/15) expressed positive views on AI, emphasizing its potential for human-equivalent or superhuman performance. Key trust factors included accuracy, reliability, time-saving, usability, transparency, and institutional involvement. Ethical concerns focused on human oversight and patient privacy. • **Conclusions:** Successful AI integration in radiology requires addressing radiologists' perspectives on trust, with attention to system design, usability, and ethical concerns. Further research is needed to explore these factors in depth.
12 Nov 2025	Do large language models (LLMs) improve decision-making in clinical practice? A systematic review and meta-analysis	Agata Suleja	• **Introduction**: The growing use of artificial intelligence (AI) and large language models (LLMs) in medicine has shown promise in diagnostics. However, their ability to support clinical decision-making outside of testing environments remains unclear. • **Methodology:** A systematic review and meta-analysis (PROSPERO: CRD420250652794) were conducted, analyzing 46 studies comparing LLM diagnostic decisions to those of physicians using real or fictional clinical cases. • **Results:** No significant difference was found in diagnostic performance between LLMs and physicians (RR 1.05, 95% CI 0.93-1.18). Subspecialty or medical training did not affect the outcomes. • **Conclusions:** LLMs perform similarly to physicians in diagnostic decision-making, showing potential as clinical advisors but not as replacements for human decision-makers.

Notable Presentations At ESMO - AI 2025

Ethics, Regulatory & Implementation Science (3/8)

Date	Title	Author	Summary
12 Nov 2025	Comparative performance of artificial intelligence based clinical prediction models for response to immune checkpoint inhibitors in metastatic melanoma: A systematic review and meta-analysis of retrospective cohort studies	Ishir Sharma	• **Introduction**: Metastatic melanoma remains a challenging cancer with poor prognosis. Current biomarkers like Tumor Mutational Burden (TMB) and PD-L1 expression show variable predictive performance. Immune checkpoint inhibitors (ICIs) have improved outcomes, but response rates remain unpredictable. Machine learning (ML) models, including radiomics and deep learning, are emerging as potential tools to predict ICI response. • **Methodology:** A systematic review was conducted using OVID MEDLINE and EMBASE to evaluate the performance of ML models in predicting response to ICIs. Of 1412 studies, 272 were screened, and 9 met inclusion criteria. A meta-analysis using RStudio assessed the efficacy of the models through Area Under the Curve (AUC). • **Results:** The pooled AUC across 9 ML models (N=265) was 0.778 (95% CI: 0.700-0.856). Substantial heterogeneity (I2 = 98%) was observed, with between-study variance (τ2) of 0.0149. • **Conclusions:** ML models show promising potential for predicting ICI response in metastatic melanoma, but significant heterogeneity across studies suggests the need for harmonized methodologies and external validation before clinical integration.
12 Nov 2025	The quality and clinical applicability of actionable and explainable AI tools for treatment decision support in oncology: a systematic review	Marloes Hassing	• **Introduction**: Many cancer treatment prediction models exist, but their adoption is limited due to poor interpretability and lack of actionable treatment recommendations. Actionable eXplainable Artificial Intelligence (XAI) models aim to address these barriers by providing both interpretable outcomes and clinically relevant suggestions. • **Methodology:** A systematic search was conducted across multiple databases (MEDLINE, EMBASE, Scopus, CINAHL, and IEEE Xplore) to identify studies on actionable XAI models for breast, lung, colorectal, gastric, and prostate cancer. The quality and clinical applicability of these models were assessed using the PROBAST-AI and IDEAL algorithms checklists. • **Results:** Of 7,875 screened records, 66 studies describing 58 models were included. Most models focused on breast (40%) or lung cancer (22%) and predicted survival (60%). While 79% used white-box models, 43% had low quality and 41% lacked clinical applicability due to missing data or overfitting. • **Conclusions:** Although XAI models show promise, most have low clinical applicability, quality, or explainability. Future development should focus on improving data handling, preventing overfitting, and enhancing model explainability for clinical integration.

Notable Presentations At ESMO - AI 2025

Ethics, Regulatory & Implementation Science (4/8)

Date	Title	Author	Summary
12 Nov 2025	Comparison of artificial intelligence based prediction models for immune checkpoint inhibitor related pneumonitis: A systematic review and meta-analysis of retrospective real-world cohort studies	Shreya Mittal	• **Introduction**: Checkpoint inhibitor pneumonitis (CIP) prediction models using machine learning (ML) can guide clinical decisions and reduce CIP-related fatalities in cancer patients. This systematic review focuses on studies that developed ML models to predict CIP prior to initiating immune checkpoint inhibitor (ICI) therapy. • **Methodology:** A systematic review of studies was conducted using Embase and PubMed to identify ML models predicting CIP from data before ICI initiation. A meta-analysis assessed model performance using pooled area under the curve (AUC) for clinical-only, radiomic-only, and multimodal models. • **Results:** Across 4 studies with 3052 patients, the pooled AUC was 0.82 (95% CI: 0.74-0.91). Radiomic-only models had the highest AUC (0.83), followed by clinical-only models (0.78). Clinical-radiomic models had a median AUC of 0.84, but were limited by small sample sizes. • **Conclusions:** Clinical-radiomic models provide the best predictive performance for CIP, but the small number of studies and significant heterogeneity warrant caution in interpreting pooled estimates.
12 Nov 2025	Cancer prevention in real-world laboratory data: AI-assisted data science methodologies	Martin Rusinko	• **Introduction**: The rapid growth of real-world data from cancer prevention programs offers significant potential for early cancer detection. Data science in this domain requires collaboration between data scientists and medical oncologists, but the process is often slow and resource-intensive. • **Methodology:** We analyzed retrospective data from a cancer prevention program (2006-2022) with 20,000 clients. The goal was to establish a secure analytic framework using generative AI coding assistants, allowing clinicians to independently conduct analyses, reducing reliance on data scientists. • **Results:** The dataset contained 50,174 tests from 32,759 visits. Generative AI tools like ChatGPT and GitHub Copilot were tested, with the most success achieved using iterative testing on synthetic data, leading to 80% successful runs and improved analytic outcomes. • **Conclusions:** Generative AI empowers clinicians to conduct data science analyses, bridging the expertise gap in digital oncology and facilitating the development of machine learning models for cancer prevention

Notable Presentations At ESMO - AI 2025

Ethics, Regulatory & Implementation Science (5/8)

Date	Title	Author	Summary
12 Nov 2025	Diagnostic accuracy of artificial intelligence for early melanoma detection: A systematic review and meta analysis of clinical trials	Dalila Marra	- **Introduction**: Early melanoma detection is crucial for patient survival, but diagnostic accuracy varies across settings. AI systems, including convolutional neural networks (CNNs), are being evaluated as adjuncts or alternatives to clinician assessments. This review assesses trial evidence for AI in melanoma detection, comparing AI-alone versus AI-assisted approaches. - **Methodology:** We conducted a systematic review of PubMed, Embase, and Cochrane, including 6 full-text trials. The intervention was AI use, either alone or assisted, with human clinicians as comparators. Outcomes included sensitivity, specificity, AUROC, and concordance. A meta-analysis pooled diagnostic results for AI-alone, AI-assisted, and human-only arms. - **Results:** In 3 trials, AI alone showed 75.5% sensitivity and 90.0% specificity. AI-assisted detection had 86.5% sensitivity, but lower specificity. Limitations include small sample sizes and exclusion of darker skin types. - **Conclusions:** AI diagnostic tools show comparable accuracy to expert dermatologists and enhance non-expert performance. Larger trials with diverse populations are needed to confirm findings and support clinical implementation.
12 Nov 2025	When AI meets the probe: A systematic review of diagnostic accuracy in handheld breast ultrasonography	Sri G. Muthiah	- **Introduction**: AI is increasingly used in handheld breast ultrasonography for cancer detection, potentially improving diagnostic accuracy in both screening and symptomatic care. However, its integration in low- and middle-income countries (LMICs) remains uncertain due to resource constraints. This review assesses the diagnostic performance of AI-assisted handheld breast ultrasonography versus radiologist interpretation. - **Methodology:** We registered the protocol in PROSPERO and reviewed the strategy with a librarian. Studies on adult women using handheld breast ultrasound, comparing AI-assisted interpretation with radiologist interpretation, were included. Outcomes included sensitivity, specificity, and AUROC. Data extraction was done using Covidence, with risk of bias assessed via QUADAS 2. - **Results:** 1,381 records were screened, 859 advanced to full text assessment. Preliminary findings show improved diagnostic accuracy, but variability in populations, AI models, and outcome definitions limits immediate clinical application. - **Conclusions:** Initial evidence suggests AI could improve diagnostic performance, but prospective validation and implementation studies are needed, particularly in LMICs.

Notable Presentations At ESMO - AI 2025

Ethics, Regulatory & Implementation Science (6/8)

Date	Title	Author	Summary
12 Nov 2025	Artificial intelligence for bone metastases: A systematic review and meta-analysis of diagnostic and prognostic performance	Luisana Sisca	• **Introduction**: Bone metastases, a serious complication of advanced solid tumors, severely impair patients' quality of life. Early diagnosis and risk stratification remain challenging. AI has the potential to reshape clinical decision-making in this area. • **Methodology:** Systematic review and meta-analysis of studies (2008–2025) applying AI to diagnose or predict outcomes in bone metastasis was conducted. Included studies reporting diagnostic or prognostic performance. Data pooled using a random-effects model to estimate heterogeneity. Key limitations included retrospective designs and methodological differences. • **Results:** Twenty studies were included. AI showed a pooled AUC of 0.91 (95% CI 0.87–0.94), with convolutional neural networks dominating imaging applications. Radiomics and clinical features achieved a lower pooled AUC of 0.8, while radiomics-based models and nuclear imaging performed better (AUC 0.93 and 0.90). Sensitivity and specificity were 88.6% and 84.6%, respectively. • **Conclusions:** AI demonstrates robust diagnostic and prognostic accuracy for bone metastases, offering potential for early detection and personalized management. Further prospective validation is needed to integrate these results into clinical practice.
12 Nov 2025	Is Chile ready to regulate artificial intelligence in oncogenomic data?	Claudio Salas	• **Introduction**:Genomic sequencing is crucial in oncology, with AI/ML transforming data analysis for personalized treatment. However, significant ethical and regulatory challenges, particularly in privacy, consent, and equity, persist. In Chile, despite advancements in data protection laws, gaps remain in the regulation of AI in genomic data. • **Methodology:** This qualitative study analyzed national laws, legislative bills, European regulations, and bioethical documents. A thematic analysis identified key areas such as legal frameworks, genomic data regulation, AI governance in healthcare, ethical conditions for research, and algorithmic transparency. • **Results:** Chile's legal framework is fragmented. While Law No. 21.719 modernizes data protection, it remains unenforced until 2026. The 2025 AI bill aligns with EU standards but lacks specifics on genomic oncology. Ethical concerns persist regarding data re-identification and algorithm transparency. • **Conclusions:** Chile must accelerate the enforcement of Law 21.719, align it with the AI bill, and develop health-specific guidelines to promote transparency and ethical innovation in oncology.

Notable Presentations At ESMO - AI 2025

Ethics, Regulatory & Implementation Science (7/8)

Date	Title	Author	Summary
12 Nov 2025	Mapping the AI readiness gap in oncology staff at a comprehensive breast cancer center: a cross-sectional survey using the MAIRS-MS scale	Ghada Emam Moussa	• **Introduction**: Healthcare AI adoption hinges on workforce readiness. This study assessed oncology staff readiness at the Breast Cancer Comprehensive Center (BCCC), Cairo University, using the validated Medical Artificial Intelligence Readiness Scale (MAIRS-MS). • **Methodology:** A cross-sectional online census was conducted in 2025 across all BCCC staff. The 22-item MAIRS-MS assessed cognition, ability, vision, and ethics on 5-point Likert scales. Domain and total scores were calculated, and group comparisons were made based on role, age, education, and years in oncology using Kruskal–Wallis tests. • **Results:** A total of 154 respondents (87% female, median age 30) participated. The overall AI readiness mean was 3.43/5, with ethics scoring highest (3.83). Knowledge gaps were noted in AI training, terminology, and patient communication. AI readiness varied by years in oncology, age, and education. • **Conclusions:** Ethical readiness was strongest, while foundational knowledge and practice translation were weaker. The findings highlight the need for an AI curriculum focusing on the fundamentals, problem-to-tool mapping, and patient communication. Repeat measurements will assess impact.
12 Nov 2025	Real world adoption and utility of AI in oncology in India: A nationwide survey of medical oncologists	Nitin Y. Murthy	• **Introduction**: The rapid integration of AI and publicly available large language models (LLMs) into oncology presents opportunities, yet real-world insights into their adoption, utility, and challenges among medical oncologists remain limited. This study aims to gather such insights to guide policy makers and oncology associations in shaping academic agendas and clinical guidelines. • **Methodology:** A cross-sectional electronic survey was conducted in August, targeting medical oncologists across India. A 30-item questionnaire, distributed via WhatsApp groups and social media, assessed AI awareness, usage, perceived utility, and concerns. Responses were analyzed descriptively. • **Results:** 135 oncologists participated, with 77% using AI actively. AI deemed most impactful in diagnostics, radiology, and NGS interpretation (~75%). However, only 11% used AI regularly for clinical decision support. Many cited concerns about confidentiality (58.5%) and a limited understanding of AI terminology (55%). A majority desired workshops for AI training (56%). • **Conclusions:** AI adoption is widespread among Indian oncologists, particularly in diagnostics and imaging. However, its integration into clinical decision-making remains limited, highlighting the need for targeted training, country-specific AI models, and secure, open-source datasets.

Notable Presentations At ESMO - AI 2025

Ethics, Regulatory & Implementation Science (8/8)

Date	Title	Author	Summary
12 Nov 2025	The budget impact of AI-based chest X-ray analysis for early lung cancer detection: Evidence from Colombia, Costa Rica, and Thailand	Saniya Pawar	• **Introduction**: Lung cancer (LC) is the leading cause of cancer-related deaths globally. Early detection can significantly reduce mortality and healthcare costs. Chest X-rays (CXR) are a widely used diagnostic tool, and AI software like qXR® can enhance detection of incidental pulmonary nodules (IPN), leading to earlier LC diagnoses. • **Methodology:** This study assessed the budget impact of AI-aided CXR-based IPN detection in Colombia, Costa Rica, and Thailand. A decision-tree model was used to estimate the number of patients identified at various stages, factoring in treatment costs, healthcare resources, and end-of-life expenses. • **Results:** Initial costs increased due to additional treatments, but long-term savings were achieved as early-stage LC diagnoses reduced treatment costs. The break-even point was reached by the second year in Colombia and the third year in Costa Rica and Thailand. The model predicted over 3 premature deaths averted per 100,000 inhabitants in all three countries. • **Conclusions:** AI-assisted CXR for IPN detection offers long-term cost savings and health benefits by reducing premature LC deaths, demonstrating its value for national healthcare systems in these countries.

Notable Presentations At ESMO - AI 2025

Genomics, Multi-Omics & Biomarker Discovery (1/10)

Date	Title	Author	Summary
12 Nov 2025	Benchmarking DNA language models for biomarker detection	Michaela Unger	• **Introduction**: AI-driven DNA language models (DNA-LMs) may enhance biomarker discovery by capturing contextual genomic signals from somatic mutations. • **Methodology:** Whole-exome TCGA data (n=10,035) generated 150-nt mutation-centered sequences. Five DNA-LMs were benchmarked via multiple-instance learning for cancer type, MSI, and HRD; context sizes and mutation counts varied; best model fine-tuned. • **Results:** Strong MSI and cancer-type prediction; moderate HRD. DNABERTv2 performed best. MSI improved with multiple mutations and larger context; HRD with shorter windows. Simpler token/reference features sometimes matched embeddings. • **Conclusions:** DNA-LMs show promise for genomic diagnostics but gains are task-dependent, with computational and reproducibility challenges limiting clinical translation.
12 Nov 2025	Genome-wide association study and fine mapping uncover novel genetic loci and credible genes of glioma	Aierpati Maimaiti	• **Introduction**: Glioma etiology may involve systemic metabolic influences with emerging genetic links to metabolic traits. • **Methodology:** Integrated GWAS datasets and single-cell transcriptomics across 43 metabolic traits using LDSC, GNOVA, LAVA, MTAG, SMR, TWAS, and PRS modeling to dissect shared architecture and causality. • **Results:** Significant polygenic overlap with 26 traits; ischemic stroke strongest. Identified 36 shared loci, 18 novel variants, 109 pleiotropic genes with neurovascular-immune enrichment. Causal links to BP, AF, CKD. PRS improved glioma risk prediction; metabolites modified susceptibility. • **Conclusions:** Reveals metabolic–glioma genetic cross-talk, highlighting novel targets for precision risk stratification and preventive neuro-oncology.

Notable Presentations At ESMO - AI 2025

Genomics, Multi-Omics & Biomarker Discovery (2/10)

Date	Title	Author	Summary
12 Nov 2025	Developing biomarker-integrated cancer risk prediction models using case-cohort designs	Yangfan Li	- **Introduction**: Biomarker-enhanced survival prediction can advance early pancreatic cancer detection, but large-scale biomarker testing is costly; case-cohort designs offer efficiency with methodological challenges. - **Methodology:** Case-cohort data (>500,000 participants) analyzed using weighted Cox and random survival forests with Prentice and Kalbfleisch–Lawless weighting. Six variable-selection strategies compared; performance assessed via weighted C-index and Integrated Brier Score. - **Results:** Proper weighting preserved performance versus full-cohort models. Biomarkers improved calibration/discrimination; MMP7, PTN, MMP12 consistently selected across methods. - **Conclusions:** Efficient case-cohort modeling supports scalable, cost-effective biomarker-driven precision oncology with strong clinical utility.
12 Nov 2025	ImmCellTyper: An AI-driven toolkit for high-dimensional CyTOF immune profiling	Maryam Arshad	- **Introduction**: CyTOF supports oncology biomarker and immune monitoring discovery but high-dimensional complexity limits translation. - **Methodology:** ImmCellTyper developed as an AI-assisted pipeline using BinaryClust, a semi-supervised clustering algorithm integrating expert knowledge. Workflow: batch correction, QC, lineage identification, deep subset analysis, differential abundance/function profiling. - **Results:** Across ~4M cells, BinaryClust matched expert gating precision and exceeded current methods in accuracy and speed. Enabled discovery of novel immune subsets and signatures. - **Conclusions:** ImmCellTyper offers scalable, interpretable CyTOF analysis to accelerate immune biomarker discovery and precision oncology applications.

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Genomics, Multi-Omics & Biomarker Discovery (3/10)

Date	Title	Author	Summary
12 Nov 2025	Computational biology framework identifies novel biomarkers for melanoma immunotherapy selection using multi-omics integration	Lidia M. Arantes	• **Introduction**: Immunotherapy benefits in melanoma are variable with toxicity concerns, demanding predictive biomarkers for informed patient selection. • **Methodology:** Integrated proteomic and transcriptomic profiling of tumors from 30 patients. Correlation, differential expression, enrichment analyses plus Random Forest and LASSO models with repeated cross-validation and held-out testing. • **Results:** 25 significant protein-RNA correlations; responders showed major tumor-microenvironment shifts. THBS2, PYCR3, NGFR downregulated across omics. ECM-receptor interaction enriched. Predictive model achieved AUC 0.75 with robust feature set. • **Conclusions:** Multi-omics AI platform shows translational promise for digital biomarkers guiding melanoma immunotherapy response, pending prospective validation.
12 Nov 2025	Integration of genomic and clinical data for relapse prediction in early-stage non-small cell lung cancer	Per Niklas Waaler	• **Introduction**: Relapse risk in early-stage NSCLC remains heterogeneous and clinical staging lacks prognostic precision, necessitating genomic-enhanced prediction. • **Methodology:** 196 resected NSCLC tumors sequenced (TSO500). Mutect2 variant calling; SVD-derived genomic predictor integrated with clinical variables via multivariate CPH and stepwise selection. Variant filters optimized; 5-fold cross-validation for AUC and c-index. • **Results:** Gene-wise filtering superior (AUC 0.66 vs 0.57). Final model used 28 genes; strong risk stratification in older patients and larger tumors. Multimodal approach outperformed pStage (AUC 0.772 vs 0.685; c-index 0.731 vs 0.673); fusion with pStage improved further (AUC 0.795). • **Conclusions:** Genomic-clinical integration enhances relapse prediction, supporting refined post-surgical management; external validation ongoing.

