

The Diagnostic Medicine Consortium: *Effector Arm of Clinical Lab2.0*



Vision

A healthcare ecosystem where every laboratory result becomes an actionable insight—powering earlier detection, smarter decisions, and better outcomes for entire populations through trusted, validated AI.

Mission

The Diagnostic Medicine Consortium (DMC) accelerates the adoption of clinically safe, equitable, and interoperable AI for laboratory medicine by delivering shared **tools**, **data services**, and **implementation playbooks** that enable laboratories to move from reactive confirmation to proactive prediction. We partner with laboratories, health systems, payers, and industry to operationalize population health solutions grounded in high-integrity diagnostic data, translate insights into closed-loop care pathways, and demonstrate measurable clinical and financial value for the communities our members serve.

Exemplar: DMC Trial Compass

Motivation

Today's trial-matching tools answer "*Which trials am I eligible for?*" but not the question patients and oncologists most need: "*Which trial is most likely to help this patient?*" DMC will transform longitudinal lab data and integrated chart context—combined with whole-genome tumor/normal NGS, curated molecular-pathology evidence, and population-level outcomes—into patient-specific forecasts that rank candidate trials by predicted likelihood of response and time-to-failure.

Expected service model

A subscription-based, cloud-delivered ***Trial Matching & Trial Forecasting*** service for health systems, oncology networks, and trial sponsors: automated eligibility screening, rapid genomic and clinical data harmonization, probabilistic odds ratios per trial arm using HMM/state-trajectory modeling, and clinician-ready reports with transparent evidence traceability—supported by DMC's concierge data science team and continuous model validation/monitoring across participating institutions.

The Building Blocks for such an approach...

- **State/trajectory modeling** (Markov / HMM / state-space models) on longitudinal biomarkers + time-to-event outcomes
- **Clinicogenomic ML** that estimates **treatment benefit heterogeneity** (who benefits more from regimen A vs B)
- **Multimodal integration** (notes + imaging reports + labs + genomics) to predict metastasis, PFS/OS, and adverse events
- **NGS/ctDNA models** (often HMM-based) to derive tumor fraction/copy-number signals that track response and progression



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Individualized survival predictions using state space model with longitudinal and survival data

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Monitoring disease progression often involves tracking biomarker measurements over time. Joint models (JMs) for longitudinal and survival data provide a framework to explore the relationship between time-varying biomarkers and patients' event outcomes, offering the potential for personalized survival predictions. In this article, we introduce the linear state space dynamic survival model for handling longitudinal and survival data. This model enhances the traditional linear Gaussian state space model by including survival data. It differs from the conventional JMs by offering an alternative interpretation via differential or difference equations, eliminating the need for creating a design matrix. To showcase the model's effectiveness, we conduct a simulation case study, emphasizing its performance under conditions of limited observed measurements. We also apply the proposed model to a dataset of pulmonary arterial hypertension patients, demonstrating its potential for enhanced survival predictions when compared with conventional risk scores.

1. Introduction

Safeguarding and enhancing patients' well-being is of paramount importance in healthcare, often necessitating ongoing monitoring. In recent years, numerous medical institutions have opted to store patients' information in electronic health records (EHRs) databases [1,2]. As time progressed, the potential inherent within this wealth of raw data, encompassing data from thousands of patients, became increasingly evident to researchers. These databases encompass a wide range of information, including diagnostic tests, laboratory results, medical procedures, their respective outcomes, and other medical occurrences that patients may encounter over their lifetimes [2–4]. The availability of such extensive healthcare data is progressively turning the aspiration of personalized treatment into a tangible reality.

Despite its advantages, EHR modelling is still relatively simplistic due to the difficulty encountered in applying conventional statistical methods [5,6]. Obtaining an accurate, parsimonious and explanatory model is hindered by many characteristics of EHRs, including heterogeneity, irregular timing of events, missing data, and lack of standardization, among others [1,2,4–6]. That being said, these databases typically contain richer and more realistic symptoms dynamics, additional biomarkers, and more frequent visits, when compared to clinical trials [1]. Despite the challenges posed by modelling such complex data, successful achievement in this endeavour holds the promise of enabling more precise outcome predictions and, consequently, the realization of personalized medicine.

“...we introduce the linear state space dynamic survival model for handling longitudinal and survival data. This model enhances the traditional linear Gaussian state space model by including survival data.”



