



AI for better cell therapy

July 2021

Thomas Clozel, MD, co-founder and CEO, OWKIN



Presentation of OWKIN



WHO WE ARE

We have assembled a unique team of top talents in clinical AI & senior pharma executives, supported by leading international investors

100 people at Owkin

- + 30 World Class Data Scientists (2 Kaggle GrandMaster) - 19 publications in high impact journals in 4 years (Nature Medicine, Nature Comm)
- + 15 Software Engineers who created a framework used for the first-ever federated deep learning model trained on histology images stored behind hospital firewalls & used by 10 pharma companies.
- + 10 marketing and sales in 3 countries
- + 15 academic partnerships people in 4 countries
- + 5 IT / 10 products / 20 support people

A high academic level

- + 95% of people with Master's degree
- + 30% of people with PhD / MD

A young and diversified population

- + 16 C-levels: 8 females, 8 males
- + Average age 33 years
- + 15 nationalities



THOMAS CLOZEL
Founder, CEO

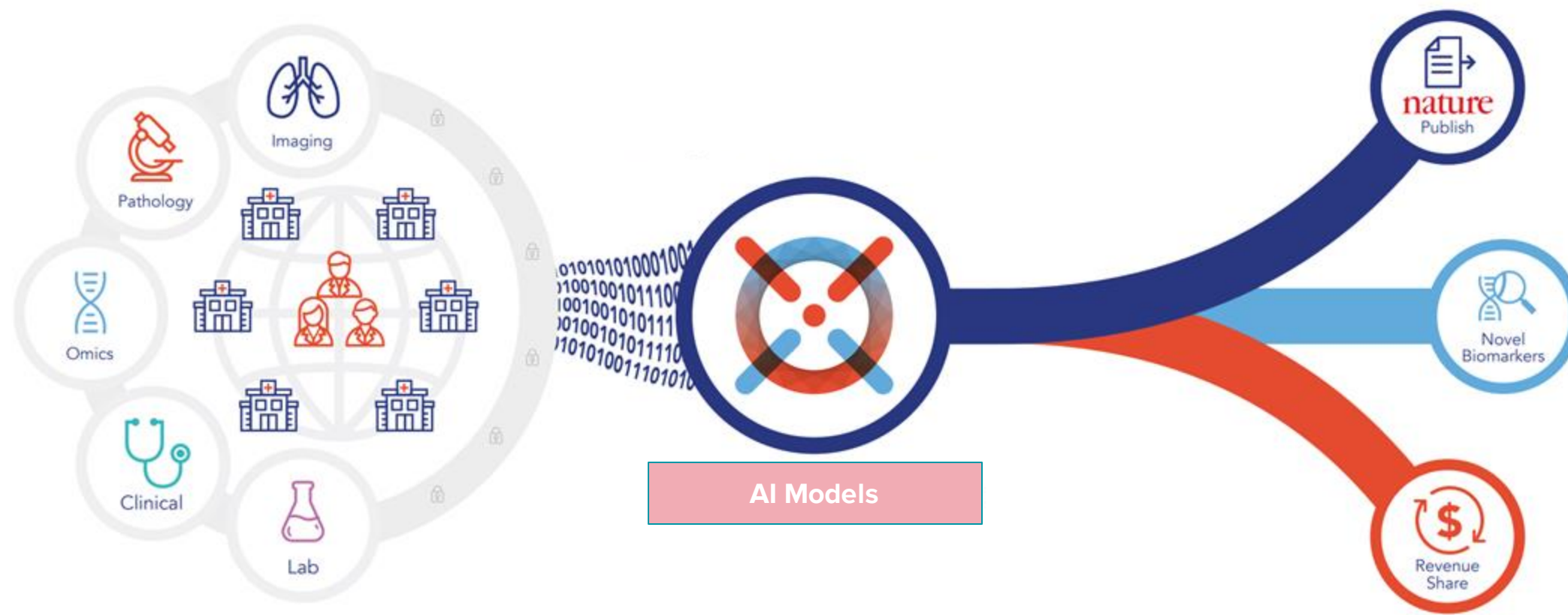


GILLES WAINRIB
Founder, CSO



OUR FEDERATED RESEARCH PLATFORM

Our AI: connecting dots between modalities and explainable



PATHOLOGY ANCHORING

MULTI MODAL BIOMARKERS

Right QUESTIONS



Questions that matter in immunotherapy and cellular therapies

General questions:

Can we predict non responders to immune therapies?

