Case Study

Talk*: *"Oncode Accelerator Summit '24, Andreas Bender, Data-driven drug discovery using AI"

Date:
28th of June, 2024

Speaker:
Prof. Andreas Bender

Affiliations:
Pharmedic

Project:
Pharmedic 2025 Internship Program
Product & Technology Dept.

Mahra.alhosani@pharmedic.ae

“How to bring the right drug to the right patient in the right way?”

-Prof. Andreas Bender

Prof. Andreas Bender serves as the Chief Technology Officer (CTO) at PangeaBIO ltd and incoming Professor for Machine Learning in Medicine at Khalifa University in Abu Dhabi, United Arab Emirates. He discussed the challenges and current status of applying Artificial Intelligence (AI) in drug discovery and model training.

While machine learning (ML) models evolved far beyond traditional linear regression, the models' ability to identify patterns in the fields of pharmacokinetics and pharmacodynamics are limited. Whether we train AI, ML, or Deep learning (DL) models, data must be labeled during the preliminary model supervised training trials. While unsupervised or semi-supervised learning are emerging to deal with unlabeled omics data, given the nature of human biology, accurately predicting the drug metabolism, bioavailability, efficacy, and safety profile is an intricate matter. Capturing the vast array of interdependent variables such as drug bioavailability, affinity, receptor subtypes (receptor selectivity, affinity, upregulation, intolerance, etc.). CYP450 polymorphisms, diagnostic history, lifestyle, chronological age, gender, prior medication history, diet, supplements, and individual tolerance.

The development of adverse drug reaction (ADR) models has played a vital role in clinical and pharmaceutical drug discovery and development. However, progress is significantly impeded by the lack of high-quality, labeled data. Supervised machine learning and deep learning methods rely on clearly defined input-output mappings, yet the biological, pathological,

Mahra.alhosani@pharmedic.ae

and chemical data relevant to ADRs are inherently complex, continuous, and often omic dependent. This makes accurate labeling extremely challenging. Numerous confounding variables, such as dosage, patient genotype, comorbidities, and drug interactions, further complicate the training process. As a result, building robust models capable of reliably assessing drug safety, interactions, efficacy, and adverse effects remains a major challenge in the field. Prof. Bender emphasized on mitigation strategies, particularly the stratification of patient data, the integration of multi-omics datasets during gene expression analysis as viable strategies for advancing precision medicine.