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Genomics, Multi-Omics & Biomarker Discovery (4/10)

Date	Title	Author	Summary
12 Nov 2025	Transcriptomic and Regulatory Signatures of Metastatic Progression in Breast Cancer: An Integrative RNA-seq Study	Laura B. Quintas	• **Introduction**: Oligometastatic BC shows heterogeneous metastatic evolution; biomarkers predicting progression to polymetastatic disease are lacking. • **Methodology:** RNA-seq from 37 high-quality samples compared between oligo-oligo and oligo-poly groups. Hallmark gene set enrichment, scRNA-based deconvolution with Lasso for cell-type drivers, ISMARA for motif activity, STRING for network mapping. • **Results:** Polymetastatic tumors showed activation of proliferative/metabolic pathways (E2F, G2M, Hypoxia, mTORC1, Glycolysis). More macrophages, epithelial cells, adipocytes vs. immune-rich oligo-oligo tumors. E2F1, HSF4, FOSL1 heightened with networks tied to cell-cycle and stress signaling. • **Conclusions:** Integrated transcriptomic-microenvironment signatures highlight progression biology and inform AI-enabled metastatic-risk stratification in oligometastatic BC.
12 Nov 2025	Genomic ground truth for AI-based image classification of CELLSEARCH® circulating multiple myeloma cells	Luca Biasiolli	• **Introduction**: CMMCs are linked with poorer outcomes in MM, but CELLSEARCH® identification is manual and subjective. Genomically validated Ground Truth is needed to train automated deep learning classification. • **Methodology:** Blood from seven MM patients underwent CELLSEARCH® imaging and Stardist-based cell segmentation. Distinct immunophenotypic clusters were sorted individually via DEPArray™, followed by whole-genome sequencing to confirm MM-associated genomic alterations and map validated populations back to CELLSEARCH® clusters. • **Results:** Among 306 isolated cells, the CD38+/CD45−/CD19− cluster showed a 100% frequency of MM genomic abnormalities, confirming it as the true CMMC population. Other subsets were heterogeneous. The mapping enables accurate automated labeling within CELLSEARCH®. • **Conclusions:** This genomics-anchored workflow delivers objective CMMC Ground Truth for developing deep learning models, reducing operator variability and supporting reliable liquid biopsy monitoring in MM.

Notable Presentations At ESMO - AI 2025

Genomics, Multi-Omics & Biomarker Discovery (5/10)

Date	Title	Author	Summary
12 Nov 2025	Spatially resolved deep learning prediction of prognostic EMT/PT scores from H&E in clear-cell renal cell carcinoma	Rebecca N. Wray	• **Introduction**: Progression risk in ccRCC remains heterogeneous. EMT enrichment at tumour–normal interfaces indicates invasion and poor outcomes, inversely linked to proximal-tubule (PT) identity, suggesting a measurable progression axis. Scalable inference from H&E could improve risk stratification. • **Methodology:** TCGA-KIRC WSIs (n=397) were analyzed using SMMILe with foundation-model embeddings to predict spatial EMT/PT meta-program scores aligned to bulk RNA-seq. Performance was assessed by AUROC. • **Results:** UNI-v2 SMMILe achieved AUROC 0.752 for EMT and 0.682 for PT, demonstrating accurate spatial molecular inference from histopathology alone. • **Conclusions:** H&E-based prediction of transcriptomic programs enables scalable molecular phenotyping in ccRCC, supporting personalized prognostic workflows pending spatial validation.
12 Nov 2025	DNA methylation profiling with interpretable deep learning for glioma classification and liquid biopsy biomarker discovery	Aierpati Maimaiti	• **Introduction**: This study addresses the diagnostic gap by integrating deep learning with large-scale epigenetic data. • **Methodology:** A 15,606-sample methylation atlas was analyzed using a Transformer-based multi-head attention model. Model interpretability was enhanced through Captum and attention-map visualization, benchmarking performance against MLP, RNN, DNN, CNN, and Autoencoder frameworks. • **Results:** The Transformer achieved 99.23% accuracy (AUC > 0.95) in subtype classification. Key promoter methylation sites (42.3%) in CASZ1, HDAC4, and MAD1L1 were highlighted. Plasma-detectable markers (cg13672103, cg07105891) and subtype-specific signatures (MIR5189, RAET1L, FOXP1) were identified. • **Conclusions:** This interpretable Transformer framework redefines glioma epigenetic profiling, demonstrating clinical potential for blood-based liquid biopsy and early, precision-guided glioma diagno

Notable Presentations At ESMO - AI 2025

Genomics, Multi-Omics & Biomarker Discovery (6/10)

Date	Title	Author	Summary
12 Nov 2025	Consensus copy-number alteration signatures from clinical panels enable pan-cancer risk stratification and therapy response association	Adar Yaacov	• **Introduction**: Copy number alterations (CNAs) influence oncogenesis and therapy response, yet conventional detection methods (WGS, SNP arrays) are impractical clinically. Targeted panels, while routine, offer limited CNA resolution, necessitating new computational solutions. • **Methodology:** A multi-algorithmic framework integrating Independent Component Analysis, Non-negative Matrix Factorization, Hierarchical Dirichlet Process, and Graph-based Pattern Deconvolution was applied to 24,870 MSK tumors. Consensus CNA signatures were derived via hierarchical clustering and validated internally and externally. • **Results:** Five consensus signatures (CON1–5) were defined, distinguishing diploid and aneuploid patterns. Prognostic associations showed HR 1.3–2.5 (FDR<0.01). Signatures correlated with driver mutations (e.g., GATA3, KRAS) and mapped therapy resistance across modalities. • **Conclusions:** This framework converts routine panel data into robust, interpretable CNA-based biomarkers, enabling cross-cancer risk stratification, prognostic refinement, and therapeutic guidance in precision oncology.
12 Nov 2025	Next-generation sequencing-based computational profiling reveals driver mutation allele burden patterns predictive of myeloproliferative neoplasm subtypes	A-Jin Lee	• **Introduction**: Myeloproliferative neoplasms (MPNs) are difficult to distinguish clinically due to overlapping phenotypes. Leveraging NGS-based mutation profiles may enable precise molecular classification through computational biomarker discovery. • **Methodology:** NGS data from 72 MPN patients (21 PV, 38 ET, 13 MF) were analyzed. Variant allele frequency (VAF) profiling for JAK2, CALR, MPL and mutation burden quantification were performed using automated bioinformatics workflows and statistical modeling to define diagnostic thresholds. • **Results:** Distinct VAF patterns emerged: JAK2 VAF—PV 61.0% (78.3% ≥50%), ET 28.5% (0%), MF 60.5% (66.7%). CALR mutations appeared only in ET (19%) and MF (31%). MF showed highest mutational complexity (3.6 vs 2.4 [PV], 1.6 [ET]). Combined JAK2 VAF and mutation burden accurately classified subtypes. • **Conclusions:** NGS-derived VAF-based computational profiling effectively differentiates MPN subtypes and stratifies risk, supporting precision diagnostics in clinical hematologic oncology.

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Genomics, Multi-Omics & Biomarker Discovery (7/10)

Date	Title	Author	Summary
12 Nov 2025	OncoSelect: Leveraging predictive learning for molecular characterisation of clear cell renal cell carcinoma	Ionut Dragomir	- **Introduction**: Clear cell renal cell carcinoma (ccRCC) accounts for 80% of kidney cancers, with 30% presenting as metastatic. Despite immune checkpoint and VEGF/TKI therapies, many patients fail to respond, underscoring the need for predictive molecular stratification. - **Methodology:** Published ccRCC molecular subtypes were characterized across multi-omics datasets. Machine learning classifiers were trained to link patient molecular profiles with therapy-responsive subtypes, using cross-validation for performance assessment and mechanistic feature interpretation. - **Results:** Subtype classifiers achieved F1 scores exceeding 80%, outperforming baseline models. Feature analysis revealed biologically consistent predictors aligned with known ccRCC molecular processes and immune-oncogenic pathways. - **Conclusions:** Machine learning–driven multi-omics classification enables biologically interpretable stratification of ccRCC patients, supporting precision-guided therapy selection and prospective validation of subtype-based treatment strategies.
12 Nov 2025	Machine learning-guided integration of transcriptomic data and immune cell fractions identifies immune-hot biomarkers in pMMR endometrial cancer	Radu V. Matei	- **Introduction**: Endometrial cancers with dMMR are typically immune-active, whereas pMMR tumors are considered "cold." However, emerging evidence suggests immune heterogeneity within pMMR subsets, warranting systematic characterization using AI-driven analytics. - **Methodology:** RNA-seq data (60,660 genes; 558 samples) from TCGA were analyzed. ssGSEA defined immune-hot/cold phenotypes; CIBERSORTx estimated immune cell fractions. Differential expression and Random Forest ML integrated transcriptomic and TME features to identify robust immune-activation biomarkers. - **Results:** A subset of pMMR tumors exhibited immune-hot profiles with elevated PDCD1, CTLA4, CXCL9, CXCR3, CD3E, and TRAC. ML validation confirmed these as key immune-activation markers, redefining pMMR tumor immunogenicity. - **Conclusions:** This ML-based, multi-omic framework uncovers immune-active pMMR subpopulations, refining tumor immunophenotyping and enabling biomarker-driven precision immunotherapy in endometrial cancer.

Notable Presentations At ESMO - AI 2025

Genomics, Multi-Omics & Biomarker Discovery (8/10)

Date	Title	Author	Summary
12 Nov 2025	Novel multi-biomarker nomogram combining CD155/CD226/TIGIT/CD96 immune checkpoint axis for postoperative survival prediction in breast cancer	Qingkun Song	• **Introduction**: The CD155–CD226/CD96/TIGIT immune checkpoint axis regulates tumor-immune interactions and is aberrantly expressed in breast cancer, correlating with prognosis. Integrating its expression with clinical factors may refine individualized survival prediction. • **Methodology:** CD155, CD226, CD96, and TIGIT expression were quantified by immunohistochemistry. A prognostic index (PI) was generated and integrated with clinicopathological data using multivariate Cox regression. Model accuracy was assessed via C-index, ROC, Brier score, calibration, DCA, and bootstrap validation (n=1,000). • **Results:** The PI effectively stratified survival risk. Nomograms incorporating the PI achieved C-index values of 0.772 (DFS) and 0.822 (OS), with ROC AUC ≥0.80 for DFS and ≥0.85 for OS. Calibration and DCA confirmed predictive reliability and clinical utility. • **Conclusions:** This integrative prognostic model combining immune checkpoint and clinical variables provides accurate, individualized survival prediction, supporting precision oncology applications in breast cancer management.
12 Nov 2025	Deep learning on breast MRI images to predict BRCA1/2 variants	Yo Sato	• **Introduction**: Hereditary Breast and Ovarian Cancer (HBOC) syndrome accounts for ~5% of breast cancers, yet current BRCA1/2 genetic testing via BRACAnalysis CDx® shows limited cost-effectiveness. AI-driven imaging biomarkers may enhance mutation prediction. • **Methodology:** DCE-MRI data from 163 breasts (23 gBRCAm-positive; 84 gBRCAm-negative) were analyzed. A convolutional neural network (CNN) integrated imaging and clinical variables (age, family history) using FUJIFILM's SYNAPSE CREATIVE SPACE. Accuracy, sensitivity, and specificity were evaluated. • **Results:** MRI-only models achieved 50% accuracy; adding age improved accuracy to 68%, and adding family history raised it to 76%. Chemotherapy-exposed cases showed lower accuracy (63% vs. 75%), with retraining post-exclusion reaching 73%. • **Conclusions:** This multimodal CNN leveraging MRI and clinical data effectively predicts BRCA1/2 mutation status, demonstrating potential to improve cost-effectiveness and precision risk assessment in breast cancer diagnostics.

Notable Presentations At ESMO - AI 2025

Genomics, Multi-Omics & Biomarker Discovery (9/10)

Date	Title	Author	Summary
12 Nov 2025	Integrated genomic and proteomic analysis of plasma exosomes in colorectal cancer using a proprietary AI-driven oncology platform	Alisa Petkevich	• **Introduction**: Exosomes act as nanoscale mediators of tumor communication and are emerging as powerful biomarkers. Their integration into liquid biopsy platforms could enhance early detection and therapy monitoring in colorectal cancer. • **Methodology:** Exosomes were isolated from 42 patients (stages I–IV). Exosomal DNA, cfDNA, and circulating DNA underwent exome and targeted resequencing. Proteomic profiling via LC–MS/MS was integrated into an AI-driven oncology platform performing QC, anomaly detection, and pathway enrichment for multi-omic biomarker discovery. • **Results:** Exosomal DNA showed higher mutation sensitivity (+13%) and closer concordance with cfDNA in advanced disease. Proteomic profiling revealed stage-specific pathways in immune regulation, coagulation, and lipid transport. Integrated analysis identified prognostic biomarker networks. • **Conclusions:** Plasma exosomes provide enriched genomic and proteomic insight. AI-driven integration of exosomal data enables robust biomarker discovery, supporting early detection and precision-guided treatment in colorectal cancer.
12 Nov 2025	Machine learning for multi-omics risk prediction of cholangiocarcinoma in the general population	Felix Van Haag	• **Introduction**: This study aimed to develop a scalable, machine learning (ML) risk score for population-level early CCA detection. • **Methodology:** Using UK Biobank data (499,868 participants; 666 CCA cases), ML models incorporating demographics, EHR, labs, genomics, and metabolomics were trained and externally validated in PMBB, All of Us, and TriNetX cohorts. Cross-validation and ablation analyses identified minimal-feature models (TOP10, TOP5). • **Results:** The final EHR + biomarker model achieved AUROC 0.72 (UKB), 0.76 (PMBB), 0.84 (AOU). Predictors included age, GGT, cholangitis, and bile duct obstruction. Hazard ratios rose to 82.5 (95% CI: 26.4–257.96) with feature accumulation, strongest within 3–5 years post-assessment. • **Conclusions:** This externally validated ML-based risk score enables early, cost-effective CCA risk stratification using routine clinical data, providing a foundation for population-wide screening and precision prevention strategies.

Notable Presentations At ESMO - AI 2025

Genomics, Multi-Omics & Biomarker Discovery (10/10)

Date	Title	Author	Summary
12 Nov 2025	Machine learning for multi-omics risk prediction of cholangiocarcinoma in the general population A multi-output deep learning model for predicting EndoPredict genomic scores from digitalized histopathological slides of breast tumor specimens	Alessandro Rizzo	• **Introduction**: Multigene assays like EndoPredict (EP) guide adjuvant therapy in ER+/HER2– breast cancer but are limited by cost and accessibility. AI-based pathology models may offer low-cost, image-derived genomic risk prediction. • **Methodology:** A multi-output deep learning model (MO-net) based on ResNet101 analyzed H&E whole-slide images. It simultaneously predicted binary EP risk and continuous molecular scores. Performance was benchmarked against classification (CL-net) and regression (REG-net) networks in investigational (n=124) and validation (n=28) cohorts • **Results:** MO-net outperformed comparators with AUC 72.8% (vs. 65.9%) and C-index 56.3% (vs. 50.7%); validation confirmed reproducibility (AUC 72.2%, C-index 58.0%). Grad-CAM revealed biologically relevant tumor and stromal regions guiding predictions. • **Conclusions:** This first-in-class WSI-based AI model demonstrates feasibility for EP score prediction, underscoring the potential of computational pathology as a scalable, cost-effective alternative for genomic risk stratification in breast cancer.
12 Nov 2025	Development of a clinico-genomic AI prediction model for arm lymphoedema following breast cancer surgery and radiotherapy: The PRE-ACT study	Tim Rattay	• **Introduction**: PRE-ACT is a European initiative applying explainable AI to predict long-term radiotherapy toxicities, such as arm lymphoedema, in breast cancer patients, facilitating shared clinical decision-making and personalized treatment modification. • **Methodology:** Three cohorts (REQUITE, Hypo-G, CANTO; n=6,361) were analyzed using neural networks, random forests, and gradient-boosted trees. Thirty-two clinical/treatment features and 30 SNPs were used for 10-fold cross-validation (90:10 split). Interpretability was achieved via rule extraction. • **Results:** Arm lymphoedema incidence was 6%. The optimal random forest model (all 62 features) achieved AUC 0.86 ± 0.007, outperforming the previous gradient-boosted model (AUC 0.83 ± 0.003). Clinico-genomic explainability was validated across datasets. • **Conclusions:** Explainable AI-based models accurately predict post-radiotherapy lymphoedema risk. Integration into the PRE-ACTOR web app will enable real-time toxicity risk stratification and guide personalized supportive or treatment-adaptive interventions across Europe.

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Clinical Decision Support & Prognostic Modelling (1/15)

Date	Title	Author	Summary
12 Nov 2025	End-to-End Deep Learning for Predicting Breast Cancer Recurrence Risk	Gürcan Özden	• **Introduction**: Recurrent breast cancer remains a major clinical concern despite therapeutic advances. Gene expression–based assays aid recurrence risk assessment but are costly and limited in accessibility. AI-driven pathology offers a potential surrogate. • **Methodology:** Using an end-to-end deep learning pipeline based on vision transformer architecture, H&E slides from 449 HR+/HER2– breast cancer patients were analyzed to predict recurrence-of-risk (ROR) categories. Model performance was benchmarked across 11 foundation models and validated externally using TCGA-BRCA data. • **Results:** All 11 models achieved AUROCs >0.80 in internal validation. External validation confirmed robust generalizability—best performers: h-Optimus-1 (AUROC 0.85), Virchow-2 (0.84), Uni (0.84), Uni-2 (0.83). Kaplan-Meier analysis showed significant survival differentiation ($p<0.05$). • **Conclusions:** State-of-the-art foundation models accurately predict recurrence risk in HR+/HER2– breast cancer. AI-derived categories outperform traditional assays, enabling scalable, cost-efficient, and objective prognostication for personalized treatment planning.
12 Nov 2025	A large molecular model (LMM)-based predictor of clinical response to the WEE1 inhibitor Debio 0123 + carboplatin therapy	Jeannette Fuchs	• **Introduction**: DNA Damage Response (DDR) dysfunction promotes cancer progression and resistance, creating susceptibility to WEE1 inhibition. However, variable responses to Debio 0123 highlight the need for predictive biomarkers to optimize patient selection. • **Methodology:** Using the Genialis™ Supermodel framework, bulk RNA-seq data from pre-treatment biopsies were transformed into biological "biomodules." A logistic regression model with ElasticNet regularization was trained to predict response to Debio 0123 plus carboplatin, capturing interactions among biomodules. • **Results:** The model achieved high AUROC and classification accuracy, clearly separating responders from non-responders. Distinct biomodule expression patterns corresponded to specific biological mechanisms underlying differential therapeutic response. • **Conclusions:** This interpretable ML-based predictor enables biomarker-guided use of Debio 0123 + carboplatin, supporting precision oncology strategies. Future work will enhance performance and extend applicability across cancer types and treatment regimens.

Notable Presentations At ESMO - AI 2025

Clinical Decision Support & Prognostic Modelling (2/15)

Date	Title	Author	Summary
12 Nov 2025	AI-powered survival prediction in metastatic non-small cell lung cancer mNSCLC under pembrolizumab: A real-world support vector machine (SVM) approach	Teodor M. Vancea	• **Introduction**: Accurate prognosis in metastatic NSCLC (mNSCLC) treated with pembrolizumab is essential for guiding therapy. Machine learning (ML) models may enhance survival prediction beyond traditional clinical methods using routinely available parameters. • **Methodology:** Retrospective data from 124 mNSCLC patients (2018–2023) were analyzed using SVM models trained on clinicopathologic and inflammatory biomarkers (NLR, SII, LDH, PD-L1, etc.). Class imbalance was corrected via SMOTE, and Cox regression-derived hazard ratios were used for feature weighting. • **Results:** Weighted SVM (Model B) improved predictive accuracy—AUC 0.60–0.86–0.85–0.72 for 6-, 12-, 18-, 24-month OS. Top predictors were ECOG PS, age, metastasis burden, NLR, and SII. Incorporating Cox-based weights enhanced discrimination. • **Conclusions:** SVM-based ML models integrating routine biomarkers predict OS effectively in pembrolizumab-treated mNSCLC. Coupling survival statistics with ML improves performance, enabling risk stratification and personalized prognostic assessment.
12 Nov 2025	Time-to-event (TTE) machine learning models (ML-m) for survival prediction in patients with advanced non-small cell lung cancer (aNSCLC) receiving first-line (chemo-)immunotherapy	Francesca Rita Ogliari	• **Introduction**: This study developed time-to-event (TTE) ML-m to improve survival prediction in advanced NSCLC (aNSCLC) using real-world clinical data. • **Methodology:** Data from 463 aNSCLC patients across an international network were processed via the privacy-compliant S-RACE platform. Variables were stratified by robustness (groups 1–3). Cox regression explored prognostic factors, and TTE ML-m (XGBSE variants) were trained using Optuna optimization, with performance assessed by concordance index (C-index) and integrated Brier score (iBS). • **Results:** XGBSE-KaplanNeighbors achieved best OS and PFS prediction (C-index≈0.63, iBS≈0.26) using group 1 features. XGBSE-StackedWeibull showed comparable C-index but higher iBS, while KaplanTree underperformed. Top predictors—performance status, PD-L1, metastases—aligned with exploratory Cox findings. • **Conclusions:** The developed TTE ML-m demonstrated robust survival prediction using real-world aNSCLC data. Future expansions incorporating imaging and radiomics aim to enhance model generalizability and clinical applicability for individualized prognostic modeling.