Can we create rationale for IO drug combination?

More specifically, can we predict responders to CART?

Can we predict CRS?

By tissue of origin:

Can we identify with multi modal biomarkers rare responders to IO in prostate cancer?

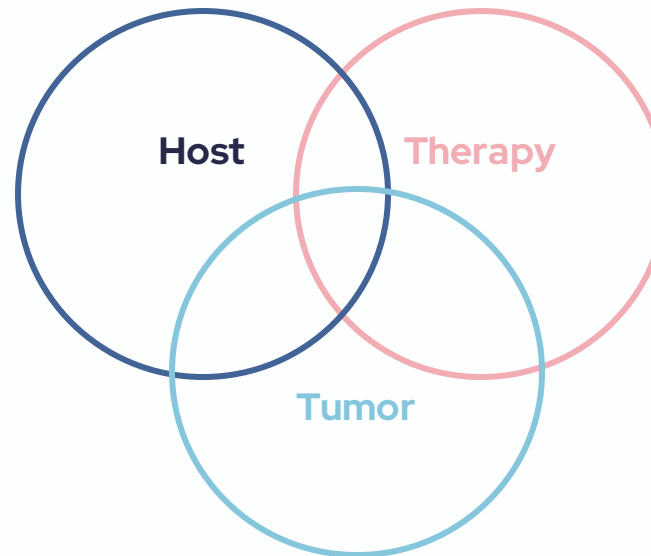
Why did CAR NK fail in NSCLC?

Can we predict whose MM patients will not respond to CART?

Can we predict toxicity to IO bitherapies in melanoma?

Cellular therapies response

Data-driven and multi modal determination of factors of response of host, tumor, and cell injected to cellular therapies



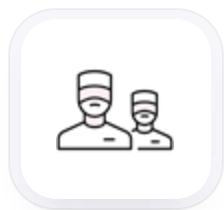
Right DATA ACCESS



Important data differentiators



Data at source
trusted origin & up
to date



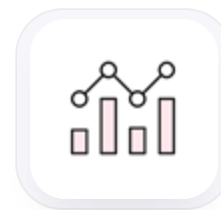
Curated by
KOLs



Highly
dimensional



CT-Scan IHC H&E Stains MRI RNA-Seq



Rich longitudinal
follow up

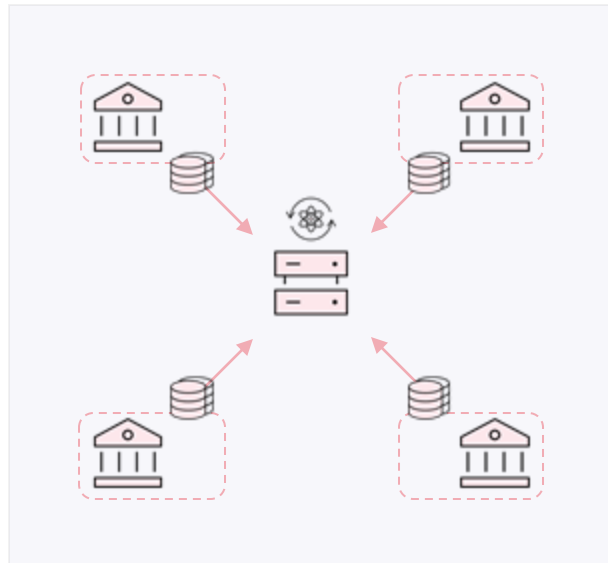


Privacy
preserving
data access

Overcoming the data sharing problem with Federated Learning

For AI models, **the more data the better** for generalization performance...

