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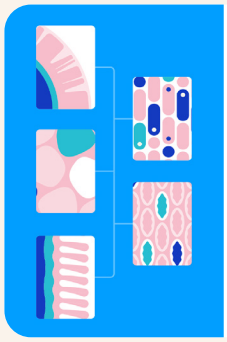
Owkin's latest publications

Get closer to our science

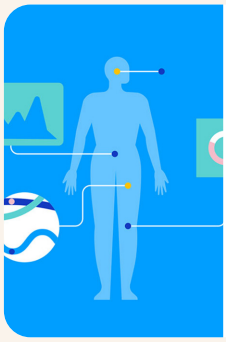
Pushing the boundaries of machine learning for biomedical applications

Our abstracts at ESMO



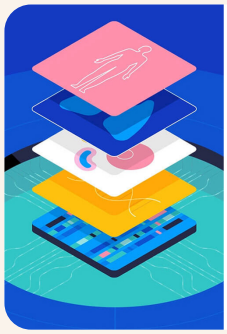
POSTER #327P

Development and validation of BRCAura: A histology model to predict germline BRCA1/2 mutations from HR+/HER2- breast cancer images



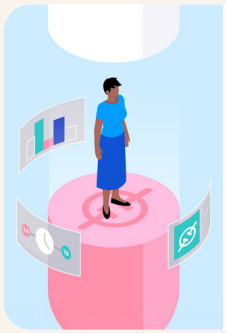
EPOSTER #1756EP

Towards achieving full MSI reflex testing in CRC, GC and EC: an efficient and streamlined approach using deep learning



EPOSTER #181EP

Harnessing Spatial Biology & AI to Optimize ADC Clinical Development Strategies



EPOSTER #238EP

Context-based drug positioning and multimodal characterization for OKN4395

AI & ML methodological innovations

We generate AI methodological innovations that push the boundaries of machine learning for biomedical applications

2025	FedECA: federated external control arms for causal inference with time-to-event data in distributed settings	nature communications
2025	OwkinZero: Accelerating Biological Discovery with AI	arXiv
2025	Towards Comprehensive Cellular Characterisation of H&E slides	arXiv
2025	H0-mini: Distilling foundation models for robust and efficient models in digital pathology	arXiv
2025	Predicting gene essentiality and drug response from perturbation screens in preclinical cancer models with LEAP: Layered Ensemble of Autoencoders and Predictors	arXiv
2024	Phikon-v2, A large and public feature extractor for biomarker prediction	arXiv
2024	Robust evaluation of deep learning-based representation methods for survival and gene essentiality prediction on bulk RNA-seq data	SCIENTIFIC REPORTS
2023	PyDESeq2: a Python package for bulk RNA-seq differential expression analysis. Code available at: github.com/owkin/PyDESeq2	Bioinformatics

AI-driven biomedical breakthroughs

Developing AI models to discover new biology

2025	Deep learning assessment of metastatic relapse risk from digitized breast cancer histological slides	nature communications
2025	MOSAIC Window: Spatial intra-tumoral heterogeneity characterization through large-scale spatial and single-nuclei multi-omics profiling	AACR
2025	Transcriptome Analysis of Archived Tumor Tissues by Visium, GeoMx DSP, and Chromium Methods Reveals Inter- and Intra-Patient Heterogeneity	nature communications
2024	MISO: A deep learning-based multiscale integration of spatial omics with tumor morphology	bioRxiv
2024	AI allows pre-screening of FGFR3 mutational status using routine histology slides of muscle-invasive bladder cancer	nature communications
2024	Histology-based prognosis prediction using deep learning outperforms and is independent of the MGMT methylation status in patients with Glioblastoma	AACR
2023	Deep learning predicts patients outcome and mutations from digitized histology slides in gastrointestinal stromal tumor	npj | precision oncology
2023	Validation of MSIntuit as an AI-based pre-screening tool for MSI detection from colorectal cancer histology slides	nature communications
2023	PACpAInt: a histology-based deep learning model uncovers the extensive intratumor molecular heterogeneity of pancreatic adenocarcinoma	nature communications
2023	HealthChain: Federated learning for predicting histological response to neoadjuvant chemotherapy in triple-negative breast cancer	nature medicine
2020	HE2RNA: A deep learning model to predict RNA-Seq expression of tumors from whole slide images. Top 50 articles of 2020 award	nature communications
2019	Deep learning predicts prognosis in mesothelioma independently of current histological classification and refines current prognostic criteria	nature medicine

73 scientific publications

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