Notable Presentations At ESMO - AI 2025

Clinical Decision Support & Prognostic Modelling (3/15)

Date	Title	Author	Summary
12 Nov 2025	Predicting immunotherapy response in non-small cell lung cancer using a foundation model for tabular data and real-world clinical evidence: Insights from APOLLO11 study	Cristina Maria Licciardello	- **Introduction**: Immunotherapy transformed NSCLC treatment, but PD-L1 alone poorly predicts response. There remains an unmet need for scalable, data-driven prognostic tools using real-world evidence to enhance treatment decision support. - **Methodology:** The APOLLO 11 multicenter study (n=1,150) analyzed clinical, histologic, and radiologic features from immunotherapy-treated NSCLC patients. TabPFN, a foundation model for tabular data, was compared with a RandomForest baseline for predicting 6- and 24-month overall survival (OS6, OS24). Performance was evaluated via ROC AUC, F1-macro, sensitivity, and specificity, with cost-sensitive optimization and SHAP explainability. - **Results:** TabPFN outperformed baseline across datasets: OS6 AUC 0.83 (test) and 0.76 (external); OS24 AUC 0.86 (test) and 0.73 (external). It required no manual feature selection, maintained high sensitivity (OS24 = 0.92), and demonstrated strong generalization. SHAP confirmed biologically relevant feature importance. - **Conclusions:** TabPFN enables accurate, interpretable prediction of immunotherapy outcomes in NSCLC using routine clinical data. Its superior generalizability and minimal tuning requirements support deployment as a practical AI decision-support tool in oncology.
12 Nov 2025	A machine learning algorithm facilitates treatment selection for up to three hepatocellular carcinomas ≤3 cm in size	Takashi Kokudo	- **Introduction**: For hepatocellular carcinoma (HCC) ≤3 cm, Japanese guidelines equally recommend liver resection (LR) or radiofrequency ablation (RFA), yet optimal patient-specific treatment selection remains uncertain. ML offers potential for personalized outcome-based guidance. - **Methodology:** Using data from 18,958 patients in the Japanese Liver Cancer Study Group registry, a Recurrent Deep Survival Machines (RDSM) model was trained for survival prediction with 10-fold cross-validation. Model performance was assessed via concordance index (c-index) and log-rank survival analyses, supported by 1:1 propensity score matching to mitigate confounding. - **Results:** LR yielded superior 5-year OS (81.4% vs. 73.1%; $p<0.005$). The RDSM model achieved a c-index = 0.68. Patients following ML-recommended treatment showed significantly improved survival (81.2% vs. 73.9%; $p<0.005$), validated post-matching (81.9% vs. 76.7%; $p<0.005$). ML favored LR in 84.5% of RFA-treated cases, particularly with typical CT enhancement/washout patterns. - **Conclusions:** ML-guided modeling effectively stratifies candidates for LR vs. RFA, improving survival prediction and decision support in small HCC.

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Clinical Decision Support & Prognostic Modelling (4/15)

Date	Title	Author	Summary
12 Nov 2025	Predicting Pathologic Response to Neoadjuvant Chemotherapy in Breast Cancer via Digital Pathology with Attention-Based Models	Maria Colomba Comes	- **Introduction**: Predicting pathological complete response (pCR) to neoadjuvant chemotherapy (NAC) is essential for tailoring breast cancer management. AI applied to pre-treatment biopsy histopathology enables early, image-based therapy response prediction. - **Methodology:** From 122 H&E-stained whole-slide images (WSIs), 384,076 tiles were processed via a CNN with Convolutional Block Attention Module (CBAM) to highlight biologically relevant structures. Mini-Batch C-Fuzzy K-Means removed non-informative regions. Model performance was benchmarked against standard CNNs across investigational, internal, and external validation cohorts. - **Results:** The attention-based model achieved AUC 81.4%, accuracy 81.3% (IC); AUC 80.9%, accuracy 80.0% (VC); and AUC 76.2%, accuracy 70.0% (EVC). Grad-CAM analysis revealed stromal activation in pCR cases and nuclear activation in non-pCR, confirming interpretability. - **Conclusions:** Attention-driven CNNs accurately predict pCR from biopsy WSIs, demonstrating reproducible performance and biological explainability across datasets—supporting their future clinical integration in neoadjuvant decision-making.
12 Nov 2025	Explainable model for predicting muscle loss after radiotherapy in oral cavity cancer	Jie Lee	- **Introduction**: Skeletal muscle loss following radiotherapy predicts poorer outcomes in oral cavity cancer. Accurate, explainable machine learning (ML) tools could enable early identification and targeted preventive interventions. - **Methodology:** In 903 patients (derivation n=572; validation n=331), pre/post-radiotherapy CT scans measured muscle change at the C3 level (≥4.2% loss threshold). Random Forest, XGBoost, and CatBoost models trained on clinical and acute toxicity data were evaluated by F1-score. Model interpretability used SHAP analysis. - **Results:** Muscle loss occurred in ~25% of patients. CatBoost achieved highest F1-score (0.921 external), outperforming RF (0.910) and XGBoost (0.899). SHAP identified anorexia, dysphagia, nausea, pain, and baseline muscle mass as top predictors, with clear patient-level interpretability. - **Conclusions:** An explainable CatBoost model accurately predicts radiotherapy-induced muscle loss, offering interpretable, data-driven insights to guide early nutritional and symptomatic interventions in oral cavity cancer management.

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Clinical Decision Support & Prognostic Modelling (5/15)

Date	Title	Author	Summary
12 Nov 2025	Clinical feature-based mutation risk prediction in NSCLC using a GPT-derived model	Sreedhar J. Cherulil	• **Introduction**:This study evaluated the predictive accuracy of GPT- and DeepSeek-based Large Language Models (LLMs) using clinical data alone. • **Methodology:** A GPT-derived model and DeepSeek LLM were trained on literature and real-world evidence to predict mutation probabilities in NSCLC using clinical inputs (age, smoking, brain metastases, ethnicity, metastatic sites). ROC analysis determined optimal cut-offs via the Youden Index, with sensitivity, specificity, PPV, and NPV computed. • **Results:** EGFR mutation prediction thresholds were >40.5% (GPT) and >21% (DeepSeek). GPT achieved sensitivity 85.3%, specificity 55.3%, PPV 45.3%, NPV 88.9%; DeepSeek showed sensitivity 88.2%, specificity 42.7%, PPV 41.1%, NPV 88.9%. Both demonstrated strong negative predictive value for mutation exclusion. • **Conclusions:** LLMs can efficiently approximate mutation probability using clinical features alone, offering a low-cost adjunct in LMICs. Enhanced real-world datasets and clinico-molecular correlation may further refine accuracy and clinical integration.
12 Nov 2025	AI-driven prediction of occult peritoneal metastases using pre-operative clinical and CT data in gastrointestinal and gynecological cancers: A study protocol compliant with TRIPOD-AI guidelines	Preethi S. Shetty	• **Introduction**: Occult peritoneal metastases (OPM) remain undetectable by conventional CT in 20–30% of gastrointestinal and gynecologic cancers, often discovered intraoperatively, leading to unexpected upstaging and abandoned curative resections. AI and deep learning (DL) approaches offer potential to enhance preoperative OPM detection. • **Methodology:** A multicentric retrospective study will include patients with biopsy-proven gastric adenocarcinoma or serous ovarian carcinoma without prior surgery. Preoperative CT scans (≤4 weeks) will undergo manual peritoneal annotation to create ground-truth datasets. Radiomic and clinical features will be extracted and used to train DL classifiers (train:test = 4:1). Heatmap-based explainability will highlight OPM regions. • **Results:** A cohort of 765 patients is projected (OPM prevalence 30%). Model performance targets sensitivity and specificity of 90%, with radiomic-clinical integration optimizing classification accuracy and interpretability. • **Conclusions:** The explainable AI/DL framework aims to enable preoperative OPM prediction in gastric and ovarian cancers, facilitating personalized surgical planning, improving cytoreductive outcomes, and advancing precision oncology in metastatic risk assessment.

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Clinical Decision Support & Prognostic Modelling (6/15)

Date	Title	Author	Summary
12 Nov 2025	Machine learning based models for prediction of tumor recurrence in patients undergoing radiotherapy for carcinoma of nasopharynx	Amit Bahl	• **Introduction**: Despite advances in chemoradiation, nasopharyngeal carcinoma (NPC) recurrence remains a major clinical problem. Machine learning (ML) can integrate multiple clinical, dosimetric, and demographic factors to enhance recurrence prediction and guide surveillance strategies. • **Methodology:** Data from 119 NPC patients (36 recurrences) with 105 clinical and treatment variables were analyzed. Missing data were imputed using mean/mode substitution. Nine ML algorithms—Logistic Regression, SVM, KNN, Naive Bayes, Neural Networks, Random Forest, Gradient Boosting, AdaBoost, and ensemble models—were trained with k-fold cross-validation and ROC analysis. • **Results:** AdaBoost and Gradient Boosting achieved perfect discrimination (AUC=1.0) with maximal classification accuracy, precision, F1, and recall. Ensemble models maintained AUC=1.0 but showed reduced overall performance due to averaging. KNN performed poorest (AUC=0.761, accuracy=0.739). • **Conclusions:** Boosting-based ML algorithms demonstrated superior accuracy for predicting NPC recurrence. These models may support individualized post-treatment risk stratification, optimizing follow-up intensity and early intervention strategies.
12 Nov 2025	Development of the user-friendly decision aid rule-based evaluation and support tool (REST) for optimizing the resources of an information extraction task	Akram Redjdal	• **Introduction**: Natural language processing (NLP) enables automated information extraction (IE) from clinical free text using rules, ML, or LLMs—each differing in interpretability, transferability, and sustainability. To simplify method selection, the REST tool was developed for NLP-agnostic annotators. • **Methodology:** REST defaults to rule-based IE due to its interpretability and low environmental impact, suggesting ML only when rules underperform. Feasibility is determined by metrics for sensitivity, PPV (>75%), linguistic homogeneity (>10%), and entity frequency (>25%). Validity was assessed on 12 cancer entities from 35 medical records annotated by two oncologists. • **Results:** REST achieved 91.7% agreement for IE method selection. Rule feasibility visualization and entity-level decision support guided optimal IE choice. A tutorial video supports user adoption. • **Conclusions:** REST is a validated, user-friendly decision aid that enables clinicians to select optimal IE strategies without NLP expertise, prioritizing rule-based extraction for sustainable and interpretable clinical text analysis.

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Clinical Decision Support & Prognostic Modelling (7/15)

Date	Title	Author	Summary
12 Nov 2025	Development of a multimodal analysis and decision support tool for adaptive radiotherapy integrating imaging, dosimetry and patient-reported toxicity data	Carolin Senger	• **Introduction**: Adaptive radiotherapy (ART) enhances precision by compensating for daily anatomical changes, yet integration of imaging, dose, and patient-reported outcomes (PROMs) into a unified toxicity-monitoring framework remains unaddressed across tumor types and institutions. • **Methodology:** A multimodal software tool built on the CuraMate platform (Fraunhofer MEVIS) was developed for ART data integration and visualization. It processes planning and daily imaging (CT, CBCT), RT structures, dose maps, and PROMs (EORTC QLQ-LC13, NCI PRO-CTCAE). **Results:** In a pilot of three stage III NSCLC patients (>90 CBCTs), automated dose mapping and registration were fully feasible. The system provided fraction-wise visualization of dose deviations across targets and seven risk structures, generating alerts for potential overdosing and facilitating near real-time ART assessment. • **Conclusions:** This integrated ART decision-support system combining imaging, dosimetry, and PROMs demonstrates feasibility for real-time toxicity prediction. It establishes a scalable, tumor-agnostic framework for online/offline ART monitoring, warranting validation in larger cohorts.
12 Nov 2025	Predicting treatment and survival outcomes in de novo metastatic hormone-sensitive prostate cancer using clinical features, routine blood tests and their early variations	Daniele Brenna	• **Introduction**: In metastatic hormone-sensitive prostate cancer (mHSPC), prognosis is traditionally assessed at diagnosis, but dynamic physiological and biochemical changes during therapy may better reflect treatment response and survival potential. • **Methodology:** A retrospective analysis of 363 de novo mHSPC patients (2014–2023) evaluated temporal variations in vital signs and blood parameters over seven months, automatically graded via CTCAE v5.0. Cox regression identified prognostic biomarkers, and machine learning (ML) models integrated dynamic data with baseline clinical factors to predict PSA response, progression-free survival (PFS), and overall survival (OS). • **Results:** Toxicities in hematologic, hepatic, renal, and electrolyte domains correlated with shorter PFS/OS ($p<0.05$). Independent predictors of poor OS included elevated alkaline phosphatase ($p=0.009$), reduced albumin ($p=0.008$), and hyponatremia ($p=0.033$). ML integration improved predictive AUCs for PSA ≤0.2 ng/mL (0.76–0.79 vs. 0.43–0.47), PFS (0.5–0.79 vs. 0.43–0.55), and OS (0.50–0.76 vs. 0.35–0.53). • **Conclusions:** This first dynamic mHSPC-specific ML model combining early biochemical variations with clinical factors enhances prediction of treatment response and survival, offering a foundation for adaptive, data-driven patient management.

Notable Presentations At ESMO - AI 2025

Clinical Decision Support & Prognostic Modelling (8/15)

Date	Title	Author	Summary
12 Nov 2025	AI-powered biomarker prediction in pathology: Opportunities and challenges for clinical translation	Mariam Gendzekhadze	• **Introduction**: AI in digital histopathology enables prediction of key biomarkers—such as MSI, TMB, PD-L1, and HER2—directly from H&E slides, potentially simplifying diagnostics and expanding global access to precision oncology, especially in resource-limited settings. • **Methodology:** A systematic review (2018–2025) analyzed AI-based studies predicting actionable biomarkers from histopathology. The review examined model architectures, validation strategies, performance benchmarks, and translational barriers, emphasizing regulatory, clinical, and technical aspects. • **Results:** AI achieved strong accuracy in MSI/TMB prediction for colorectal and gastric cancers, and enhanced reproducibility in PD-L1/HER2 scoring. Novel AI models identified morphological correlates of molecular alterations. Barriers include data heterogeneity, bias, and insufficient multi-center validation. • **Conclusions:** AI-powered biomarker prediction could democratize molecular diagnostics. Clinical translation demands validation, interpretability, regulatory clarity, and integration into pathology workflows through collaboration between AI scientists, oncologists, and pathologists.
12 Nov 2025	Multi-Agent for clinical decision support in Molecular Tumor Board	Loic Verlingue	• **Introduction**: Automating clinical trial and therapy matching remains challenging as most AI systems analyze isolated data types, limiting accuracy. Emulating expert reasoning through multi-source integration could improve oncologic decision support. • **Methodology:** The Multi-PASS system combines four specialized agents: (1) Adapted PubMed Search for literature-based treatment discovery; (2) CGI-clinics for molecular alteration pathogenicity; (3) Cellvit for cellular quantification on pathology slides; and (4) BiomedParse for RECIST tumor segmentation. A GPT-4o-mini orchestrator integrates outputs to produce clinically contextual recommendations. Evaluation used virtual patient cases simulating tumor board scenarios. • **Results:** Across four virtual oncology cases, Multi-PASS delivered consistent, clinically sound recommendations, all validated by an oncologist. Outputs demonstrated accurate synthesis of genomic, imaging, and textual data, confirming system coherence and decision relevance. • **Conclusions:** The Multi-PASS multi-agent AI system successfully integrates diverse clinical and molecular inputs, establishing proof-of-concept for automated, explainable decision support in tumor boards and precision trial matching.

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Clinical Decision Support & Prognostic Modelling (9/15)

Date	Title	Author	Summary
12 Nov 2025	Adaptive recurrence risk prediction to optimise prostate cancer follow-up using updateable machine learning	Joran Schoorlemmer	• **Introduction**: After radical prostatectomy (RARP), prostate cancer survivors require frequent PSA testing to detect biochemical recurrence (BCR). Current fixed follow-up schedules are inefficient and not evidence-based. Dynamic machine learning (ML) models using longitudinal data could individualize monitoring and reduce unnecessary testing. • **Methodology:** Data from 3,191 RARP patients in the Dutch Prostate Cancer Network were analyzed. Random Forest classifiers predicted BCR (PSA ≥0.2 ng/mL) at 1–5 years post-surgery, incorporating baseline clinicopathologic features and evolving PSA trajectories. Patient-specific PSA schedules were compared with EAU guideline-based testing. • **Results:** Model performance improved with longitudinal updates (AUC: year 1 = 0.82; year 2 = 0.83; year 3 = 0.86; year 4 = 0.92; year 5 = 0.93). Personalized scheduling reduced PSA tests by 59% without compromising safety. Low-risk patients underwent significantly fewer follow-ups while maintaining recurrence detection accuracy. • **Conclusions:** This dynamic ML model enables precise, adaptive prediction of BCR, supporting individualized PSA monitoring and major workload reduction. External validation and clinical integration will facilitate patient-centered, efficient post-prostatectomy care.
12 Nov 2025	Machine learning enhances the prognostic value of PD-1/PD-L1 expression in non-small cell lung cancer (NSCLC): A systematic review and meta-analysis	Prakash Ramdass	• **Introduction**: While PD-1/PD-L1 expression is central to NSCLC immunotherapy, its prognostic utility remains inconsistent. Machine learning (ML) can integrate multimodal data to enhance prognostic interpretation beyond conventional biomarker analyses. • **Methodology:** A systematic review (PubMed, Scopus, Embase, CINAHL; inception–Aug 2025) identified studies applying ML to evaluate PD-1/PD-L1 prognostic value in NSCLC. Two reviewers independently screened records. A random-effects meta-analysis synthesized pooled accuracy using RStudio, assessing heterogeneity via I^2 and τ^2 statistics. • **Results:** Of 95 records, 9 studies (n=847) met inclusion criteria. Pooled ML accuracy for prognostic PD-1/PD-L1 assessment was 0.84 (95% CI: 0.79–0.89), with study accuracies ranging 0.73–0.96. Moderate-to-high heterogeneity was observed (I^2=68.7%, τ^2=0.2422, p=0.0012). • **Conclusions:** ML models demonstrate strong predictive accuracy for PD-1/PD-L1-based prognosis in NSCLC, confirming their potential as complementary tools for patient stratification. Prospective, standardized validation is needed to reduce heterogeneity and enable clinical integration.

Notable Presentations At ESMO - AI 2025

Clinical Decision Support & Prognostic Modelling (10/15)

Date	Title	Author	Summary
12 Nov 2025	Personalised recurrence-risk stratification after meningioma resection: An AI-driven decision aid	George Brown	• **Introduction**: Meningioma, the most common primary brain tumor, frequently recurs despite surgery. Current prognostic tools rely on broad categories (WHO grade, Simpson resection) rather than individualized prediction. Machine learning (ML) offers more precise recurrence-risk estimation. • **Methodology:** A retrospective cohort of 441 post-surgical meningioma patients (Addenbrooke's, 2014–2024) was analyzed. Predictors included age, sex, WHO grade, Simpson grade, and MIB-1 index. Cox and ML survival models underwent 5-fold cross-validation and 200 bootstrap replicates. Model performance used Harrell's C-index and calibration • **Results:** Over 1,720 days' median follow-up, 38 recurrences occurred. MIB-1 was the top predictor (HR 1.45 per 5% increase). WHO II–III and incomplete resections raised recurrence risk. The combined model achieved C≈0.79 and good 5-year calibration, confirmed in sensitivity analyses. • **Conclusions:** MIB-1 independently predicted recurrence. The Cox/ML model showed high accuracy and interpretability, supporting potential use in personalized surveillance and adjuvant planning after external validation.
12 Nov 2025	Bringing AI to the table: A simulating clinical reasoning in oncology with experts and AI assistance	Diogo R. Ribas Silveira	• **Introduction**: AI is transforming oncology through decision support and training, yet current large language models (LLMs) lack reproducibility and structured diagnostic reasoning. To bridge this gap, a generative AI platform was created to simulate multilevel oncology workflows using structured patient data for diagnostic, staging, and treatment reasoning. • **Methodology:** A web-based interface processes structured clinical inputs. The generative AI model simulates reasoning, staging, and evidence-based management. A validation protocol assessed accuracy, reproducibility, and consistency across ten oncologic case complexities. • **Results:** Across ten simulated cases, AI-generated diagnostic and therapeutic outputs showed 87% concordance with clinical guidelines. The interactive platform, accessible via QR code, allows real-time testing and structured feedback on accuracy and usability. • **Conclusions:** This demonstration highlights generative AI's role in structured, reproducible oncology reasoning, enabling real-time clinical simulation and education. The platform supports transparent, collaborative decision-making and future clinical workflow integration.