Longitudinal latent overall toxicity (LOTox) profiles in osteosarcoma: a new taxonomy based on latent Markov models

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Abstract

Due to the presence of multiple types of adverse events (AEs) with different levels of severity, the analysis of longitudinal toxicity data is a difficult task in cancer research. The current literature primarily relies on descriptive-based methods and lacks models that can effectively quantify the overall toxic burden experienced by patients over treatment without losing details of the impact of each AE. In this work, a novel taxonomy based on latent Markov models and compositional data techniques is proposed to model the Latent Overall Toxicity (LOTox) condition of each patient over cycles of treatment. Starting from observed categories of severity of multiple toxicities, the goal is to delineate distinct LOTox conditions and retrieve patients' probabilities of being in a specific condition at a given cycle, as well as their risk of experiencing "worse" overall toxicity statuses compared to a reference "good" toxic condition. The proposed approach is applied to longitudinal toxicity data from the MRC BO06/EORTC 80931 randomized controlled trial for patients with osteosarcoma. The population of interest includes 377 patients who had successfully completed the six-cycle treatment. Personal characteristics and observed information on six toxicities are used to infer the unobserved LOTox status over the six cycles of chemotherapy. Provided that longitudinal toxicity data are available, the developed procedure is a flexible approach that can be adapted and applied to other cancer studies.

Keywords Categorical data · Compositional data · Latent Markov models · Longitudinal data · Osteosarcoma · Toxicity

1 Introduction

Being of interest in several research fields, including social, economic, and behavioral sciences, education, and public health, longitudinal data have prompted the development of numerous statistical models (see Fitzmaurice et al. (2009) for a

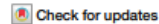
Extended author information available on the last page of the article

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“...Provided that longitudinal toxicity data are available, the developed procedure is a flexible approach that can be adapted and applied to other cancer studies.”

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Joint AI-driven event prediction and longitudinal modeling in newly diagnosed and relapsed multiple myeloma



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Multiple myeloma management requires a balance between maximizing survival, minimizing adverse events to therapy, and monitoring disease progression. While previous work has proposed data-driven models for individual tasks, these approaches fail to provide a holistic view of a patient's disease state, limiting their utility to assist physician decision-making. To address this limitation, we developed a transformer-based machine learning model that jointly (1) predicts progression-free survival (PFS), overall survival (OS), and adverse events (AE), (2) forecasts key disease biomarkers, and (3) assesses the effect of different treatment strategies, e.g., ixazomib, lenalidomide, dexamethasone (IRd) vs lenalidomide, dexamethasone (Rd). Using TOURMALINE trial data, we trained and internally validated our model on newly diagnosed myeloma patients ($N = 703$) and externally validated it on relapsed and refractory myeloma patients ($N = 720$). Our model achieved superior performance to a risk model based on the multiple myeloma international staging system (ISS) ($p < 0.001$, *Bonferroni corrected*) and comparable performance to survival models trained separately on each task, but unable to forecast biomarkers. Our approach outperformed state-of-the-art deep learning models, tailored towards forecasting, on predicting key disease biomarkers ($p < 0.001$, *Bonferroni corrected*). Finally, leveraging our model's capacity to estimate individual-level treatment effects, we found that patients with IgA kappa myeloma appear to benefit the most from IRd. Our study suggests that a holistic assessment of a patient's myeloma course is possible, potentially serving as the foundation for a personalized decision support system.

Multiple myeloma, the second most common blood cancer, has a global incidence of ~20,000 cases per year¹. Clinical management of multiple myeloma patients is complex, both in terms of the factors that impact physician decision-making as well as the overall goals of care. Several factors, including the stage of the disease, transplant status, functional status, and genetic profile, are considered in the initial treatment decision^{2,3}. Furthermore, effective care aims to maximize patient survival and time to disease progression while minimizing adverse events from therapy. When deciding on a treatment, striking an appropriate balance between optimizing patient survival while maintaining quality of life by limiting adverse events is intricate and requires frequent follow-up with patients. The International Myeloma Working Group recommends monthly (or bimonthly, depending on the therapy given as part of a follow-up or maintenance regimen) monitoring of patients receiving

initial chemotherapy for response to treatment, disease complications, and toxic sequelae of therapy⁴.

However, despite prior work focusing on prediction of individual aspects of cancer management, such as overall survival (OS)⁵⁻⁸, progression free survival (PFS)⁹, adverse events (AEs)¹⁰, or biomarker forecasting¹¹, no previous approach provides a holistic view of the patient's disease course by modeling the different facets of multiple myeloma management simultaneously. This narrow focus limits the clinical applicability of such models.