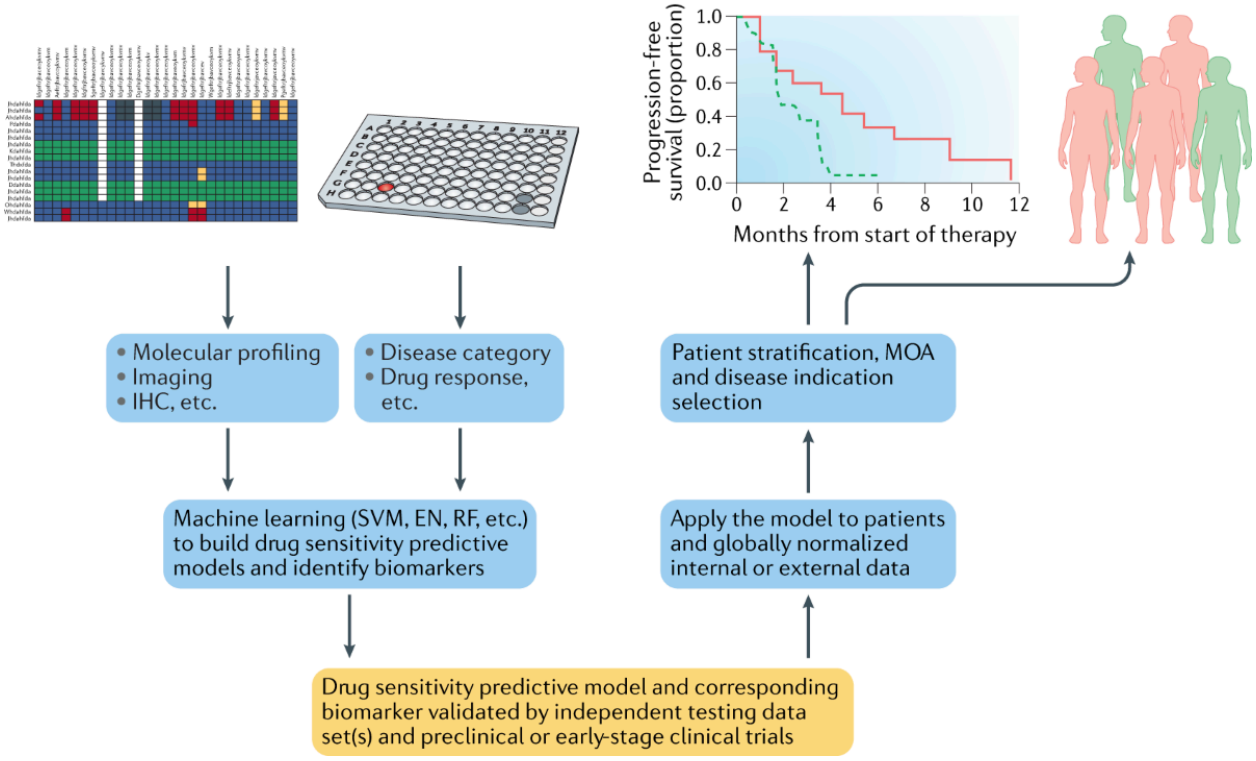


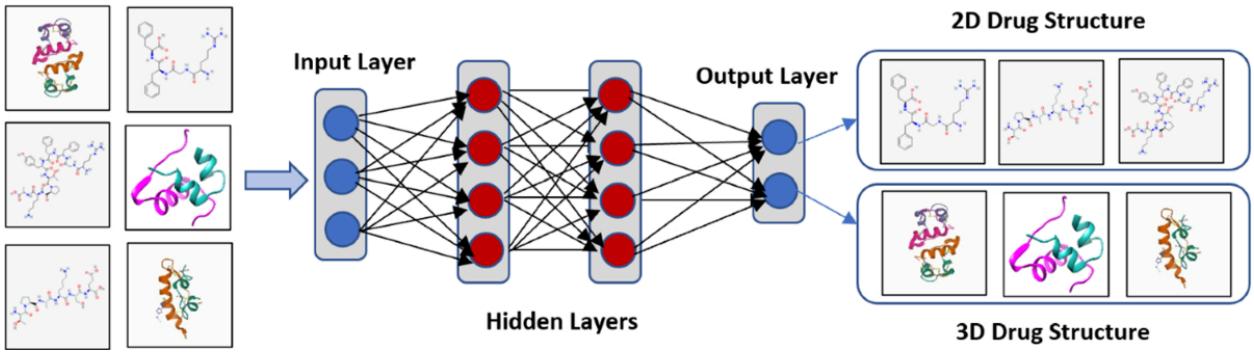
Fig 1. Workflow for predictive drug modeling.

Current research using omics data to select compounds that induce stem cells differentiation, for instance into cardiomyocytes serve as a testament towards regenerative medicine. Additionally, the speaker touched on the use omics-guided compound selection to transform cancer cells into dendritic-like cells (CDC1). These approaches can be employed to chemically reprogram specific cell types into immune-activating cells at a more feasible rate compared to chimeric antigen receptor (CAR) T-cell therapy. For example, in CAR-T cell therapy, T cells are

Mahra.alhosani@pharmedic.ae

extracted from patients, engineered to express CARs, and reinfused to stimulate the immune system to target and destroy immunogenic cancer cells. This illustrates the potential success of cell-based immunotherapies in inducing effective anti-tumor immune mediated responses.

As per my studies in Data Science at CISCO, inferred data utilised with tree-based classifiers and neural networks DL models yield accurate predictions. These models provide extensive nodes and hidden layers that excel at capturing non-linear and multi-factorial physiological responses. Whether it be enzyme polymorphisms and drug interactions, which are often challenging to model using AI or ML linear regression algorithms. They are particularly effective in managing dimensional omics data and clinical variables. Thus, when integrated with patient stratification data, these models play a crucial role in supporting precision medicine pipelines as per patients genetic profile.



Thus to ensure the right drug is prescribed to the right patient in the right manner, we must eliminate the wage between computer scientists, data analysts, pharmacists, and physician pave the integration multi-omics data into clinical workflows and patient care. Aiming to enable tailored treatment as per biological profiles of individual patients.

Abbreviations

- AI: Artificial Intelligence
- ML: Machine Learning
- DL: Deep Learning
- ADR: Adverse Drug Reaction
- CYP450: Cytochrome P450

Mahra.alhosani@pharmedic.ae

- CAR: Chimeric Antigen Receptor
- CAR-T: Chimeric Antigen Receptor T-cell Therapy
- CDC1: Conventional Dendritic Cell Type 1
- ANN: Artificial Neural Network
- CNN: Convolutional Neural Network
- RNN: Recurrent Neural Network
- CISCO: Cisco Systems, Inc.
- UAE: United Arab Emirates
- T-cell: T Lymphocyte

References

1. Böttcher JP, Reis e Sousa C. The Role of Type 1 Conventional Dendritic Cells in Cancer Immunity. Trends Cancer. 2018 Nov;4(11):784-792. doi: 10.1016/j.trecan.2018.09.001. Epub 2018 Sep 29. PMID: 30352680; PMCID: PMC6207145.
2. Andreas Bender. Oncode Accelerator Summit '24: Data-driven drug discovery using AI. YouTube, 2024. Available at: https://www.youtube.com/watch?v=PJvJDrx6phI

Mahra.alhosani@pharmedic.ae

Mahra.alhosani@pharmedic.ae