Notable Presentations At ESMO - AI 2025

Clinical Decision Support & Prognostic Modelling (11/15)

Date	Title	Author	Summary
12 Nov 2025	AI-powered data extraction in Von Hippel-Lindau (VHL) syndrome: A feasibility study highlighting the role of digital document structure	Vaia Mentesidou	• **Introduction**: This study evaluated the real-world performance and barriers of oncoAI Clinician, an experimental LLM integrated into oncoEHR®. • **Methodology:** A retrospective review identified VHL patients. An oncologist manually extracted “ground truth” data for four domains—treatment history, side effects, disease evaluation, and molecular results—from full records (JSON, PDFs). oncoAI Clinician was tasked to extract the same data. Root cause analyses differentiated technical versus analytical extraction errors. • **Results:** Fourteen records were analyzed; 57.1% failed technically due to non-parsable PDFs with complex layouts. For machine-readable files (42.8%), oncoAI Clinician achieved 100% concordance with manual review across all domains. • **Conclusions:** LLM-based extraction is highly accurate with structured, digital data. The main limitation is unstructured documentation. Future AI deployment requires a “data-first” approach emphasizing standardized, machine-readable clinical records.
12 Nov 2025	MediMind: AI-powered integrated therapy decisions in oncology	Mathias Witzens-Harig	• **Introduction**: Oncology decisions require rapid integration of molecular, genetic, and imaging data with guidelines and trial evidence. Manual synthesis is slow and inconsistent, often leading to suboptimal treatment choices. • **Methodology:** MediMind is an AI-based, MDR Class IIb–certifiable decision-support system integrating structured and unstructured hospital data via HL7/FHIR. Using fine-tuned LLMs (LLaMA 3, Mistral) with retrieval-augmented generation (RAG), it synthesizes patient findings and aligns recommendations with evidence and guidelines. Outputs include structured summaries, explainable therapy suggestions, and patient-friendly reports. • **Results:** MediMind reduces case review time from hours to minutes, generating transparent, evidence-linked treatment recommendations and trial options. Prospective studies at comprehensive cancer centres will assess clinical utility and physician acceptance. • **Conclusions:** MediMind enables GDPR-compliant, real-time, explainable integration of multimodal oncology data. Its validated design supports precision, efficiency, and standardization in cancer therapy decision-making.

Notable Presentations At ESMO - AI 2025

Clinical Decision Support & Prognostic Modelling (12/15)

Date	Title	Author	Summary
12 Nov 2025	Dynamic overall survival prediction for patients with metastatic esophagogastric cancer	Irene Cara	• **Introduction**: Existing survival models for metastatic esophageal/gastric cancer (EGC) predict overall survival (OS) only at diagnosis. Dynamic models, which update predictions during treatment, may improve prognostic accuracy and clinical utility. • **Methodology:** Data from 857 metastatic EGC patients (2016–2021) were extracted from the Netherlands Cancer Registry and hospital records. Dynamic Cox regression and random survival forest (RSF) models were trained using clinical, biochemical, and pathological predictors, evaluated by time-dependent C-index, AUC, and Brier score. • **Results:** WHO performance status, BMI, treatment type, and lab markers were most predictive. Cox and RSF models achieved highest accuracy at treatment onset (C-index = 0.70 and 0.67; AUC = 0.72–0.76). Predictive strength declined over time as sample size decreased. • **Conclusions:** Dynamic survival modeling provides robust, time-updated OS predictions in metastatic EGC. WHO performance status remains the key determinant. External validation will support multi-center deployment.
12 Nov 2025	Development and validation of a living decision support tool (Living-DST) in non-small cell lung cancer (NSCLC) using agentic AI-augmented systematic literature review (SLR)	Anna Forsythe	• **Introduction**: The exponential growth of NSCLC data from trials, congresses, and regulatory updates makes evidence synthesis challenging. Manual curation is time-intensive, hindering timely clinical decisions. • **Methodology:** A living Decision Support Tool (DST) was built using agentic AI (GPT-5, o3, Claude Sonnet-4) emulating Cochrane-compliant SLR workflows. It automatically annotated studies with 36 total variables, validated against 2,136 human annotations, and benchmarked against ChatGPT-5, Perplexity, Consensus, and OpenEvidence using six evidence-precision criteria. • **Results:** Review accuracy was 93–97%; extraction accuracy exceeded 90% (half >95%). AI completed 2,136 annotations in 7.75 h versus 778 h for humans. DST achieved 100% compliance across criteria, outperforming other chatbots (16–37%). • **Conclusions:** The Living-DST integrates AI-driven, continuously updated evidence with guidelines and regulatory data, offering oncologists real-time, patient-specific NSCLC treatment insights with substantial efficiency gains.

Notable Presentations At ESMO - AI 2025

Clinical Decision Support & Prognostic Modelling (13/15)

Date	Title	Author	Summary
12 Nov 2025	Predicting solid-tumor behavior over time with explainable GenAI for precision oncology	Anna Tidstam	• **Introduction**: Personalized breast cancer therapy demands treatment-specific risk–benefit prediction, but current models rely on population-level trial data. Previous ISPY2 pCR models (AUC = 0.81) ignored treatment effects, limiting clinical utility. • **Methodology:** Cancer4D, a multimodal generative AI (GenAI) framework, generates image-based, time-resolved predictions with visual explanations. Using ISPY2 MRI data (n = 985; 13 arms), logistic regression models based on imaging features (diameter, FTV, sphericity, BPE) simulated ΔpCR—the predicted pCR change under alternative regimens—to identify optimal regimen switches. • **Results:** Two treatment groups were defined (A: pCR 34.1%; B: pCR 21.5%). ΔpCR identified 26 patients (11 A→B, 15 B→A) with higher projected efficacy post-switch, supporting individualized neoadjuvant therapy adaptation • **Conclusions:** This proof-of-concept demonstrates treatment-specific ΔpCR feasibility using imaging-based modeling. Larger datasets will enable full Cancer4D GenAI deployment for real-time, image-explained, treatment-personalized counterfactual predictions.
12 Nov 2025	The TrustedMDT multi-agent ai copilot for tumour boards: Protocol for a two-phase evaluation of performance, safety, and feasibility	Andrew A. Soltan	• **Introduction**: Multidisciplinary team meetings (MDTs) are central to oncology decision-making but face mounting challenges from increasing caseloads, leading to potential delays and inconsistencies in treatment planning. • **Methodology:** TrustedMDT-Copilot, an Oxford-developed modular AI system, supports MDTs through automated case summarization, AJCC/UICC staging, and guideline-based draft treatment plans. Integrated into Microsoft Teams via the Healthcare Agent Orchestrator, the study includes: Phase 1a: Benchmarking against 250 synthetic cases using TBFact/BERTScore, Phase 1b: Expert review of 200 anonymized colorectal cases for safety and completeness, Phase 2: Three simulated MDTs assessing clinical impact and usability. • **Results:** Setup phase ongoing. Primary endpoint: rate of clinically significant errors. Secondary endpoints: feasibility, usability, and technical reliability in real-time MDT simulations. • **Conclusions:** This first-in-kind evaluation will determine the safety, feasibility, and performance of a multi-agent AI MDT copilot, informing its refinement and readiness for prospective clinical integration.

Notable Presentations At ESMO - AI 2025

Clinical Decision Support & Prognostic Modelling (14/15)

Date	Title	Author	Summary
12 Nov 2025	Development and validation of AI models to predict grade ≥3 chemotherapy toxicities in solid tumors: Retrospective study at tertiary care centre India	V Niveditha	• **Introduction**: Severe chemotherapy-related toxicities such as neutropenia and mucositis often cause treatment interruptions and hospitalizations. AI-driven risk prediction could enable early intervention and personalized supportive care. • **Methodology:** EHR data from 450 adult solid tumor patients (Jan 2022–May 2025) were analyzed using demographics, treatment, labs, comorbidities, and NLP-extracted clinical notes. Logistic regression, random forest, and gradient boosting models were trained to predict grade ≥3 toxicity within four cycles; performance was evaluated by AUC, precision, and recall. • **Results:** Grade ≥3 toxicity occurred in 29%. Gradient boosting achieved the best performance (AUC = 0.79, 95% CI 0.72–0.85). Key predictors were baseline neutrophils, albumin, prior delays, cumulative dose, and NLP-detected fatigue/oral ulcers. Calibration was well-aligned. • **Conclusions:** AI-based EHR models demonstrated reliable toxicity prediction, supporting early risk stratification and individualized care. Prospective validation will assess real-world clinical utility.
12 Nov 2025	Transformer-based framework for explainable cancer prediction	Ditsuhi Iskandaryan	• **Introduction**: Colorectal cancer (CRC) remains a major global health burden where early detection significantly improves survival. Leveraging EHR data for predictive modeling is promising but limited by data heterogeneity and complexity. Transformer architectures offer a solution by capturing longitudinal, multimodal patterns. • **Methodology:** ExCaPT, a transformer encoder-based model, was developed to predict CRC risk using PADRIS EHR data incorporating demographics, comorbidities, drug exposure, and disease trajectories. Explainability was achieved through attention and embedding-based analyses. Performance was benchmarked against an LSTM model. • **Results:** ExCaPT achieved superior performance (ROC-AUC = 92.1 ± 0.06, Balanced Accuracy = 81.6 ± 0.1, Recall = 74.8 ± 0.2). Compared with LSTM, it improved accuracy by >20%, precision by 23%, and MCC by 43%. • **Conclusions:** Transformer-based modeling markedly enhances CRC risk prediction from EHR data, offering interpretable, scalable tools for precision screening and proactive oncology care.

Notable Presentations At ESMO - AI 2025

Clinical Decision Support & Prognostic Modelling (15/15)

Date	Title	Author	Summary
12 Nov 2025	Predictive model for the risk of carrying a homologous recombination repair (HRR) gene alteration in patients with metastatic castration-resistant prostate cancer (mCRPC) using Big Data and Artificial Intelligence	Joel Greshock	• **Introduction**: Metastatic castration-resistant prostate cancer (mCRPC) is highly lethal, with 20–30% of cases harboring homologous recombination repair (HRR) gene alterations—key biomarkers for targeted therapy eligibility. Predicting HRR mutation risk could streamline genetic testing and optimize patient selection. • **Methodology:** AIPredicts retrospectively analyzed harmonized clinical data from 948 mCRPC patients in the MAGNITUDE and GALAHAD trials. Machine learning models (LR, LASSO, DT, RF, XGB) were trained using 10-fold cross-validation, random split, and bootstrap evaluation. Predictors included PSA metrics, LDH, NLR, BMI, age, and disease duration. • **Results:** HRR alterations were present in 52%. XGB achieved the highest bootstrap AUC (0.80 [0.77–0.83]), followed by DT (0.75 [0.72–0.78]). Consistent top predictors across models reinforced their clinical validity. • **Conclusions:** ML-based prediction of HRR alterations in mCRPC is feasible, highlighting reproducible clinical predictors. Future models integrating real-world data and NLP could enhance predictive precision and guide targeted testing strategies.
13 Nov 2025	Collaborative Human-Agent for Therapeutic Decision-Making In Cancer Immunotherapy prediction	Federica Corso	• **Introduction**: Clinical decision-making (CDM) in advanced NSCLC requires integration of multimodal data. While large language models (LLMs) show promise, generic systems are computationally heavy and task-limited. Specialized AI agents can orchestrate multiple tools efficiently, enabling personalized, data-driven oncology reasoning. • **Methodology:** A privacy-preserving AI agent used Qwen3-14B for orchestration, Deepseek-r1-8B for guideline retrieval, MedGemma-4B for imaging, and HistroBistro for molecular analysis. LORIS predicted immunotherapy response, with Tavily/PubMed supporting literature access. Tested on 20 NSCLC patients (IRCCS Milano), two oncologists evaluated tool use and accuracy. • **Results:** Specialized tools were applied in 95% of cases (87 total; 4.4/patient). Among 170 statements, 78.8% were accurate, 21.2% incorrect, and none harmful—demonstrating safe, consistent reasoning. • **Conclusions:** The immune-specialized AI agent effectively integrated multimodal data for NSCLC CDM, showing high accuracy and safe outputs. Further validation will enhance transparency and clinical trust.

Notable Presentations At ESMO - AI 2025

LLMs, NLP & Data Extraction in Oncology (1/12)

Date	Title	Author	Summary
12 Nov 2025	SCRIPT: Stratified clinical risk prediction from pathology reports using large language models	Chiara M. Loeffler	- **Introduction**: Accurate risk stratification in oncology is critical for treatment planning but remains limited by unstructured data such as pathology reports. These reports contain valuable prognostic details not easily integrated into quantitative models. Large language models (LLMs) may extract and synthesize this data into unified survival risk scores. - **Methodology:** Using LLaMA 3.3 70B, risk scores were generated from free-text pathology reports of three gastrointestinal cancers. The model was prompted to produce quantitative survival risk values, which were correlated with overall survival (OS), progression-free survival (PFS), and disease-specific survival (DSS) outcomes. - **Results:** In colorectal cancer, LLM-generated scores showed strong prognostic significance—OS (HR=2.77, 95% CI: 1.92–3.97), PFS (HR=2.93, 95% CI: 2.11–4.08), and DSS (HR=5.85, 95% CI: 3.66–9.36), all p<0.001. - **Conclusions:** LLMs can effectively extract prognostic information from unstructured pathology reports, generating robust quantitative survival risk scores that may enhance personalized oncology risk assessment and stratification.
12 Nov 2025	Self-hosted open-source large language models for autonomous clinical agents	Li Zhang	- **Introduction**: This study introduces a self-hosted medical AI agent integrating a novel multi-dimensional confidence assessment framework. - **Methodology:** A fully on-premises autonomous agent using open-source LLMs was tested on complex MIMIC-IV acute care cases simulating oncology workflows. A dual-agent setup evaluated diagnostic reasoning. Confidence was quantified via token-level probabilities, linguistic redundancy, and cross-run consistency, forming a composite reliability score - **Results:** The self-hosted agent achieved 89.4% diagnostic accuracy, comparable to a proprietary model (88.9%). The consistency metric best predicted correctness (AUC=0.910). Applying a ≥0.85 threshold increased accuracy to 98.9%, resolving 63.5% of cases autonomously. - **Conclusions:** The self-hosted agent achieved 89.4% diagnostic accuracy, comparable to a proprietary model (88.9%). The consistency metric best predicted correctness (AUC=0.910). Applying a ≥0.85 threshold increased accuracy to 98.9%, resolving 63.5% of cases autonomously.

Notable Presentations At ESMO - AI 2025

LLMs, NLP & Data Extraction in Oncology (2/12)

Date	Title	Author	Summary
12 Nov 2025	Large language model-based feature extraction to find patient similarity in precision oncology	Oguz Serbetci	**Introduction**:This study assessed large language model (LLM)–based extraction from pathology reports to improve patient similarity retrieval. **Methodology:** Pathology reports from 4,761 patients across eight tumor types were analyzed using Nemotron-49B, extracting 56 features (1,607 variables) from macroscopy, molecular, and immunohistochemistry data. Retrieval performance was compared with BM25 and BGE-M3 embeddings using 228 test queries, stratified by tumor type and treatment intent. **Results:** Feature extraction achieved an F1-score of 70%, and 89–95% for immunohistochemistry/molecular alterations. Similarity retrieval outperformed benchmarks (precision@10 = 8.51, recall@10 = 13.50) vs. BM25 (4.78/7.12) and BGE-M3 (4.12/6.07). **Conclusions:** LLM-based extraction enhances therapy-aligned patient similarity retrieval, supporting precedent-driven decision-making and enabling institutional case libraries for precision oncology evidence generation.
12 Nov 2025	Text-to-treatment: Explainable ML predicts systemic therapy choice in cutaneous melanoma	Vladimir Evdokimov	**Introduction**: This study evaluated whether explainable machine learning (ML) can predict physician-selected systemic therapy and key clinical drivers in metastatic cutaneous melanoma. **Methodology:** From 1,201 tumour-board records (July–Dec 2024), an LLM (Claude 3.7 Sonnet) extracted structured data via a KNIME pipeline (95% accuracy). The curated cohort included 307 cutaneous melanoma cases. Predictors: ECOG, therapy line, LDH, BRAF status, disease burden, CNS involvement, steroids, age, and sex. Models: Random Forest, Bayesian, CatBoost; explainability: SHAP, LIME, XGBoost importance. **Results:** Median age 66; 56% female; ECOG 0–1 ≈ 73%. ROC-AUC macro = 0.922, micro = 0.926. First-line accuracy = 82%. Key metrics: combo-IO (sens 0.80/spe 0.93), mono-IO (0.73/0.97), BRAF/MEK (1.00/0.87). Top predictors: ECOG, therapy line, LDH, BRAF. **Conclusions:** LLM-assisted ML accurately replicated tumour-board therapy decisions and identified interpretable clinical patterns. This approach enables scalable conversion of routine notes into structured, decision-support data for future prospective validation.

Notable Presentations At ESMO - AI 2025

LLMs, NLP & Data Extraction in Oncology (3/12)

Date	Title	Author	Summary
12 Nov 2025	Structuring real-world molecular pathology reports using a large language model for oncology documentation	Isabella Wiest	- **Introduction**: Large language models (LLMs) can extract structured data from unstructured medical reports, enabling automation in oncology documentation. Yet, their real-world integration and accuracy evaluation remain limited. This study assessed an open-source LLM for structuring molecular pathology reports in lung cancer - **Methodology:** Using 472 pathology reports from the nNGM Dresden center, a Llama 3.1–based pipeline extracted 187 elements across 27 genes. Outputs (25,676 items) were compared with 21,184 manually documented entries. Accuracy was validated by exact match and manual physician review. - **Results:** The LLM achieved 98% accuracy (19,332/19,783) versus manual data, correctly identifying mutation/wild-type status in 98% (10,412/10,604) of genes. Errors (2%) were mainly missing or misclassified PD-L1/mutation data. When documentation was absent, the LLM filled gaps correctly in 90% of cases. - **Conclusions:** Open-source LLMs can accurately structure molecular pathology data for oncology documentation. However, human verification remains essential before integration into clinical systems to ensure data integrity and patient safety.
12 Nov 2025	Evaluating large (LLM) versus small language models (SLM) in summarizing real-life oncology clinical narratives in Spanish	Beatriz Villaescusa Gonzalez	- **Introduction**: This study evaluated small language models (SLMs) for secure, local EHR summarization. - **Methodology:** Two models were compared: GPT-4.1 (OpenAI API) and an open-source SLM deployed via Ollama. Fifty oncology EHR summaries were evaluated across hallucinations, omissions, and readability (scored 1–3). A weighted Final Score (0.4×Hallucinations + 0.4×Omissions + 0.2×Readability) classified summaries as Adequate (≥0.8), Fair (0.6–0.8), or Insufficient (<0.6). - **Results:** Mean Final Score: 71.3% (SD 16.9); Adequate 36%, Fair 34%, Insufficient 30%. Hallucinations were rare, but omissions reduced quality. Readability was rated level 2–3, indicating generally understandable summaries with partial structural coherence. - **Conclusions:** SLMs enable privacy-compliant, resource-efficient EHR summarization for oncology. Despite minor omissions, they demonstrate feasibility for safe, local AI integration within public healthcare environments.

Notable Presentations At ESMO - AI 2025

LLMs, NLP & Data Extraction in Oncology (4/12)

Date	Title	Author	Summary
12 Nov 2025	How to generate open-source annotated cancer clinical datasets with LLMs to support the development of smaller language models	Emmanuelle Kempf	• **Introduction**: This study aimed to create open-source, annotated synthetic clinical datasets for developing smaller cancer-focused models. • **Methodology:** Using Mistral Large, complex prompts combined real-world French national claims data, cancer guidelines, and randomized administrative details to generate realistic hospitalization reports with structured annotations. Reports were evaluated by two physicians (oncologist, information specialist) across five domains on a 10-point scale for realism and quality. • **Results:** AI-generated reports matched clinicians in language quality (9.3 vs 9.2) and overall impression (9.3 vs 9.2) but scored lower in medical consistency (7.9 vs 9.3) due to occasional logical inconsistencies. Structured annotations were highly accurate and consistent with prompts. • **Conclusions:** LLMs can produce clinically realistic synthetic data with precise annotations, supporting dataset creation for smaller medical models. Minor medical inconsistencies can be mitigated through prompt refinement and expert review.
12 Nov 2025	Comprehensive comparison of on-premise large language models (LLMs) for data abstraction in rare cancers from unorganized non-English medical documentation	Pawel Teterycz	• **Introduction**:This study evaluated open-source, on-premise LLMs for automated data abstraction from unprocessed oncology EHRs of rare bone sarcoma patients. • **Methodology:** EHRs from 302 patients (2016–2022) were annotated for five variables—pathology type, tumor size, localization, grade, and resection status. Four models (Llama 3.1 8B, DeepSeek-R1 8B, Mixtral 8×7B, Bielik-11B-v2.3-Instruct) were tested with multiple prompts. Accuracy was compared to expert annotation using mixed-effects logistic regression; majority voting was applied for performance boosting. • **Results:** Standalone accuracy ranged 17.5–30.3%, highest for Mixtral (OR = 1.14, $p < 0.001$); tumor localization reached 44–67.7% accuracy. DeepSeek underperformed with few-shot prompting. Majority voting improved overall accuracy to 83.6%, reaching 90% for resection type. • **Conclusions:** Though unstructured EHRs challenge automation, combining optimized prompting and ensemble voting enables robust, privacy-preserving data extraction. Local lightweight LLMs show strong promise for accelerating oncology data curation and research.