The **standard approach** requires data pooling and central coordination:



More:

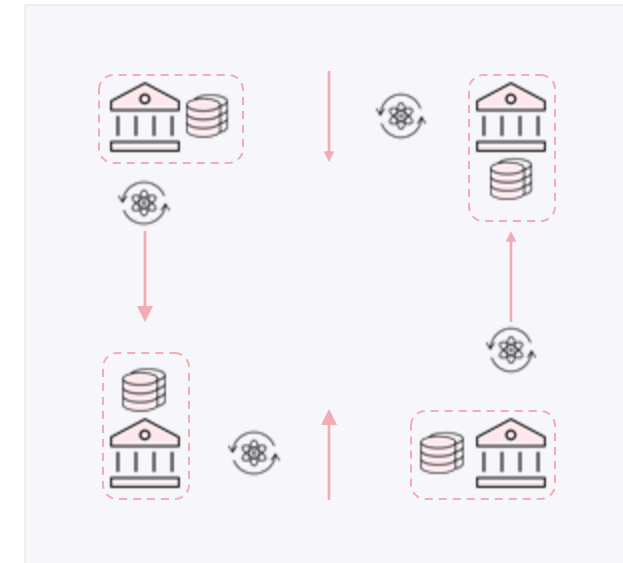
SECURE

COMPLIANT

COLLABORATIVE

...and building models on **non-located datasets** is possible with **Federated Learning**:

FL algorithms can be trained remotely, preserving the security and privacy of distributed data



Our platform is powered by Owkin Connect: an end-to-end software for Federated Learning



Collaboration
Insight generation



Compliance
Data management



Confidentiality
Privacy-preserving FL

- Owkin Connect is **deployed in Owkin hospital network** to enable federated data collaborations.
- Owkin Connect is also **deployed in the MELLODDY consortium (IMI)**, connecting **10 large pharmaceutical companies** to develop machine learning models for drug discovery across their molecular libraries databases, demonstrating the **high level of security and privacy** offered by our software.

MELLODDY
PHARMA PARTNERS

AMGEN

astellas

AstraZeneca

BAYER

**Boehringer
Ingelheim**

gsk

janssen
Janssen-Cilag

Merck

NOVARTIS

SERVIER

Right AI technology



Horizontal versus Vertical approaches for biomarker discovery and prediction accuracy

Vertical Approach
Mono Data

Benefits of the multi-modal approach

1. We deal with very complex phenomena where **we need the full picture** of a patient to understand what really happens
2. One modality alone [ex: bulk sequencing data] is often very hard to decrypt due to the mixture of many different signals, combining information with other modalities [ex: images] helps a lot to **deconvolute the molecular data and better understand the underlying patterns**