Notable Presentations At ESMO - AI 2025

LLMs, NLP & Data Extraction in Oncology (5/12)

Date	Title	Author	Summary
12 Nov 2025	LLM-On-Hub: A User-Friendly Platform for cancer medications and timelines extraction with Large Language Models	Vittoria Peppoloni	• **Introduction**: Electronic health records (EHRs) contain rich oncology data, but most remain unstructured and hard to analyze. Manual review is slow and error-prone. LLM-On-Hub was developed as a user-friendly, privacy-compliant platform for extracting structured data and reconstructing patient timelines from oncology EHRs. • **Methodology:** The system extracted drug, dosage, frequency, route, and molecular markers from 186 NSCLC EHRs, linking events to dates. Multiple locally deployable LLMs were tested (Llama3.1:8B, Mistral:7B, Gemma-3:27B, Devstral:24B). Evaluation metrics included precision, recall, F1-score, and accuracy, with 20% of records manually annotated as reference. • **Results:** Medication and dosage extraction achieved near-perfect results; frequency and duration were moderate (F1 = 0.58–0.63), molecular markers low (F1 ≤ 0.32). Mistral 7B had the best overall F1 (0.75). Gemma-3:27B led in biopsy and imaging events (F1 = 0.67, 0.63), while Devstral:24B excelled in progression tracking (F1 = 0.67). • **Conclusions:** LLM-On-Hub effectively structures oncology EHRs, improving data accessibility and reducing clinician workload. Despite challenges with complex extractions, it represents a practical step toward real-world LLM deployment in oncology documentation and research.
12 Nov 2025	Finetuning language models for extracting and structuring data in clinical documentation	Ahmadreza S. Ramezanzadeh	• **Introduction**:This study assessed whether fine-tuned smaller LLMs can match larger models while remaining efficient and privacy-compliant. • **Methodology:** Using MIMIC-IV admission notes, Low-Rank Adaptation (LoRA) with automated hyperparameter optimization was applied to TinyLlama, Llama-2-7B, SmolLM-1.7B, Llama-3.2-1B, and Llama-3.1-8B, benchmarked against Llama-3.1-70B. Performance was evaluated via precision, recall, and F1, with efficiency and resource use also assessed. • **Results:** Fine-tuned Llama-3.1-8B achieved the best F1 = 0.55, surpassing Llama-3.1-70B (0.53). LoRA improved performance across models—Llama-3.1-8B (0.10→0.55), Llama-2-7B (0.23→0.41), Llama-3.2-1B (0.22→0.39)—highlighting fine-tuning's strong impact on smaller architectures. • **Conclusions:** Fine-tuning significantly boosts smaller LLMs, narrowing the gap with large models while improving efficiency and deployability in healthcare. Future studies should validate these models prospectively and standardize fine-tuning protocols for clinical implementation.

Notable Presentations At ESMO - AI 2025

LLMs, NLP & Data Extraction in Oncology (6/12)

Date	Title	Author	Summary
12 Nov 2025	Large language models in clinical oncology: Comparative analysis of colorectal cancer recurrence identification	Evelyn Y. Wong	- **Introduction**: This study developed an automated recurrence detection algorithm and benchmarked it against top-performing LLMs. - **Methodology:** A two-step pipeline combined: (1) radiology screening via fine-tuned GatorTron to flag progression, and (2) NLP extraction to confirm recurrence and metastatic sites. Validation included 95 Stage I–III CRC patients (2018–2020), with manual chart review as the gold standard. Performance was compared with GPT-4-o, Claude 3.5, gpt-oss-20B, Qwen3-8B, Gemma-3-12B, and SEA-LION. - **Results:** The algorithm achieved 100% sensitivity, 96.6% specificity, and 97.9% accuracy, outperforming all LLMs. GPT-4-o and Claude 3.5 achieved ~94.6% sensitivity and 93–95% specificity, while open-source gpt-oss-20B had the highest specificity (98.3%). SEA-LION (91.9%) surpassed Qwen3 (89.2%), and Gemma-3-12B showed the lowest sensitivity (67.6%). - **Conclusions:** The algorithm exceeded generalist LLMs in CRC recurrence detection, enabling scalable, accurate progression-free survival analytics and reducing manual workload. Prospective, large-scale validation will confirm its clinical utility.
12 Nov 2025	Exploring large language model (LLM) for TNM categorizing and re-categorizing nasopharyngeal carcinoma (NPC) from structured text reports	Junru Zhong	- **Introduction**: This study assessed whether large language models (LLMs) can autonomously deduce and recategorize T and N classifications of nasopharyngeal carcinoma (NPC) from structured MRI reports following UICC/AJCC guidelines. - **Methodology:** Eleven LLMs (9 general-purpose, 2 medical-specific) were evaluated on 379 pre-treatment NPC MRI reports labeled under the 7th edition TNM system. LLMs performed two tasks: (i) deducing 7th-edition T/N categories and (ii) recategorizing 100 cases to the 8th edition, compared against expert and junior radiologists. - **Results:** High-performing models included DeepSeek-R1 (T=85.8%, N=80.7%) and GPT-4o (T=84.0%, N=80.7%), comparable across editions. Smaller or medical-tuned models (MedGemma, HuatouGPT) underperformed (<50%). Human readers remained superior (T=89–93%, N=88–90%). - **Conclusions:** LLMs demonstrate strong potential in radiologic TNM inference, with accuracy driven by model scale rather than domain specialization. However, human expertise remains indispensable for precise oncologic staging.

Notable Presentations At ESMO - AI 2025

LLMs, NLP & Data Extraction in Oncology (7/12)

Date	Title	Author	Summary
12 Nov 2025	A fine-tuned large language model for literature screening and exclusion reason prediction in lung cancer clinical practice guideline development	Yuki Katsuya	- **Introduction**: This study advanced a fine-tuned LLM to predict explicit exclusion reasons, improving transparency and reproducibility in guideline development**.** - **Methodology:** Using 3,000+ abstracts from the 2025 Japanese lung cancer CPG, five exclusion categories were defined: inappropriate design, mismatch with clinical question, lack of Japanese applicability, poor meta-analysis, and other. The fine-tuned LLM predicted both inclusion/exclusion and exclusion reasons. Its performance was validated against expert committee decisions across in-domain and out-of-domain clinical questions. - **Results:** The model retained high accuracy comparable to previous binary classifiers, while effectively classifying exclusion reasons. Performance remained consistent across domains, demonstrating strong generalizability and reliability. - **Conclusions:** The LLM's ability to predict exclusion categories enhances transparency, consistency, and auditability in CPG development, significantly reducing manual burden and marking a key step toward trustworthy AI integration in evidence-based oncology.
12 Nov 2025	From clinical reports to patient journeys: LLM-based reconstruction of longitudinal clinical trajectories	Hania Paverd	- **Introduction**: This study evaluated LLMs for automated reconstruction of pre-transplant lesion and treatment timelines from free-text reports. - **Methodology:** Timelines for 20 patients (8 with hepatocellular carcinoma) were reconstructed using LIRADS lesion grading and prior liver-directed treatments. Reports from radiology and liver transplant assessments were analyzed by Llama 3.3 70B and Llama 3.1 8B. Extracted lesion and treatment data were compared with manually curated ground truth for accuracy, recall, precision, and hallucinations. - **Results:** Llama 70B achieved recall 0.97, precision 0.81, identifying 139 correct vs. 33 hallucinated lesions, outperforming 8B (recall 0.85, precision 0.73; 121 correct, 44 hallucinated). Lesion-type hallucinations were fewer with 70B (1 vs. 6). For treatment data, hallucinations were 12 (70B) vs. 6 (8B) in radiology and fewer with LTA input. - **Conclusions:** LLMs enable accurate, scalable extraction of longitudinal disease trajectories, with larger models offering superior precision. Despite limited hallucinations, such tools can accelerate structured chronic disease analytics and inform AI-assisted clinical decision systems.

Notable Presentations At ESMO - AI 2025

LLMs, NLP & Data Extraction in Oncology (8/12)

Date	Title	Author	Summary
12 Nov 2025	Comparative evaluation of rule-based natural language processing (NLP) and fine-tuned large language model (LLM) for clinical data extraction in non-small cell lung cancer (NSCLC): A real-world study from China	Jian Sun	• **Introduction**: Although NLP has been increasingly used for structured data extraction, its real-world use in China remains limited due to transparency and reproducibility challenges. This pilot study compared a rule-based NLP system with a fine-tuned LLM for oncology EHR data extraction. • **Methodology:** Clinical records from 480 NSCLC patients (2018–2023) in the National Anti-tumor Drug Surveillance System were analyzed. Models included: (1) a BERT/ALBERT-based NLP with entity and relation extraction, and (2) a Qwen3-30B LLM fine-tuned for few-shot learning. Accuracy and F1-scores across key variables and time efficiency were benchmarked against manual review. • **Results:** Overall F1-scores: LLM 76.0% vs. NLP 72.0%. NLP excelled in structured data (TNM 88%, ECOG 79%), while the LLM surpassed in contextual variables—treatment start (88%), end (65%), and progression (92%). LLM reduced manual QC time from 168 to 40 hours. • **Conclusions:** Fine-tuned LLMs outperform traditional NLP for complex, contextual variable extraction, enabling faster, scalable real-world oncology data curation in China. Continued refinement will enhance robustness and compliance for clinical research integration.
12 Nov 2025	A comparative benchmarking of large language models (LLMs) for clinical data abstraction from real-world oncology records	Harendra Guturu	• **Introduction**: This study developed and benchmarked a Retrieval-Augmented Generation (RAG) LLM framework to automate oncology data extraction. • **Methodology:** A multi-query RAG pipeline was implemented using custom prompts for 13 event types and structured validation. Model performance was tested on 50 de-identified oncology records, benchmarked via precision, recall, Gwet's AC, runtime, and cost. Multiple LLMs—Claude Sonnet, Gemini, GPT-5, and Grok—were compared for domain-specific accuracy. • **Results:** Performance varied across tasks: Claude Sonnet and Grok excelled in cancer diagnosis (AC = 0.97); Gemini models in metastasis detection (AC = 0.80–0.83); and Gemini Pro/GPT-5 in medication extraction (AC = 0.87). No model demonstrated universal superiority, and treatment regimen abstraction remained challenging. • **Conclusions:** LLMs enable scalable oncology data extraction, but accuracy depends on clinical context. A multi-model, retrieval-optimized framework may yield the best balance between precision, cost, and operational speed for real-world oncology data abstraction.

Notable Presentations At ESMO - AI 2025

LLMs, NLP & Data Extraction in Oncology (9/12)

Date	Title	Author	Summary
12 Nov 2025	Interpreting Small Generative LLMs for Oncology Trial Matching Using Gradient-Based Attribution under Low-Resource Settings	Clement BRUTTIMAIRE SSE	- **Introduction**: Matching patients to clinical trials remains an essential yet complex task, hindered by the opaque decision-making of current LLM-based systems. Interpretability is crucial to ensure clinician trust and accurate eligibility evaluation. - **Methodology:** Fourteen virtual oncology patients with 84 French clinical notes were matched to 200 English trial criteria. Expert annotators labeled each patient-criterion pair as met, unmet, or insufficient data and identified supporting or contradicting text. Small-scale LLMs (10B parameters)—including Nemo, LLaMA, and Qwen—were tested. A novel fidelity metric measured overlap between model attributions and annotated proofs; robustness was assessed via sensitivity to input changes. - **Results:** The best-performing model achieved 57% accuracy, F1 = 68%. However, alignment between model attributions and expert-identified evidence occurred in only 20% of cases. Gradient-based explainability methods (Integrated Gradients, SmoothGrad, SHAP) showed limited sensitivity to clinical context. - **Conclusions:** Small-scale LLMs show potential for trial eligibility matching but lack consistent interpretability and reliability. Improved attribution alignment and explanation fidelity are essential for safe AI-assisted clinical deployment in Molecular Tumor Boards.
12 Nov 2025	ClinNotes: A large language model-based tool for semi-automated structuring of oncological clinical notes	Carlota Gozalbo Barriga	- **Introduction**: Manual abstraction of oncology clinical notes (CNs) is labor-intensive and limits data scalability. ClinNotes, a web-based tool, leverages LLMs to semi-automatically extract structured data while retaining human validation. - **Methodology:** Ten anonymized CNs (5 colorectal, 5 breast cancer) were processed using GPT-4o-mini and LLaMA 3.3 70B. Models were dynamically prompted via metadata for up to 81 variables in REDCap. Extracted data were validated by data curators (DCs) and auto-imported into REDCap through API integration. - **Results:** GPT achieved higher accuracy and faster responses than LLaMA—breast: 67.1% vs 57.7%; colorectal: 77.9% vs 73.8%. Mean response times were markedly lower for GPT (31.4 s vs 2280 s for BC; 24.1 s vs 1201 s for CRC). Simpler CNs produced higher accuracy. - **Conclusions:** ClinNotes enables semi-automated, curator-supervised data structuring with substantial efficiency gains. Further prompt optimization and resource tuning will improve accuracy, supporting scalable oncology data transformation.

Notable Presentations At ESMO - AI 2025

LLMs, NLP & Data Extraction in Oncology (10/12)

Date	Title	Author	Summary
12 Nov 2025	LLM-based reasoning framework for MedDRA adverse event coding: Toward scalable automation	Naghme Dashti	- **Introduction**: Manual MedDRA annotation of adverse events (AEs) in oncology trials is slow and error-prone due to term overlap and semantic ambiguity. LLMs with structured reasoning may streamline AE-to-LLT mapping with interpretability and scalability. - **Methodology:** A LLaMA-3.3-70B-Instruct model integrated with Retrieval-Augmented Generation (RAG) retrieved top-10 semantically similar Low Level Terms (LLTs) via MiniLM embeddings. Stepwise reasoning guided final LLT selection. Performance was tested on AML trial datasets (MOSAIC, DELTA, DaunoDouble) and validated by experts using both exact and fuzzy matching. - **Results:** Clinical correctness reached 98.8% (MOSAIC), 95.5% (DELTA), and 95.0% (DaunoDouble). Exact LLT match ranged 61–66%, PT-level accuracy 83–87%. Discrepancies mainly reflected synonymy or medical equivalence. UMAP clustering confirmed stable semantic grouping across System Organ Classes. - **Conclusions:** Combining LLM reasoning with semantic retrieval achieves near-human MedDRA coding accuracy. Despite lexical variability, outputs were clinically valid, supporting future expansion toward CTCAE grading and autonomous pharmacovigilance workflows.
12 Nov 2025	Autoevaluation of open-source LLMs: General purpose vs. medical finetuned models	Annika Domres	- **Introduction**: This study introduces a Fact Checking algorithm to identify and correct misinformation in oncology-related outputs, comparing generalist versus medical fine-tuned LLMs. - **Methodology:** Within a RAG framework, generated answers were decomposed into atomic facts and validated for truthfulness. False statements were corrected. Models tested included Gemma3 27B vs MedGemma3 27B, Llama3 70B vs OpenBioLLM 70B, and Qwen3 32B vs Qwen3Medical 32B across 40 prostate cancer Q&As and the AMEGA benchmark. Evaluation combined human review, GPT-4o judging, and automatic metrics. - **Results:** Fact Checking improved AMEGA scores by 2–4 points across models. MedGemma3 achieved top sensitivity (83%), balanced accuracy (90%), and overall answer improvement (30%). Generalist models (Llama3, Qwen3) benefited most from Fact Checking, reducing hallucinations and factual inaccuracies. - **Conclusions:** Fact Checking enhances factual reliability and interpretability of open-source LLMs in clinical Q&A. MedGemma3 demonstrated superior performance, surpassing the GPT-4o baseline, supporting its integration into medical AI reasoning frameworks.

Notable Presentations At ESMO - AI 2025

LLMs, NLP & Data Extraction in Oncology (11/12)

Date	Title	Author	Summary
12 Nov 2025	Validating large language model-assisted data extraction from clinical notes in head and neck oncology	Josephine W. Van Koevorden	- **Introduction**: Administrative workload limits clinical efficiency, with documentation consuming twice the time of direct care. LLMs offer potential to automate structured data extraction from clinical notes, but rigorous prospective validation is required to ensure safety and reliability. - **Methodology:** A prospective validation was performed on 60 head and neck cancer patients using real-world clinical data (referrals, pathology, radiology). A pretrained open-source LLM extracted information across 29 categories, benchmarked against human consensus. Two expert rounds assessed accuracy, impact, and time savings. - **Results:** The LLM achieved an F1-score of 0.85 (precision 0.81, recall 0.91, accuracy 0.81). Per-category accuracy was 74–90%. Hallucinations were minimal (0.16%, low impact). Processing time dropped from 8.6 to 1.9 minutes/patient, and inter-expert disagreement remained high (~33%). - **Conclusions:** Validated LLM-assisted data extraction effectively reduces clinician workload while maintaining accuracy and safety. Clinical deployment demands contextual reasoning and expert oversight, reinforcing LLMs' role in accelerating oncology's digital transformation.
12 Nov 2025	A Framework for Evaluating Performance of LLM-Based Extraction From the Electronic Health Record Across Different Healthcare Systems	Kathi Seidl-Rathkopf	- **Introduction**: The adoption of LLMs for oncology data curation introduces new data quality concerns across healthcare systems. The VALID framework (Validation of Accuracy for LLM/ML-Extracted Information and Data) provides a structured method to evaluate accuracy and contextual variability across regions such as the UK and Germany. - **Methodology:** A GDPR-compliant duplicate abstraction platform was implemented to compare LLM and human data extraction. Two expert reviewers independently abstracted identical patient records; one served as the reference to calculate precision, recall, and F1-scores. This established local human baseline metrics for cross-country benchmarking of LLM accuracy. - **Results:** The framework quantified market-specific performance differences influenced by documentation and treatment variability between UK and German systems. Benchmarking LLMs against local human baselines allowed identification of context-dependent limitations and improvement priorities. - **Conclusions:** This initial VALID application demonstrates scalable, country-specific validation of LLM data extraction quality. Future work will integrate automated verification and replication checks, ensuring trustworthy and fit-for-purpose oncology real-world data globally.

Notable Presentations At ESMO - AI 2025

LLMs, NLP & Data Extraction in Oncology (12/12)

Date	Title	Author	Summary
12 Nov 2025	Structuring GDPR-compliant private networks to enable LLM-extracted oncology data on pseudonymized patient EHR data in Europe	Lauren Ellsworth	• **Introduction**: Expanding real-world oncology data across global markets requires scalable, high-quality EHR curation. Manual abstraction is accurate but inefficient, while automated approaches risk lower reliability. A hybrid LLM–human abstraction system was developed to balance scalability, privacy, and data integrity under GDPR compliance. • **Methodology:** Using EHR data from Flatiron Health's European partners, a GDPR-compliant private network was built employing a "lock box" approach with pseudonymization and restricted access. Pretrained LLMs extracted key clinical variables within secure, isolated environments, and expert reviewers validated outputs. The architecture ensured no internet data transfer or model retraining from patient data. • **Results:** Across multiple European sites, the platform enabled secure, isolated data processing while integrating state-of-the-art LLMs for oncology data extraction. The private network maintained full regulatory compliance and protected patient confidentiality. • **Conclusions:** This secure hybrid abstraction system demonstrates that high-performance LLM tools can operate under stringent GDPR safeguards, ensuring privacy-preserving, scalable, and compliant oncology data extraction suitable for multinational research and regulatory contexts.

Notable Presentations At ESMO - AI 2025

Clinical Trial Matching & Drug Development Applications (1/8)

Date	Title	Author	Summary
12 Nov 2025	Real-Time Integration of ChatGPT into Multidisciplinary Tumor Boards: A Prospective Study in General Medical Oncology	Beatriz F. Perez	• **Introduction**: Clinical oncology decisions are increasingly complex, requiring multidisciplinary team (MDT) input. This study prospectively evaluated ChatGPT's real-time integration into MDT meetings as a clinical support tool. • **Methodology:** Between April–August 2025, ChatGPT participated in 58 eligible MDT cases, providing independent and revised opinions on diagnosis and management • **Results:** Initial concordance with MDT was 67.2%. ChatGPT expanded diagnostic (2.47 vs. 1.92) and management options (2.24 vs. 1.74). MDT decisions were maintained (86.2%), refined (10.3%), or replaced (3.4%). • **Conclusions:** ChatGPT improved discussion breadth and meeting quality, supporting its complementary role in oncology MDT workflows.
12 Nov 2025	Analysis of ChatGPT5-recommendations as a support toll for multidisciplinary team decisions for the adjuvant treatment of breast cancer	Sara Plavic-Radeka	• **Introduction**: This study assessed ChatGPT-5's ability to generate adjuvant therapy recommendations for breast cancer within multidisciplinary team (MDT) workflows. • **Methodology:** From May–July 2025, 107 MDT cases were analyzed. ChatGPT-5 used structured prompts referencing AGO 2025 guidelines and German drug-approval rules to propose adjuvant recommendations. • **Results:** Full concordance with MDT decisions occurred in 75.7% of cases; partial concordance in 24.3%. Highest alignment was for endocrine (100%) and radiotherapy (95%) recommendations, while genetic testing (47%) and surgery (33%) showed lower agreement. • **Conclusions:** ChatGPT-5 achieved high overall concordance with MDT decisions, supporting its potential as an adjunctive decision-support tool in breast cancer management pending further optimization.

Notable Presentations At ESMO - AI 2025

Clinical Trial Matching & Drug Development Applications (2/8)

Date	Title	Author	Summary
12 Nov 2025	Effects of a vibe-coded, rule-based trial-matching application on screening efficiency and coverage: A multi-physician study	Masahiro Kuno	• **Introduction**: Eligibility screening for early-phase oncology trials is hindered by complex criteria and changing slot availability. This study evaluated a clinician-built, rule-based “vibe-coded” web app for patient-to-trial matching. • **Methodology:** Six physicians screened nine simulated cases, alternating app use. The app matched patient data to 63 active trials using preset eligibility rules. • **Results:** Mean screening time was 190.1 s; app use reduced time by 25.6 s (p=0.171). Significant gains occurred in two cases (−77 s, −74 s). Recall improved from 0.776 to 0.860. • **Conclusions:** A physician-built AI-assisted screening tool improved trial coverage and efficiency, showing promise for adaptive, clinician-led deployment.
12 Nov 2025	LungTrial-LLMX: An Explainable On-Premises LLM System for Clinical Trial Matching in Lung Cancer	Vittoria Peppoloni	• **Introduction**: Matching oncology patients to trials remains labor-intensive due to complex eligibility rules and privacy limitations of cloud-based AI. LungTrial-LLMX was developed as an on-premises, explainable dual-LLM system for automated, privacy-preserving lung cancer trial matching. • **Methodology:** Llama 3.1 8B extracted nine structured features from electronic records; Gemma3-27B aligned them to eligibility criteria from 17 active trials at INT and generated rationale explanations. • **Results:** LungTrial-LLMX achieved 83% overall matching accuracy, correctly identifying the top trial in 15/18 patients. Extraction accuracy was high (diagnosis 83%, stage 88%, demographics >90%). The explainable interface supported criterion-level transparency. • **Conclusions:** LungTrial-LLMX demonstrates accurate, interpretable, and privacy-preserving trial matching. Its dual-LLM design enables scalable clinical integration while maintaining data security.

Notable Presentations At ESMO - AI 2025

Clinical Trial Matching & Drug Development Applications (3/8)

Date	Title	Author	Summary
12 Nov 2025	Early international uptake of an AI-powered oncology clinical trial knowledge platform	Tony Kin Wai Hung	• **Introduction**: Low provider awareness limits trial enrollment. This study assessed adoption of an AI-powered oncology trial platform with real-time updates and decision support. • **Methodology:** Engagement data (Feb 2022–Aug 2025) from 595 downloads and 426 users across 15+ countries were analyzed. • **Results:** Users generated 216,055 events (507/user) and 4,458 engaged sessions (~8 min/session). Top modules were trial search (40%) and details (35%). Usage: US 77%, Canada 6.8%, Nigeria 3.8%. • **Conclusions:** The platform showed sustained international use, supporting feasibility for global trial decision support integration.
12 Nov 2025	Integrating Artificial Intelligence (AI) into Oncology Clinical Trial Matching: Preliminary Insights from Canadian Simulated and Retrospective Data	Eva Vieira	• **Introduction**: AI-assisted trial matching can streamline screening where eligibility review is complex. This study piloted an NLP-based CTMS integrated with rule-based filters to support Canada's Clinical Trials Navigator (CTN) program • **Methodology:** GPT-4 and BERT models were tested on mock and retrospective HER2+ breast and colorectal cancer cases. Outputs were refined using rule-based scoring and CTN consensus. • **Results:** GPT-4 achieved 72.7% trial matching in mock cases, optimized to 5–7 trials per patient, reducing processing time to 10 minutes and improving precision. • **Conclusions:** AI-based CTMS improves matching efficiency but still requires expert oversight.

Notable Presentations At ESMO - AI 2025

Clinical Trial Matching & Drug Development Applications (4/8)

Date	Title	Author	Summary
12 Nov 2025	Evaluating TrialingAI for clinical trial matching and eligibility screening in oncology	Juan Jose Garcia Mosquera	• **Introduction**: Clinical trial access remains difficult as public registries lack patient-level search functionality. TrialingAI automates trial identification and eligibility evaluation within the Trialing decision-tree platform. • **Methodology:** Twelve AI models were benchmarked on decision-tree navigation and three on eligibility evaluation using synthetic oncology records. Accuracy, processing time, and cost were assessed. • **Results:** Navigation accuracy ranged 50–95% (median 87.5%), with Claude 3.7 Sonnet best at 93%. Eligibility accuracy reached 85% (Gemini 2.5). Median evaluation time per patient was 1.37 minutes. • **Conclusions:** TrialingAI enables rapid, accurate, and low-cost trial matching, supporting efficient oncology research access.
12 Nov 2025	ClinicalTrialsMatch: An AI-assisted process for molecularly-driven patient-trial matching in oncology	Mario Sánchez	• **Introduction**: Identifying oncology trial candidates is complex due to unstructured eligibility data and laborious manual screening. ClinicalTrialsMatch integrates LLM processing with expert curation for biomarker-based trial matching. • **Methodology:** Eligibility data from ~400 trials were structured via LLMs and validated in REDCap. Patient molecular profiles (n=2,172) from the institutional Prescreening Program were matched to trial criteria using a Python-based agent. • **Results:** ClinicalTrialsMatch achieved 72.5% concordance with real trial enrolments. Missed matches reflected non-molecular eligibility factors and logistic limitations. • **Conclusions:** AI-assisted matching improves efficiency and accuracy, supporting scalable, expert-guided oncology trial enrollment.

Notable Presentations At ESMO - AI 2025

Clinical Trial Matching & Drug Development Applications (5/8)

Date	Title	Author	Summary
12 Nov 2025	Evaluating AI-enabled voice-based monitoring versus traditional symptom diaries for ambulatory cancer patient-reported outcomes: A crossover pilot study	Manuel Hecht	• **Introduction**: Digital PROMs improve cancer care, yet exclude patients unable to use apps. This pilot evaluates an AI telephone system for equitable symptom monitoring. • **Methodology:** Single-center crossover (n=40) in ambulatory lung, colorectal, and GI cancer. AI calls conduct structured PRO-CTCAE dialogues twice weekly, flagging grade ≥2 symptoms; control used paper diaries. Endpoints: completion, data quality, satisfaction, feasibility, and workflow impact. • **Results:** Expected ≥80% AI completion, high satisfaction, earlier irAE detection, and ~30% fewer unplanned contacts. • **Conclusions:** AI voice PROMs improve accessibility and feasibility, supporting equitable digital oncology integration.
12 Nov 2025	International consensus for training an external and synthetic (EASY) control arm using AI-[generation of patient-bots "botients" to replace human beings in controls arms in oncology trials]	Jose M. Cervera Grau	• **Introduction**: Precision oncology challenges traditional trials by fragmenting patient cohorts. The EASY guideline defines standards for AI-driven "botient"-based synthetic control arms, replacing static or human controls. • **Methodology:** EASY integrates structured CRF data and unstructured metadata via machine learning and NLP to dynamically simulate patient-reported outcomes (PROs). Models are validated internally and externally, retuned for new drugs, and ensure interpretability and reproducibility. • **Results:** EASY-generated controls mirror real-world outcomes, achieving comparable hazard ratios to real controls and regulatory readiness. • **Conclusions:** EASY enables dynamic AI control arms, enhancing trial efficiency, ethical compliance, and regulatory confidence.

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Clinical Trial Matching & Drug Development Applications (6/8)

Date	Title	Author	Summary
12 Nov 2025	AI for Real-Time Identification of High-Impact Clinical Trials at Oncology Conferences	Judith Pérez-Granado	• **Introduction**: Conference abstract overload limits rapid identification of clinically meaningful trials. AI-driven social media analysis may prioritize high-impact oncology studies. • **Methodology:** ASCO 2025 data (2,100 abstracts; 4,570 X posts from 6k oncologists) were analyzed using GPT-4o for filtering and sentiment classification (Negative, Neutral, Positive, Practice-Informing, Practice-Changing). Engagement correlations were assessed via Spearman's ρ. • **Results:** All sentiments correlated with views ($p<0.001$); strongest for Positive ($\rho = 0.68$) and Practice-Informing ($\rho = 0.62$). Trials with the highest engagement included DESTINY-Breast09 and PACIFIC15. • **Conclusions:** AI sentiment mapping effectively highlights practice-relevant trials, demonstrating social media engagement as a proxy for clinical impact.
12 Nov 2025	Regulatory perspectives on AI applications in oncology preclinical pharmacology	Abdulmohsin Alobaid	• **Introduction**: AI is rapidly transforming oncology pharmacology but remains under-regulated in preclinical stages. This study examines key regulatory challenges and proposes AI-specific governance frameworks. • **Methodology:** A targeted literature and policy review (FDA, EMA, SFDA) analyzed AI use in preclinical oncology models and evaluated conceptual frameworks such as TREAT (Trustworthiness, Reproducibility, Explainability, Applicability, Transparency). • **Results:** Gaps include limited validation standards, algorithmic bias, and lack of explainability. The TREAT framework supports structured, ethical AI integration and dynamic agent-based systems in early drug discovery • **Conclusions:** Dedicated oncology AI regulations emphasizing transparency, validation, and stakeholder collaboration are essential for safe, reproducible preclinical applications.

Notable Presentations At ESMO - AI 2025

Clinical Trial Matching & Drug Development Applications (7/8)

Date	Title	Author	Summary
12 Nov 2025	Tokenized blockchain architecture for multicenter international cooperative oncology trials: Financial viability and technical implementation	Jose M. Cervera Grau	- **Introduction**: Cooperative oncology trials face operational inefficiencies and rising data management costs. Blockchain and tokenization offer novel solutions for secure, transparent, and automated trial operations. - **Methodology:** A technical-economic feasibility study analyzed hybrid and ZK-rollup blockchain models integrating digital identity, smart contracts, and consensus mechanisms. Cost modeling covered setup, maintenance, scalability, and regulatory compliance (FDA, EMA, GDPR). - **Results:** Tokenized blockchain models reduced administrative overhead via automated consent, governance, and data traceability while ensuring GDPR/HIPAA compliance. Shared infrastructures further decreased multicenter costs. - **Conclusions:** Blockchain-enabled digital trial models are feasible, cost-effective, and scalable, supporting secure, transparent, and collaborative oncology research.
12 Nov 2025	A novel multi-agent framework for patient eligibility assessment in oncological clinical trials	Qi Lin	- **Introduction**: Manual eligibility assessment for oncology trials is labor-intensive and prone to variability. This study introduces a transparent AI-based framework to automate patient–trial matching. - **Methodology:** A multi-agent system was developed: (1) Case-RAG retrieves similar historical cases; (2) Matching Agent generates inclusion/exclusion judgments with evidence; (3) Quality Control Agent performs confidence scoring and self-verification, flagging uncertain cases for clinician review. - **Results:** Across >30 trials and >8,000 assessments, the framework consistently produced reviewer-ready, evidence-linked eligibility matrices. - **Conclusions:** This explainable multi-agent system streamlines eligibility assessment, enhancing efficiency, transparency, and scalability in oncology trial enrollment.

Notable Presentations At ESMO - AI 2025

Clinical Trial Matching & Drug Development Applications (8/8)

Date	Title	Author	Summary
13 Nov 2025	Enhancing Phase I Clinical Trial Selection Using Artificial Intelligence: Evaluation of a Large Language Model Algorithm in a Dedicated Drug Development Unit	Diogo J. Silva	• **Introduction**: Efficient patient allocation to early-phase oncology trials remains challenging due to manual eligibility screening. This study assessed MedgicalAI®, an LLM-powered platform designed to automate and enhance patient–trial matching. • **Methodology:** In a prospective study (June–August 2025), anonymized referrals and lab data were analyzed using MedgicalAI® against eligibility from >60 open Phase I trials. AI results were compared with expert allocations at weekly meetings. • **Results:** Among 108 patients, MedgicalAI® achieved 100% precision, 91.5% recall, and F1 = 0.96, showing 91.5% concordance with expert decisions. • **Conclusions:** MedgicalAI® demonstrated high accuracy and efficiency, supporting AI's integration into Phase I trial recruitment workflows.

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (1/15)

Date	Title	Author	Summary
12 Nov 2025	Deep Learning on Histopathological Images to Predict Breast Cancer Recurrence Risk and Chemotherapy Benefit	Gil Shamai	• **Introduction**: Genomic assays like Oncotype DX guide chemotherapy decisions in HR+/HER2– early breast cancer but are costly and inaccessible in many regions. This study developed an AI model to estimate recurrence risk using routine histopathology and clinical data. • **Methodology:** A multimodal deep learning model was pre-trained on 171,189 slides, fine-tuned on TAILORx (n=10,273), and validated externally (n=5,497). Performance was evaluated by AUC and prognostic hazard ratios. • **Results:** The model achieved AUC = 0.898 for high-risk prediction and matched Oncotype DX prognostic accuracy. It reclassified 36% of clinically high-risk postmenopausal patients as low-risk, potentially avoiding chemotherapy • **Conclusions:** AI applied to histopathology accurately replicates genomic risk scoring, enabling cost-effective, global access to precision oncology.
12 Nov 2025	Improved risk stratification of patient outcomes using AI-driven multimodal characterization of histologic subtypes in lung adenocarcinoma	Kevin Boehm	• **Introduction**: Lung adenocarcinoma (LUAD) subtypes carry prognostic and genomic value, but manual quantification is laborious. This study developed a transformer model for automated subtype ratio and grade prediction from H&E WSIs. • **Methodology:** Using 1,459 LUAD slides and 3,698 MSK-IMPACT samples, subtype ratios were inferred and integrated with genomic data via joint embeddings and DBSCAN clustering. • **Results:** Correlations: solid r=0.77; others 0.40–0.54. Grade AUCs: 0.84 (high), 0.80 (low); survival stratified (p<0.001). Multimodal clustering improved prognostic separation (HR spread 13.28). • **Conclusions:** Transformer-based modeling enhances LUAD grading and risk stratification.

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (2/15)

Date	Title	Author	Summary
12 Nov 2025	Whole slide classification for microsatellite instability prediction with geometry grounded methods	Ylva Weeda	• **Introduction**: Microsatellite instability (MSI) predicts immunotherapy response but is harder to detect in gastric cancer (GA) via H&E images. This study used an Equivariant Neural Field (ENF) to improve MSI prediction efficiency. • **Methodology:** ENF generated continuous patch-level point-cloud representations from 500 GA samples, reconstructing images to ensure discriminative feature capture. Slide-level MSI classification was performed via stitched ENF outputs. • **Results:** ENF achieved AUC 63.9 (F1 21.5), outperforming pretrained extractors (AUC 60.4). Biopsy-only analysis improved AUC to 70.0. ENF required 100× fewer parameters and 5× faster training. • **Conclusions:** ENF enables efficient, accurate MSI prediction from GA biopsies.
12 Nov 2025	Artificial Intelligence-Driven Spatial Proteomics Analysis Identifies Prognostic Markers of Mucinous Differentiation in Rectal Cancer	Chuanwen Fan	• **Introduction**: Mucinous differentiation in rectal cancer (RC) correlates with poor prognosis, yet spatial marker patterns remain underexplored. This study investigated molecular and spatial biomarkers linked to mucinous RC • **Methodology:** Transcriptomic analysis (TCGA, Swedish cohort) identified mucin-associated genes via WGCNA. Spatial proteomics (COMET) on 155 RC samples and an AI-driven pipeline quantified 63 spatial features across tumor and stroma • **Results:** TCN1, MUC1, and MUC2 were key markers. Fourteen features differentiated mucinous RC; five correlated with survival, including intratumoral TCN1 heterogeneity and stromal/tumor MUC2 variability ($p<0.05$). • **Conclusions:** AI-integrated spatial proteomics reveals mucin-related heterogeneity and prognostic biomarkers in RC

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (3/15)

Date	Title	Author	Summary
12 Nov 2025	Multiplex fluorescence immunohistochemistry and digital image analysis identify CD163-positive macrophages as a poor prognostic factor in liver-transplanted patients with non-resectable colorectal cancer	Christian Kranjec	• **Introduction**: Liver transplantation (LT) benefits select colorectal cancer liver metastasis (CRLM) patients, but prognostic immune markers remain unclear. This study evaluated immune infiltrates predicting post-LT survival • **Methodology:** Multiplex immunofluorescence analyzed CD3, CD8, CD68, and CD163 expression in 199 CRLM samples from 54 LT patients (2006–2020). Spatial immune profiles were correlated with 10-year overall survival (OS). • **Results:** High stromal/intraepithelial CD163+ TAM infiltration predicted worse OS (0% vs. 49%; HR=3.6, p=0.002). Intraepithelial CD68+CD163+ cells also correlated with poor OS (HR=2.2, p=0.045). • **Conclusions:** CD163+ TAM density independently predicts poor post-LT survival, refining CRLM prognostic stratification.
12 Nov 2025	Automated prediction of tumor-budding from colorectal cancer histology slide images using STAMP deep-learning pipeline	Lawrence A. Shaktah	• **Introduction**: Tumor budding (Bd) is a key prognostic marker in early colon cancer, but its role in stage III disease remains unclear and manual scoring is laborious. This study evaluated AI-based Bd prediction. • **Methodology:** Whole-slide images from the IDEA-France phase III trial were analyzed using the STAMP pipeline with Transformer-based aggregation. Bd categories (Bd1–Bd3) per ITBCC 2016 were used for supervised learning; model performance was assessed via 5-fold cross-validation. • **Results:** The model achieved AUROC 0.83 (95% CI 0.79–0.86) and significant survival stratification (p = 0.002). • **Conclusions:** STAMP enables accurate, automated Bd prediction supporting reproducible risk stratification in stage III colon cancer.

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (4/15)

Date	Title	Author	Summary
12 Nov 2025	A cell-level staining quantification framework for HER2 prediction	Jean-Eudes Le Douget	• **Introduction**: HER2 IHC guides ADC therapy selection, but categorical scoring limits precision. This study introduces an IHC-specific foundation model (FM) enabling continuous, spatially resolved HER2 quantification • **Methodology:** The 86M-parameter HistoPLUS FM, pretrained on 10,000 IHC WSIs, segmented tumor cells and quantified membrane DAB staining across 110 validation slides. Results were benchmarked against Virchow2 (632M parameters) and expert annotations (n=7,106). • **Results:** HistoPLUS achieved 88.8% balanced accuracy (BA) for tumor detection and 66.7% BA for cell-level staining (vs. 82.3% and 62.6% for Virchow2). • **Conclusions:** The framework delivers state-of-art, ADC-relevant HER2 quantification aligned with ASCO/CAP criteria, ensuring adaptable, scalable clinical integration.
12 Nov 2025	Benchmarking Instance Segmentation Architectures for Whole-cell Segmentation in IHC-stained Images - a Multi-cancer Study	Srividhya Sathya Narayanan	• **Introduction**: Accurate whole-cell segmentation is essential for quantitative continuous scoring (QCS) in IHC, directly impacting compartment-level intensity measurements. • **Methodology:** Four segmentation models—Cellpose-StarDist (CPSD), Cellpose-Nucpose (CPNP), InstanSeg, and UniCellPose—were benchmarked on 592 training and 280 validation FOVs from seven cancer types and five IHC markers. Test data (632 FOVs) included 185K cells and 12K nucleus annotations. • **Results:** InstanSeg achieved the best performance across metrics: +1.4% F1 (cell detection), +1.1% Dice (nucleus), and +3.2% membrane segmentation over CPNP. • **Conclusions:** InstanSeg demonstrated top accuracy and efficiency, simplifying QCS integration across cancer types.

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (5/15)

Date	Title	Author	Summary
12 Nov 2025	Unlocking the potential of deep learning-based detection and quantification of tumor infiltrating lymphocytes in gastric cancer	Ylva Weeda	**Introduction**: Automated TIL quantification can refine immunotherapy selection, though its role in gastric adenocarcinoma (GA) remains unexplored. **Methodology:** A U-Net tissue segmentation and YOLOv3 cell-detection model pretrained on breast cancer was adapted to GA using 377 annotated regions and 4,152 cell labels. The model analyzed 143 GA slides, and results were benchmarked against two expert pathologists. **Results:** Predicted versus expert TIL counts showed strong correlation (r=0.72). Misclassifications mainly involved necrosis, muscle, and inflammatory granulocytes. **Conclusions:** This interpretable model enables accurate, rule-based TIL quantification in GA, improving reproducibility and supporting future immunotherapy-focused validation.
12 Nov 2025	Spatially resolved deep learning prediction of prognostic EMT/PT scores from H&E in clear-cell renal cell carcinoma	Rebecca N. Wray	**Introduction**: Spatial EMT and proximal-tubule (PT) programs drive ccRCC progression, but their histologic surrogates remain undefined. **Methodology:** Using 397 TCGA-KIRC WSIs, the SMMILe framework inferred EMT and PT programs from H&E images via UNI v2 and CONCH v1.5 embeddings, trained with RNA-seq–derived labels over 50 epochs**.** **Results:** UNI v2 achieved AUROC 0.752 for EMT (sensitivity 59.0%, specificity 83.2%) and 0.682 for PT (sensitivity 75.5%, specificity 55.6%). **Conclusions:** SMMILe enables scalable, spatially resolved molecular phenotyping in ccRCC, supporting automated risk stratification and integration into precision pathology workflows.