Horizontal Approach - Multi-modal data



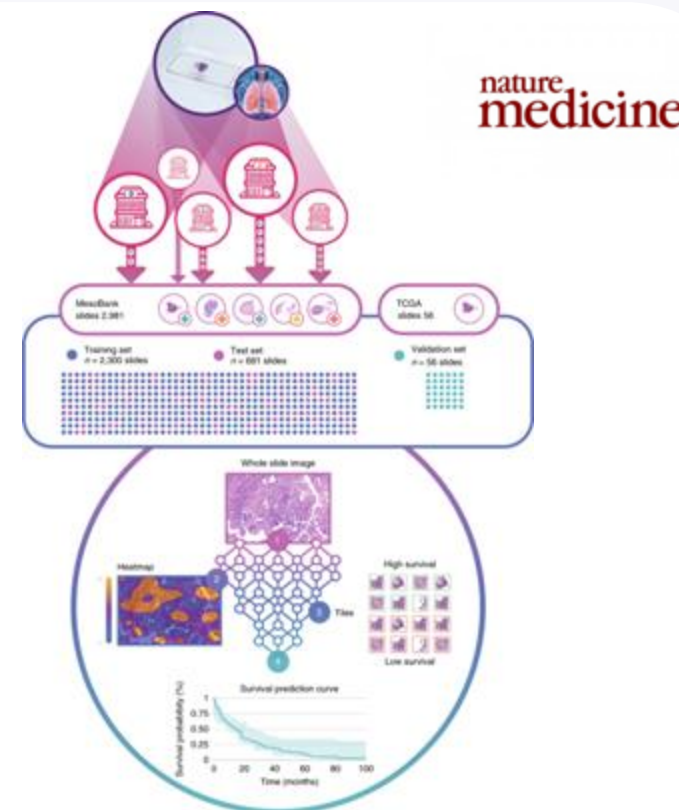
MESONET: A Model to Predict Overall Survival

Owkin used its AI technology to better predict and explain overall survival in patients with mesothelioma, outperforming current pathology practices

Deep learning-based classification of mesothelioma improves prediction of patient outcome

- Accessed top-tier research cohort Mesopath/Mesobank (N=2,981)
- Identified tiles of interest from WSIs using Owkin's **proprietary technology CHOWDER** – the deep learning architecture uniquely suited to extract **interpretable features** from images
- Discovered **new biomarkers predictive of prognosis in collaboration with expert mesothelioma pathologists**: stroma, tumor cell localization, inflammation, cellular diversity & vascularisation
- Being investigated to optimize mesothelioma clinical trials

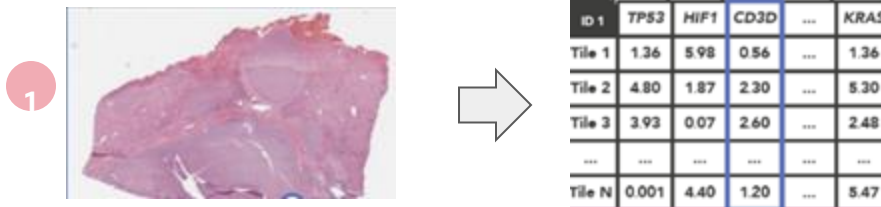
MesoNet



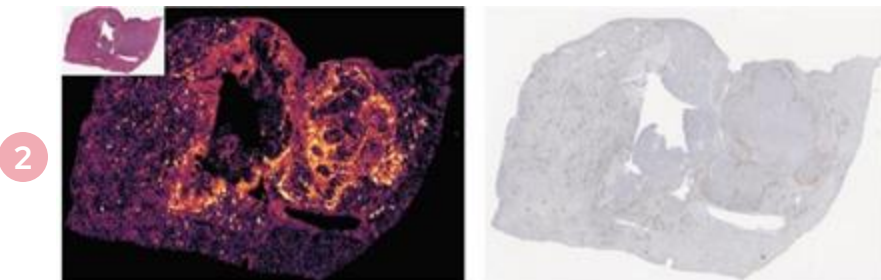
HE2RNA: A model to predict gene expression

Owkin developed a model able to extract molecular features from histology images alone, providing a powerful tool to enhance clinical practice – from diagnosis to treatment optimization.

A deep learning model to predict RNA-Seq expression of tumours from whole slide images



Transcriptome prediction from histology images without associated RNA-seq



For each predicted gene, a score is calculated and may be used to generate "heatmaps" of gene expression

HE2RNA

nature
COMMUNICATIONS



The virtual spatial representation of a gene expression profile is especially important for predicting immune response, and may be used to:

- Determine eligible patients for immunotherapy from routine histological information, **without the need for NGS**
- Identify **novel biomarkers in images** of specific tumoral regions that are important for the development of cancer



Thank you

November 2021