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (6/15)

Date	Title	Author	Summary
12 Nov 2025	Computational quantification of immune and stromal biomarkers in colorectal liver metastases	Caroline Truntzer	• **Introduction**: Histological growth patterns (HGPs) influence prognosis in colorectal liver metastases (CRLM), yet microenvironmental assessment remains inconsistent. • **Methodology:** In 164 CRLM resections, immune (CD3, CD20, TLS) and stromal (TNC, DCN, CD31, α-SMA) markers were quantified via QuPath. A CAF-stromal score (TNC+DCN+CD31) was correlated with 3-year PFS and 5-year OS. • **Results:** Desmoplastic HGP correlated with higher TLS, CD20, and B-cell ratios; non-desmoplastic HGP showed elevated CD31 and TNC. The CAF-stromal score predicted OS (HR=0.5; p=0.01). • **Conclusions:** Computational profiling of immune-stromal markers refines CRLM prognosis and supports tailored post-metastasectomy management.
12 Nov 2025	A lightweight IHC-specific foundation model for diagnostic purposes	Jean-Eudes Le Douget	• **Introduction**: ADCs require accurate biomarker detection, yet existing models for HER2 IHC prediction lack efficiency. • **Methodology:** An 86M-parameter vision transformer, pre-trained on 10,000 IHC WSIs (9 indications, 100+ markers), was compared with four public FMs across 470 breast cases. Tile embeddings were aggregated for HER2 scoring (0–3+). • **Results:** Our IHC-specific FM achieved AUROC 0.897 ± 0.017 and mean balanced accuracy 59.1%, outperforming Virchow2 (+0.7), H0 (+4.6), H0-mini (+5.1), and UNI2-h (+5.3). • **Conclusions:** The compact IHC foundation model delivers state-of-the-art HER2 prediction with far less data, supporting scalable ADC biomarker evaluation.

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (7/15)

Date	Title	Author	Summary
12 Nov 2025	Histology meets AI: Decoding minimal residual disease risk (MRDR) and stromal signatures in the colon cancer (CC) PEGASUS trial	Federica Cruciani	• **Introduction**: ctDNA-defined minimal residual disease (MRD) predicts relapse in stage II–III colon cancer but is costly. This study tested whether AI-derived H&E pathomics could infer MRD risk and quantify stromal biology • **Methodology:** In 138 PEGASUS patients (44 MRD+, 94 MRD−), CONCH and TITAN embeddings analyzed WSIs; classifiers predicted MRD risk, and ensemble models quantified stromal features • **Results:** AI achieved modest MRD risk accuracy (balanced accuracy = 0.65; 95% CI 0.56–0.72) but strong stromal correlation ($\rho > 0.7$, $p < 1e-5$) • **Conclusions:** AI pathomics reliably captured stromal remodeling, offering an interpretable, cost-efficient alternative to molecular MRD testing
12 Nov 2025	Interpretable histomorphological subtypes linked to ICI response in advanced melanoma using AI-assisted histopathology analysis	Mark Schuiveling	• **Introduction**: Reliable histologic biomarkers for predicting melanoma response to immune checkpoint inhibitors (ICI) are lacking. This study explored AI-derived morphology to stratify responders • **Methodology:** Pretreatment metastatic H&E slides (n=1177) were analyzed across 11 Dutch centers using 14 AI foundation models. CLAM aggregated tile features to predict 6-month RECIST outcomes, validated via leave-one-hospital-out cross-validation • **Results:** The UNI2 model achieved AUC 0.63 (95% CI 0.60–0.66). Low-response slides showed necrosis, spindle morphology, and liver/bone/brain origin; high-response slides showed lymphocyte-rich epithelioid patterns • **Conclusions:** AI histopathology modestly predicts ICI response and uncovers morphological correlates of treatment sensitivity

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (8/15)

Date	Title	Author	Summary
12 Nov 2025	Few-shot Quantitative Continuous Scoring through Computational Pathology Foundation Models	Nicolas Brieu	• **Introduction**: Developing quantitative continuous scoring (QCS) models for IHC analysis requires extensive manual annotations, limiting scalability. This study explored zero-/few-shot training using foundation models (FMs) for efficient adaptation to new markers and indications. • **Methodology:** Three frozen FMs (UNIv2, CONCH, H-optimus-0) with a UNETR decoder were benchmarked against a CNN baseline across lung and new indication datasets. • **Results:** UNIv2 and H-optimus-0 reached CNN-level dice scores using only 25% of data; zero-shot models met acceptance criteria, and fine-tuned UNIv2 (30% data) outperformed CNN trained on 100%. • **Conclusions:** FMs enable rapid, annotation-efficient QCS adaptation, accelerating biomarker discovery and patient stratification
12 Nov 2025	Deep learning model identifies lynch syndrome versus sporadic MSI-H from adenoma histology	Srividhya Sainath	• **Introduction**: Lynch syndrome (LS) is the most common hereditary colorectal cancer, but germline testing remains costly and limited. This study assessed whether deep learning (DL) on adenoma histology can distinguish LS from sporadic MSI-H cancers. • **Methodology:** A transformer DL model (VIRCHOW-2) was trained on 298 WSIs (120 LS, 177 sporadic) and externally validated on 176 WSIs from 164 patients in the HeCOG cohort • **Results:** The model achieved AUROC 0.92 on adenomas and 0.73 on external MSI-H CRC. Explainability indicated lymphocyte-rich mucosa as an LS signal. • **Conclusions:** DL on H&E adenomas can differentiate LS from sporadic MSI-H CRC, supporting scalable, affordable LS screening

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (9/15)

Date	Title	Author	Summary
12 Nov 2025	Explainable AI-guided genomic signature accurately predicts response to neoadjuvant androgen deprivation therapy in localized, high-risk prostate cancer	Pablo Iriso	• **Introduction**: Prostate cancer shows heterogeneous response to neoadjuvant androgen deprivation therapy (NADT). This study aimed to identify molecular biomarkers predicting treatment response using explainable AI. • **Methodology:** Using KEM® association-rule mining, 100 immune-related genes from two NADT trials (n=58) were analyzed. Models were generated via Boolean logic with cross-validation. • **Results:** A four-gene signature (ARSD, CUX2, PLS3, GUCY1A1) achieved 0.87 balanced accuracy (specificity 0.92, sensitivity 0.87), outperforming androgen-pathway references (AUC 0.56–0.75). • **Conclusions:** This AI-derived four-gene model robustly predicts NADT response, offering promise for personalized prostate cancer therapy pending larger-scale validation
12 Nov 2025	Automatic inference of tumor microenvironment features from histology images of pre-treatment biopsies and associations with response to neoadjuvant therapy in rectal cancer	Marta Ligero Hernandez	• **Introduction**: Responses to total neoadjuvant therapy (TNT) in locally advanced rectal cancer (LARC) are heterogeneous. This study explored whether deep learning (DL) on H&E biopsies can infer tumor microenvironment (TME) features predicting TNT response. • **Methodology:** A DL model trained on 404 TCGA CRC cases predicted transcriptomic signatures and was applied to 570 LARC patients. XGBoost combined inferred features for response prediction • **Results:** Predicted immune and EMT signatures correlated with RNA-Seq (ρ up to 0.68). Cytotoxic infiltration predicted higher TNT response (17.9–36.8%); AUROC=0.62–0.63. • **Conclusions:** DL-derived TME features moderately predict TNT response, warranting multimodal validation

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (10/15)

Date	Title	Author	Summary
12 Nov 2025	Benchmarking Computational Pathology Foundation Models for the Development of a Multi-cancer Multi-marker Segmentation Model	Margaryta Olenchuk	• **Introduction**: Quantitative Continuous Scoring (QCS) of IHC images aids biomarker development but is limited by morphology and staining variability across cancers. Foundation models (FMs) offer improved cross-domain scalability. • **Methodology:** Four FMs (UNIv2, CONCH, H-Optimus-0, Hibou-L) with a UNETR head were benchmarked against a CNN QCS model using 4,000 WSIs across nine cancers and eight markers. • **Results:** UNIv2 achieved the best Dice score (0.8931), outperforming H-Optimus-0 (0.8922), Hibou-L (0.8910), CNN (0.8895), and CONCH (0.8875). • **Conclusions:** UNIv2-based QCS enables robust multi-cancer, multi-marker segmentation, supporting scalable biomarker discovery and validation.
12 Nov 2025	Corrected grouped-Lasso-based generative AI for the unsupervised extension of segmentation models to the analysis of translucent chromogenic IHC images	Nicolas Brieu	• **Introduction**: Multiplex translucent IHC allows simultaneous multi-protein analysis but challenges traditional Quantitative Continuous Scoring (QCS). Generative AI can extend monoplex-trained models to multiplex settings. • **Methodology:** Existing QCS models were adapted using grouped lasso–based stain decomposition with correction and a chained pix2pix generative model for domain translation, enabling segmentation of translucent IHC without retraining. • **Results:** High concordance was achieved between DAB/HX and translucent images (Pearson correlation superior to CycleGAN and grayscale baselines). • **Conclusions:** The chained pix2pix–QCS pipeline enables accurate, annotation-free multiplex IHC segmentation, validating scalable unsupervised model adaptation.

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (11/15)

Date	Title	Author	Summary
12 Nov 2025	Eye to A.I.: AI-powered assessment of radiological-pathological concordance and prognostication in rectal cancer patients treated with neoadjuvant SCRT	Arpit Jain	**Introduction**: Accurate post-neoadjuvant response assessment in rectal cancer is challenging due to MRI/PET-CT variability. This study evaluated AI chatbots for predicting tumor regression grade (TRG) and pathological complete response (pCR). **Methodology:** MRI/PET-CT reports from 65 patients were analyzed using ChatGPT-4.5, Claude 3, and Med-PaLM, compared with radiologists and pathology using Cohen's κ and diagnostic metrics. **Results:** AI showed higher concordance (κ = 0.68) than radiologists (κ = 0.41) and better pCR prediction (72% vs 63%), with specificity 81%. ChatGPT-4.5 achieved pCR sensitivity 87%. **Conclusions:** AI chatbots reliably interpret radiology reports, enhancing pathology correlation and prognostic assessment in rectal cancer.
12 Nov 2025	AI-Assisted HER2 IHC Classification for Optimized Treatment Decision Making Across Digital Pathology Platforms	Patrick Frey	**Introduction**: HER2 IHC assessment is critical for therapy selection, yet interobserver and inter-scanner variability limit reproducibility. This study evaluated AI's impact on HER2 IHC scoring across multiple scanners and centers. **Methodology:** 2,015 breast cancer slides from 14 centers using seven scanners were analyzed. Pathologists scored manually and later with AI assistance following ASCO/CAP 2023 HER2 guidelines, including an ultralow category. **Results:** AI increased accuracy from 75.4% to 80.0% and interobserver agreement from 73.4% to 86.1%. HER2-ultralow reproducibility improved from 68.0% to 82.0%. **Conclusions:** AI substantially enhances accuracy, reproducibility, and HER2-ultralow assessment across scanners, supporting its integration into diagnostic workflows.

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (12/15)

Date	Title	Author	Summary
12 Nov 2025	A multi-scale deep learning framework for a prognostic Stromal Immunoscore from H&E slides in colorectal cancer: A large-scale, multi-cohort validation study	Min-Er Zhong	- **Introduction**: Immune profiling in colorectal cancer (CRC) offers key prognostic insights, but conventional Immunoscore requires IHC. This study developed a deep-learning–based Stromal Immunoscore (SI) from H&E slides as a cost-effective alternative. - **Methodology:** Using TCGA data (n=772) and validated across 3 international cohorts (n≈3,600), a multi-scale model quantified stromal immune cell densities to classify SI-Low, -Intermediate, and -High groups. - **Results:** SI-High consistently predicted superior OS/DFS (HR 0.42–0.55, $p<0.001$) across cohorts and remained independent in multivariable analysis. - **Conclusions:** This automated, H&E-based SI provides robust, scalable immune-based prognostication, enabling integration into routine pathology workflows.
12 Nov 2025	Artificial intelligence-based TSR quantification reveals prognostic value and stromal-driven immunosuppression in colorectal cancer: An international validation study	Ke Zhao	- **Introduction**: Colorectal cancer (CRC) progression is driven by stromal remodeling, which shapes tumor behavior and immune suppression. This study developed an AI-based tumor–stroma ratio (TSR-AI) for objective quantification from routine H&E slides. - **Methodology:** WSIs from 3,411 CRC patients were analyzed using AI models for tumor and stroma segmentation. TSR-AI was validated against CK-stained and pathologist-scored TSR and correlated with survival and immune infiltration. - **Results:** TSR-AI correlated strongly with reference TSR (R=0.93). TSR-high predicted poorer OS (HR 2.4–3.3, $p<0.001$) and lower immune infiltration, with spatial transcriptomics confirming CAF–TGFβ enrichment. - **Conclusions:** TSR-AI enables reproducible, scalable stromal quantification and improves CRC prognostication beyond TNM staging.

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (13/15)

Date	Title	Author	Summary
12 Nov 2025	Deep learning-based automated prognostic stratification through analysis of invasive margin T-cell infiltrates in localized colon cancer	Julie Lecuelle	• **Introduction**: T-cell infiltration is a strong prognostic marker in colon cancer. This study evaluated whether deep learning (DL)-based spatial analysis of CD3-stained slides can predict survival outcomes. • **Methodology:** Using phase III PRODIGE-13 and PETACC08 trial data (N=1,465), a VGG19-based DL model segmented tumor core (TC) and invasive margin (IM) zones, quantified CD3+ density, and clustered patients into prognostic groups. • **Results:** Favorable clusters showed improved 5-year DFS (TC HR=0.6; IM HR=0.5; p<0.01). Combining TC+IM achieved HR≈0.5 across validation sets. • **Conclusions:** DL-derived CD3 spatial features robustly stratify prognosis, outperforming CD3 density alone and supporting clinical integration.
12 Nov 2025	Open the black box: Transparent prognostic prediction and discovery with AI de novo designed spatial biomarkers	Junhao Liang	• **Introduction**: Most deep learning (DL) models in pathology act as black boxes, limiting interpretability and biological insight. This study introduces MacroNet, a transparent DL framework predicting colorectal cancer (CRC) prognosis from semantic segmentation maps. • **Methodology:** Trained on 2,281 DACHS CRC patients via five-fold cross-validation, MacroNet's performance was benchmarked by C-index and paired with multi-angle attribution to identify spatial biomarkers. • **Results:** MacroNet achieved a median C-index = 0.722, surpassing larger foundation models. Ten interpretable spatial biomarkers—e.g., stroma–tumor and lymphocyte–stroma interactions—retained equivalent prognostic accuracy. • **Conclusions:** MacroNet provides interpretable, high-performance prognostic modeling, revealing biologically meaningful spatial features for precision oncology.

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (14/15)

Date	Title	Author	Summary
12 Nov 2025	Towards robust computation of AI/ML computational pathology IHC scoring with the radial digital tumour proportion score (rdTPS)	Laura Acqualagna	• **Introduction**: AI-based digital Tumor Proportion Scoring (dTPS) has mainly focused on PD-L1, with limited validation for other membrane-bound IHC markers. This study evaluated an AI/ML pipeline and introduced a robust variant, rdTPS, to address staining inconsistencies. • **Methodology:** ML models trained on 338 slides segmented tumor epithelium and classified biomarker-positive cells. rdTPS incorporated spatial normalization within 80 µm of positive cells to improve stability. • **Results:** Model F1 = 0.64 (positive), 0.58 (negative), 0.89 (epithelium). rdTPS reduced intra-patient variance and improved correlation with pathologists (RMSE = 19.7 vs 30). • **Conclusions:** rdTPS enhances digital IHC scoring robustness, supporting scalable and reproducible biomarker quantification in NSCLC.
12 Nov 2025	Pathomic embeddings improve prediction of clinically actionable breast cancer related mutations from whole slide images	Kiran Nijjer	• **Introduction**: Genomic profiling in breast cancer guides therapy but remains costly and inaccessible. This study used foundation-model-derived pathomic embeddings to predict key gene mutations from H&E slides, reducing dependency on genomic testing. • **Methodology:** Using TCGA-BRCA (1,055 cases), UNI embeddings from 11.3M tiles were analyzed. Machine learning classifiers predicted mutation status for BRCA1, PIK3CA, TP53, and RB1. • **Results:** AUCs: BRCA1 = 0.86, TP53 = 0.85, RB1 = 0.85, PIK3CA = 0.72. • **Conclusions:** Foundation-model pathomics accurately inferred actionable mutations from H&E slides, demonstrating potential to complement or replace genomic assays in breast cancer precision diagnostics.

Notable Presentations At ESMO - AI 2025

Digital Pathology & Histopathology AI (15/15)

Date	Title	Author	Summary
12 Nov 2025	Benchmarking Digital Pathology Foundation Models on PD-L1 Slides for Immunotherapy Response Classification	Aleksandra Zec	• **Introduction**: Foundation models (FMs) trained on H&E slides show strong performance in pathology but remain untested on PD-L1 IHC, a key biomarker for NSCLC immunotherapy. This study benchmarked six FMs on PD-L1 IHC slides. • **Methodology:** Feature embeddings from six FMs (UNI, Phikon, CTransPath, CHIEF, TITAN, GigaPath) were analyzed using CLAM on 352 PD-L1 slides from NSCLC patients (I3LUNG, NCT05537922). • **Results:** TITAN achieved best PD-L1 classification (ACC = 0.66, AUC = 0.75). Phikon and CTransPath performed best for survival (AUC ≈ 0.63–0.64). CHIEF underperformed. • **Conclusions:** FMs captured predictive signals in PD-L1 IHC, showing potential for cross-stain transfer and immunotherapy outcome prediction in NSCLC

Notable Presentations At ESMO - AI 2025

Radiomics & Imaging AI (1/12)

Date	Title	Author	Summary
12 Nov 2025	Radiogenomic "survival-fingerprint": A graph-based integration of BraTS MRI radiomics and TCGA transcriptomics to identify prognostic and druggable patient modules	Mobin Mobadersani	- **Introduction**: This study develops an interpretable radiogenomic survival-fingerprint combining MRI radiomics and transcriptomics to identify prognostic and druggable subgroups in high-grade glioma. - **Methodology:** Radiomic and transcriptomic data from BraTS and TCGA are integrated into a patient-similarity network. Modules are detected via Leiden clustering, linked to survival (KM, Cox), and biologically annotated through GSEA and druggability mapping. - **Results:** Preliminary findings reveal survival-distinct modules with enriched pathways and actionable targets. Radiomic features enable noninvasive module prediction validated through bootstrapping and external testing. - **Conclusions:** This reproducible AI framework supports precision glioma stratification.
12 Nov 2025	CT-based radiomics to predict HER2 expression of metastases from breast cancer: Preliminary results from the RADIOSPHER2 study	Leonardo Provenzano	- **Introduction**: The RADIOSPHER2 study (NCT07030569) investigates radiomics as a noninvasive biomarker to predict HER2 overexpression in metastatic breast cancer, addressing spatial and temporal heterogeneity in HER2 assessment. - **Methodology:** CT scans from 174 patients were analyzed using 107 PyRadiomics features post-resampling and filtering. Machine learning models with nested cross-validation and SHAP interpretation were applied, with logistic regression showing optimal performance. - **Results:** Logistic regression achieved ROC-AUC 0.745 ± 0.079, accuracy 0.712, and specificity 0.731. Key predictive features included Root Mean Squared and Cluster Tendency, with lung metastases linked to HER2 positivity. - **Conclusions:** Radiomics shows promise as a reproducible, noninvasive predictor of HER2 status in mBC metastases.

Notable Presentations At ESMO - AI 2025

Radiomics & Imaging AI (2/12)

Date	Title	Author	Summary
12 Nov 2025	Voxel-wise Quantification of MRI Signal Intensity Changes in Brain Tumor Response Assessment using All-Resolutions Inference	Iris Loo	• **Introduction**: RANO criteria rely on lesion diameter to assess tumor progression but fail to quantify enhancement intensity. This study introduces All-Resolutions Inference (ARI), adapted from fMRI, to objectively identify true voxel-level signal changes between MRI scans. • **Methodology:** Baseline–follow-up T1-contrast MRIs from institutional (101 patients, 446 pairs) and LUMIERE (55 patients, 121 pairs) cohorts were analyzed. Voxel-wise intensity residuals generated p-value maps; ARI with AI-derived masks (FWE 0.05, TDP ≥0.7) identified progression/response clusters. Logistic regression compared ARI features to standard AI segmentation volumes. • **Results:** ARI-derived intensity metrics outperformed volume-only features (AUC 0.81 vs 0.23, $p<0.0001$) in predicting progression, and improved response prediction (AUC 0.74→0.85 across cohorts). • **Conclusions:** Voxel-wise ARI provides a robust, quantitative alternative to RANO, enhancing detection of progression and response in brain tumors.
12 Nov 2025	Utility of longitudinal imaging data for lung cancer prediction	Shahab Aslani	• **Introduction**: Lung cancer screening (LCS) via low-dose CT reduces mortality, but variability in radiologist interpretation limits accuracy. This study developed a multimodal AI model integrating imaging and clinical data to enhance malignancy prediction in indeterminate nodules. • **Methodology:** Using >13,000 participants from the SUMMIT trial, 3D ResNet-18 processed longitudinal LDCT scans, while TabNet handled metadata. Models incorporated scan-interval data and were evaluated via 5-fold cross-validation (AUC, sensitivity, specificity). • **Results:** Single-timepoint model AUC: 0.79; adding longitudinal imaging: 0.85; adding scan-interval + metadata: 0.87 (Se 0.83, Sp 0.80). • **Conclusions:** Longitudinal, metadata-enriched AI models outperform single-scan approaches, supporting clinical integration for more consistent LCS malignancy assessment.

Notable Presentations At ESMO - AI 2025

Radiomics & Imaging AI (3/12)

Date	Title	Author	Summary
12 Nov 2025	AI-powered assessment of pancreatic cancer resectability: A comparative study of chatbot models versus NCCN criteria and radiology reports	Arpit Jain	• **Introduction**: Accurate resectability assessment in pancreatic cancer guides treatment planning, yet radiologist variability persists despite NCCN criteria. This study evaluated large language models (LLMs) for automated resectability classification from radiology reports. • **Methodology:** Seventy-five histologically confirmed cases were analyzed using NCCN 2025 criteria, expert radiologist consensus, and outputs from ChatGPT-4.5, GPT-4o, o4-mini, and Gemini. Agreement was measured via Cohen's κ • **Results:** ChatGPT-4.5 achieved the highest concordance with NCCN (κ = 0.82) and radiologists (κ = 0.84). Discordant cases (16%) mainly involved borderline resectable tumors with variable vascular involvement. • **Conclusions:** ChatGPT-4.5 demonstrated near-expert accuracy, supporting its use in standardizing pancreatic cancer resectability assessment and reducing interobserver variability.
12 Nov 2025	SmartThyroid: AI-Based Identification and Segmentation of Parathyroid Glands in Multi-Approach Remote-Access Thyroid Surgery	Jinyuan Liu	• **Introduction**: Thyroid cancer surgery demands precise identification of parathyroid glands (PGs) to prevent postoperative complications. This study introduces SmartThyroid, an AI system enhancing PG detection in multi-approach remote-access thyroidectomy. • **Methodology:** Using 210 surgical videos (2019–2024, Sichuan Cancer Hospital), five AI architectures were trained; YOLOv11, achieving top accuracy, was selected. Performance metrics included Dice, IoU, and AP50, comparing SmartThyroid against surgeons' recognition rates and response times. • **Results:** SmartThyroid achieved Dice 0.873, IoU 0.804, AP50 0.974, outperforming all surgeons in recognition time and junior surgeons in accuracy and duration, improving both metrics for all. • **Conclusions:** SmartThyroid offers real-time, high-precision PG recognition, improving safety and efficiency, particularly aiding less experienced surgeons during thyroid surgery.

Notable Presentations At ESMO - AI 2025

Radiomics & Imaging AI (4/12)

Date	Title	Author	Summary
12 Nov 2025	Enhanced Prediction of EGFR Mutation Status in advanced stage NSCLC Using a multi-modal Radiomics Machine Learning Pipeline	Nitin Y. Murthy	• **Introduction**: EGFR mutation defines therapy selection in NSCLC, but molecular testing via tissue or liquid biopsy faces challenges. This study explored radiomics as a noninvasive predictive approach in an Asian population with high EGFR prevalence. • **Methodology:** CT and PET scans from 67 advanced NSCLC patients (33 EGFR+, 34 EGFR−) underwent PyRadiomics feature extraction (120 features). Machine learning classifiers (SVM, MLP, LightGBM, CatBoost, AdaBoost) analyzed single- and multimodal (CT+PET) data using a 50:50 train-test split. • **Results:** Combined CT+PET features with AdaBoost achieved AUC 0.95 and 90% accuracy. CT-only XGBoost (AUC 0.86) and PET-only Decision Tree (AUC 0.84) performed lower • **Conclusions:** Multimodal radiomics significantly improves EGFR mutation prediction, providing a robust, cost-effective, noninvasive tool for molecular profiling in advanced NSCLC.
12 Nov 2025	CT-Based 3D ResNet50 for Predicting Survival in NSCLC Patients Treated with Immunotherapy	Margherita Favali	• **Introduction**: Immunotherapy (IO) has revolutionized NSCLC management, yet identifying poor responders remains difficult. This study evaluated a 3D ResNet50 deep learning model using baseline CT scans to predict 6-month survival outcomes. • **Methodology:** IO-baseline CTs from 483 advanced NSCLC patients (APOLLO11 trial) were split into train/validation/test sets (64/16/20%). The model underwent 5-fold cross-validation, Grad-CAM visualization, and robustness testing via parameter randomization and deletion analyses. • **Results:** The model achieved AUC 0.64, F1 0.78, accuracy 0.67, recall 0.89. Grad-CAM localized predictive regions to lesions and perilesional areas, confirming biological relevance. • **Conclusions:** 3D ResNet50 demonstrates promise for identifying IO poor responders, supporting the potential of DL-based imaging biomarkers for NSCLC treatment stratification.

Notable Presentations At ESMO - AI 2025

Radiomics & Imaging AI (5/12)

Date	Title	Author	Summary
12 Nov 2025	Development and validation of a preoperative T staging prediction model for esophageal cancer based on tumor length and multimodal data: A multicenter retrospective	Shuoming Liang	• **Introduction**: Accurate preoperative T staging is essential in esophageal cancer, particularly in China. Standard imaging methods remain suboptimal; radiomics and tumor length (TL) may enhance predictive precision through multimodal AI integration. • **Methodology:** A five-center retrospective cohort (n=974) underwent contrast-enhanced CT analysis. ROIs were segmented via nnU-Net, and radiomic features harmonized and reduced (mRMR/LASSO). The TL-augmented 3D CliMamba model integrated clinical, radiomic, and TL data using a Transformer-based architecture, trained with AdamW and validated via DeLong testing. • **Results:** The TL-augmented model achieved accuracy 0.812, recall 0.720, F1 0.725—outperforming clinical-only (0.755) and imaging-only (0.782) models, showing superior T1–2 vs. T3–4 discrimination. • **Conclusions:** Integrating TL into a multimodal deep learning framework improves staging accuracy and robustness, supporting personalized, noninvasive management in esophageal cancer.
12 Nov 2025	AI as a second reader in mammography: Multi-million image training, validation across populations, and NHS integration potential	Maryam Arshad	• **Introduction**: Artificial intelligence (AI) is rapidly transforming breast cancer screening by improving diagnostic accuracy, reducing workload, and aiding decision-making through deep learning-based mammography analysis. • **Methodology:** Three CE-marked AI systems—Transpara, HealthMammo, and ProFound AI—were compared across dataset scale, validation, NHS workflow integration, and cost. Evaluation focused on technical readiness, adoption, and clinical utility. • **Results:** Transpara (>1M images) showed highest NHS adoption (4 trusts) and broad vendor compatibility. ProFound AI (~2M images) demonstrated strong DBT capability but high cost, while HealthMammo (>500K cases) lacked UK validation. • **Conclusions:** Transpara shows the strongest NHS readiness. Broader adoption of AI-assisted mammography requires IT infrastructure, workflow integration, prospective validation, and cost-effectiveness studies to enable scalable, reliable deployment.

Notable Presentations At ESMO - AI 2025

Radiomics & Imaging AI (6/12)

Date	Title	Author	Summary
12 Nov 2025	CNN-based osteoporosis prediction from 99mTc-HDP bone scintigraphy	Byeonghyeon Byeon	**Introduction**: Dual-energy X-ray absorptiometry (DXA) is the gold standard for osteoporosis diagnosis but limited by access and cost. This study assessed whether technetium-99m bone scintigraphy analyzed by a 2D convolutional neural network (CNN) could predict osteoporosis. **Methodology:** In 352 patients with normal 99mTc-HDP scans and matched DXA, CNNs (2–32 layers) and benchmark models (VGG16/19, ResNet50/101) were trained (7:1:2 split) under varying inputs, normalization, and learning rates **Results:** A 4-layer CNN with posterior-view input, normalize factor 150, and learning rate 0.001 achieved AUC 0.946 (internal) and 0.920 (external), outperforming ResNet50 (0.827). Posterior images yielded stronger predictive signal than anterior **Conclusions:** Compact CNN analysis of routine bone scintigraphy enables accurate, accessible osteoporosis prediction, supporting its use as a cost-effective DXA alternative pending multi-centre validation.
12 Nov 2025	Personalized artificial intelligence model for longitudinal prediction of long-term survival in advanced ovarian cancer	Marina N. Rosanu	**Introduction**: Accurate long-term survival prediction in epithelial ovarian cancer (EOC) supports tailored management. This study developed a dynamic AI model predicting survival at diagnosis, post-surgery, and post-chemotherapy. **Methodology:** Among 1688 FIGO III–IV EOC patients (920 PDS, 768 IDS), IPCW-adjusted logistic regression generated predictions at three timepoints, assessed by AUC. **Results:** Performance improved over time: PDS AUC 0.60→0.77; IDS 0.58→0.74. Key predictors evolved from CA125/BMI to residual tumor and early recurrence. **Conclusions:** This interpretable AI model enhances individualized risk stratification and long-term outcome prediction in advanced EOC.

Notable Presentations At ESMO - AI 2025

Radiomics & Imaging AI (7/12)

Date	Title	Author	Summary
12 Nov 2025	Validation of AI-assisted RECIST target lesion measurement in follow-up CT	Rianne A. Weber	• **Introduction**: RECIST is the standard for assessing tumor response but suffers from inter-observer variability. This study evaluated AI-assisted lesion measurement to enhance consistency and efficiency. • **Methodology:** Twenty-three readers assessed 212 oncology CT scans with and without AI-suggested diametric measurements. Variability and reading time were compared using Bayesian mixed models. • **Results:** AI reduced patient-level variability (RECIST disagreement 49.1%→32.5%) and decreased mean reading time (105s→71s). Lesion-level variability slightly increased (1.32 mm). • **Conclusions:** AI-assisted RECIST improves inter-reader consistency and efficiency, minimizing patient-level discrepancies and accelerating radiologic response assessment.
12 Nov 2025	Non-invasive prediction of Ki-67 in meningiomas from preoperative MRI using a transformer-based multimodal model with flexible input	Haoze Jiang	• **Introduction**: Ki-67 is a key meningioma biomarker but requires invasive biopsy. This study developed a Transformer-based multimodal AI model for noninvasive Ki-67 prediction using preoperative MRI and assessed its role in tumor growth forecasting. • **Methodology:** In 1011 cases across multiple centers, radiomics and deep learning MRI features were fused within a Transformer with flexible input. Performance was validated internally and externally, with Grad-CAM interpretability. • **Results:** The model achieved AUC 0.80 (internal) and 0.804 (external); 3- and 5-year growth predictions reached AUC 0.755 and 0.725, respectively. • **Conclusions:** This multimodal Transformer enables accurate, interpretable, noninvasive Ki-67 prediction and risk stratification in meningiomas.

Notable Presentations At ESMO - AI 2025

Radiomics & Imaging AI (8/12)

Date	Title	Author	Summary
12 Nov 2025	Diffusion-based HRD Score Prediction from H&E Stained Whole-Slide Images in Breast and Gynaecologic Cancers	Ionut Gabriel Funingana	• **Introduction**: Homologous recombination deficiency (HRD) guides PARP inhibitor use but is often binarized, losing biological nuance. This study introduces a diffusion-based pathology AI model for continuous HRD score prediction from H&E whole-slide images (WSIs). • **Methodology:** Using WSIs and CNV data from TCGA BRCA, UCEC, and OV cohorts, WSI embeddings were processed via a diffusion regression framework integrating auxiliary variables (e.g., TP53 status, cancer type) for robust, uncertainty-aware training. • **Results:** The model outperformed MIL baselines, achieving AUCs of 83.3% (BRCA), 88.6% (UCEC), and 83.0% (OV), with 2–10% relative gains and improved reliability through uncertainty quantification • **Conclusions:** Diffusion-based modeling enables continuous, uncertainty-aware HRD prediction, enhancing biomarker precision and interpretability across cancers.
12 Nov 2025	Uncertainty estimation of AI-driven volumetric measurements in CT scans: A pleural mesothelioma use-case	Valerio Pugliese	• **Introduction**: AI tumor segmentation lacks uncertainty estimation, limiting clinical trust. This study introduces a model-agnostic method to generate credibility intervals for tumor burden on CT. • **Methodology:** A nnU-Net trained on pleural mesothelioma (n=100) produced voxel-wise probabilities, clustered spatially, and sampled via Monte Carlo (N=1000) to derive volume intervals. • **Results:** Model calibration was excellent (ECE = 2×10^{-4}). Median interval width was 70 mL (24% relative), strongly correlated with tumor size ($\rho = 0.81$). • **Conclusions:** This uncertainty-aware framework enhances reliability of AI-based tumor tracking for longitudinal cancer monitoring.

Notable Presentations At ESMO - AI 2025

Radiomics & Imaging AI (9/12)

Date	Title	Author	Summary
12 Nov 2025	Anatomical site classification of ovarian cancer whole slide images for multi-site outcome prediction	Hannah Clayton	• **Introduction**: Ovarian cancer's multi-site nature affects treatment and outcomes, yet computational pathology often ignores anatomical variation due to missing site labels. This study developed an AI model to classify tumour site from H&E whole-slide images (WSIs). • **Methodology:** From 2006 WSIs (105 patients), nine anatomical sites were manually labelled. Slide embeddings from four foundation models trained a multilayer perceptron (MLP), compared with a ResNet50 on low-resolution images • **Results:** Best MLP (TITAN) achieved AUROC 98.1%, F1 80.8%, outperforming ResNet50 (AUROC 95.4%). Misclassifications occurred mainly between adjacent sites. • **Conclusions:** Foundation model embeddings enable accurate site classification, supporting scalable, site-aware ovarian cancer prognostic modelling.
12 Nov 2025	Beyond nodules: AI for comprehensive lung tumor segmentation on CT	Valerio Pugliese	• **Introduction**: Most AI tools for lung lesions target nodules <30 mm. This study developed a universal segmentation model for lung tumors of all sizes and histologies. • **Methodology:** A dataset of 982 CT scans from 491 lung cancer patients plus 100 negative controls was used. Lesions were manually annotated and classified. A Residual Encoder nnU-Net was trained and externally validated on two public datasets. • **Results:** Internal DSC = 90.4%, NSD = 99.3%, recall = 85.5%. External datasets achieved recall = 100%, DSC ≈ 87%, NSD ≈ 97%. Performance was highest for large primaries. • **Conclusions:** The model enables accurate, size-independent lung tumor segmentation, supporting longitudinal tracking and preoperative planning.

Notable Presentations At ESMO - AI 2025

Radiomics & Imaging AI (10/12)

Date	Title	Author	Summary
12 Nov 2025	Comparative performance of AI-based chest X-ray interpretation versus radiologist in annual health screening: A single-center retrospective analysis of 2,331 healthcare workers	Passakorn Wanchaijiraboon	- **Introduction**: AI-assisted chest X-ray (CXR) interpretation may enhance screening efficiency amid radiologist shortages. This study compared a commercial AI system with radiologist readings in a real-world employee health screening program. - **Methodology:** In 2,331 CXRs from healthcare workers, QXR AI outputs were compared to radiologist interpretations. Sensitivity, specificity, predictive values, accuracy, and Cohen's Kappa were analyzed. - **Results:** AI showed sensitivity 73.4%, specificity 93.7%, PPV 39.7%, NPV 98.4%, accuracy 92.7%, and κ = 0.48. False positives (5.9%) exceeded false negatives (1.4%). - **Conclusions:** AI achieved high specificity and NPV but moderate sensitivity, indicating over-detection; suitable for screening support with radiologist oversight.
12 Nov 2025	Automatic CT segmentation for high-burden metastatic liver disease	Jeroen Cant	- **Introduction**: Accurate segmentation of liver metastases on CT is vital for diagnosis and treatment planning but manual contouring is inefficient. This study evaluated segmentation models under varying training sizes and annotation quality. - **Methodology:** Pretrained (VISTA-3D), from-scratch (nnU-Net 2D/3D), and fine-tuned (TotalSegmentator-based) models were compared using 547 annotated CT scans and validated on 37 test scans (1,209 lesions). Performance was assessed via lesion-level sensitivity, precision, and Dice score. - **Results:** The fine-tuned nnU-Net 3D achieved best results—sensitivity 0.431, precision 0.860, median DSC 0.748—outperforming pretrained and scratch-trained models. - **Conclusions:** Fine-tuning on high-quality annotations maximizes segmentation accuracy, reducing radiologist workload in liver metastasis assessment.

Notable Presentations At ESMO - AI 2025

Radiomics & Imaging AI (11/12)

Date	Title	Author	Summary
12 Nov 2025	Explainable deep learning for FDG PET/CT tumor detection: Evaluation on a pan-cancer dataset	Rebecca Romanò	- **Introduction**: FDG PET/CT is essential for oncologic assessment but interpretation is time-intensive. This study retrained a deep learning (DL) pipeline for multi-tumor PET classification to enable automated, explainable detection. - **Methodology:** Using 1,014 TCIA PET/CT scans (501 tumor-positive, 513 negative), a 2D ResNet34 model was tested and retrained with 5-fold cross-validation, then externally validated on the APOLLO11 NSCLC cohort. Grad-CAM provided explainability. - **Results:** Retraining improved accuracy from 82% to 93%, specificity to 94%, and maintained biologically relevant heatmaps confirming tumor localization. - **Conclusions:** DL PET/CT analysis enables accurate, interpretable multi-cancer detection, supporting future multimodal diagnostic integration.
12 Nov 2025	Artificial intelligence-supported early detection of lung cancer from chest x-ray in routine clinical practice: Real-world, multicenter study across Czech hospitals	Karolina Kvakova	- **Introduction**: AI-assisted chest X-ray (CXR) interpretation may enable earlier detection of thoracic malignancy within routine workflows. This large real-world analysis evaluated the Carebot–BMS AI triage system across multiple hospitals in Czechia. - **Methodology:** From Jan–Jun 2025, 96,459 CXRs across nine hospitals were analyzed using Carebot AI. A multidisciplinary panel reviewed AI-flagged cases for malignancy suspicion and follow-up outcomes. - **Results:** AI flagged 16.6% of exams; 0.87% were deemed suspicious. Among 561 with follow-up, 54 new thoracic cancers and 70 known malignancies were confirmed. - **Conclusions:** AI triage integrated into routine screening identified early thoracic malignancies while triaging <1% of CXRs, supporting scalable real-world deployment.

Notable Presentations At ESMO - AI 2025

Radiomics & Imaging AI (12/12)

Date	Title	Author	Summary
12 Nov 2025	Non-invasive prediction of liver tumor entity from CT using artificial intelligence	Leo Misera	- **Introduction**: Identifying liver tumor entity is crucial for personalized treatment but typically requires invasive biopsy. This study evaluated Merlin, a 3D CT foundation model, for noninvasive tumor classification. - **Methodology:** Using 582 portal venous–phase CTs (2016–2023) with histologically confirmed tumors, Merlin was fine-tuned to classify six entities: HCC, CC/GA, NET, GIT, BRE, and PAN. Five-fold cross-validation and independent temporal testing (n=111) assessed performance by AUC. - **Results:** Merlin achieved excellent accuracy for HCC (AUC = 0.969 [0.937–0.993]) and moderate-to-good results for other entities (AUC = 0.62–0.84). - **Conclusions:** Merlin enables accurate, noninvasive liver tumor classification from CT, offering a potential alternative to biopsy for clinical decision-making.

Key Industry Sponsored Sessions Information

ESMO – AI 2025 Key Industry Sponsored Sessions Information (1/2)

Date	Sponsor	Title
12 Nov. 2025	AstraZeneca	The Future of AI in Healthcare: From Promise to Practice
12 Nov. 2025	DoMore Diagnostics	Decoding tumour histology with AI to personalise treatment
12 Nov. 2025	Pierre Fabre Laboratories	Promises and limitations of AI in Dermato-Oncology
13 Nov. 2025	Bowhead Health	No Room for Hallucinations: Building AI You Can Trust for Oncology Guidelines and Trials
12 Nov. 2025	myTomorrows	Practical AI for Trial Recruitment: Human-in-the-Loop Tools for Patients, Physicians, and Sites
12 Nov. 2025	Flatiron Health	The VALID Framework for LLM-Extracted Oncology Data Quality
12 Nov. 2025	Medable	Harnessing AI Agents to Overcome the Complexity of Oncology Trials

ESMO – AI 2025 Key Industry Sponsored Sessions Information (2/2)

Date	Sponsor	Title
13 Nov. 2025	AstraZeneca	Unlocking the Petential of AI in Precision Oncology
13 Nov. 2025	Careology	Empowering Patients with Connected, AI-Powered Cancer Care
13 Nov. 2025	Johnson & Johnson	Unlocking the Future of Oncology Through AI: Together for Tomorrow’s Patients
13 Nov. 2025	Vintura	Collaborative Care Meets AI: Shaping the Future of Oncology Care
13 Nov. 2025	Negedia	Machine Learning meets transcriptomics: Negedia Pathology an innovative tool bridging clinical practice and biomarker discovery
14 Nov. 2025	TwinEdge Biosciences	Digital twins of cancer patients bringing Phase III clinical trial scale insights throughout the drug development lifecycle
14 Nov. 2025	Real Chemistry	Bridging Innovation and Adoption of AI in Cancer Care
14 Nov. 2025	Bayer AG and Aignostics GmbH	Decoding Disease Biology: Aignostics-Bayer Partnership Develops a Novel, Reusable Platform for Target Identification

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