To address this gap, we developed a novel machine learning model called SCOPE, Simultaneous Cancer Outcome Prediction Estimator for multiple myeloma, which utilizes a transformer architecture¹² and techniques from survival analysis. Transformer architectures are attention-based models that have emerged as a powerful approach for capturing long-range dependencies and

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Automated real-world data integration improves cancer outcome prediction


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The digitization of health records and growing availability of tumour DNA sequencing provide an opportunity to study the determinants of cancer outcomes with unprecedented richness. Patient data are often stored in unstructured text and siloed datasets. Here we combine natural language processing annotations^{1,2} with structured medication, patient-reported demographic, tumour registry and tumour genomic data from 24,950 patients at Memorial Sloan Kettering Cancer Center to generate a clinicogenomic, harmonized oncologic real-world dataset (MSK-CHORD). MSK-CHORD includes data for non-small-cell lung ($n = 7,809$), breast ($n = 5,368$), colorectal ($n = 5,543$), prostate ($n = 3,211$) and pancreatic ($n = 3,109$) cancers and enables discovery of clinicogenomic relationships not apparent in smaller datasets. Leveraging MSK-CHORD to train machine learning models to predict overall survival, we find that models including features derived from natural language processing, such as sites of disease, outperform those based on genomic data or stage alone as tested by cross-validation and an external, multi-institution dataset. By annotating 705,241 radiology reports, MSK-CHORD also uncovers predictors of metastasis to specific organ sites, including a relationship between *SETD2* mutation and lower metastatic potential in immunotherapy-treated lung adenocarcinoma corroborated in independent datasets. We demonstrate the feasibility of automated annotation from unstructured notes and its utility in predicting patient outcomes. The resulting data are provided as a public resource for real-world oncologic research.

The ubiquity of electronic health records offers a largely untapped data substrate for translational medicine. Although abstraction of key elements from free-text patient visit, radiology, histopathology and procedural notes has traditionally limited analysis, natural language processing (NLP) now allows for automatic annotation of such features^{1,2}. Massive, context-aware transformer architectures³, including those pretrained on health records^{4,5}, have reshaped the NLP landscape and have shown promise at a number of medical tasks including predicting hospital readmission⁶ and providing medical advice⁷. In oncology, immunohistochemistry⁸ and clinical tumour sequencing⁹ are standard

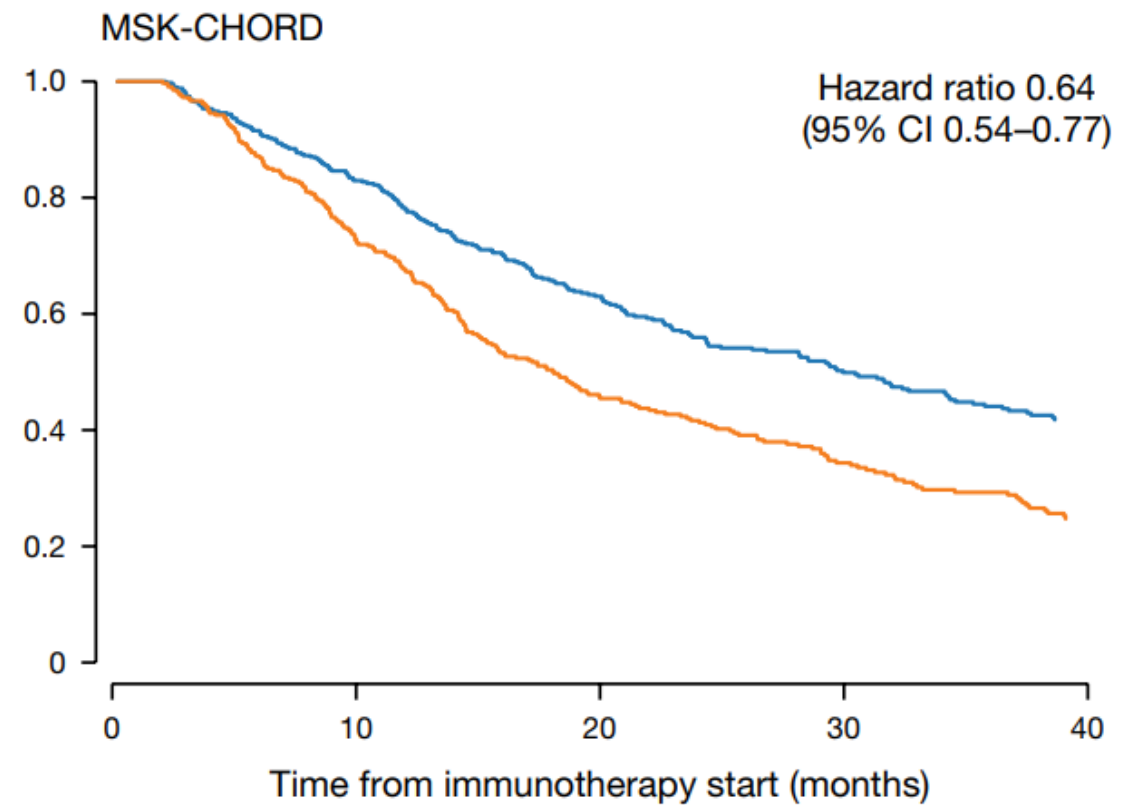
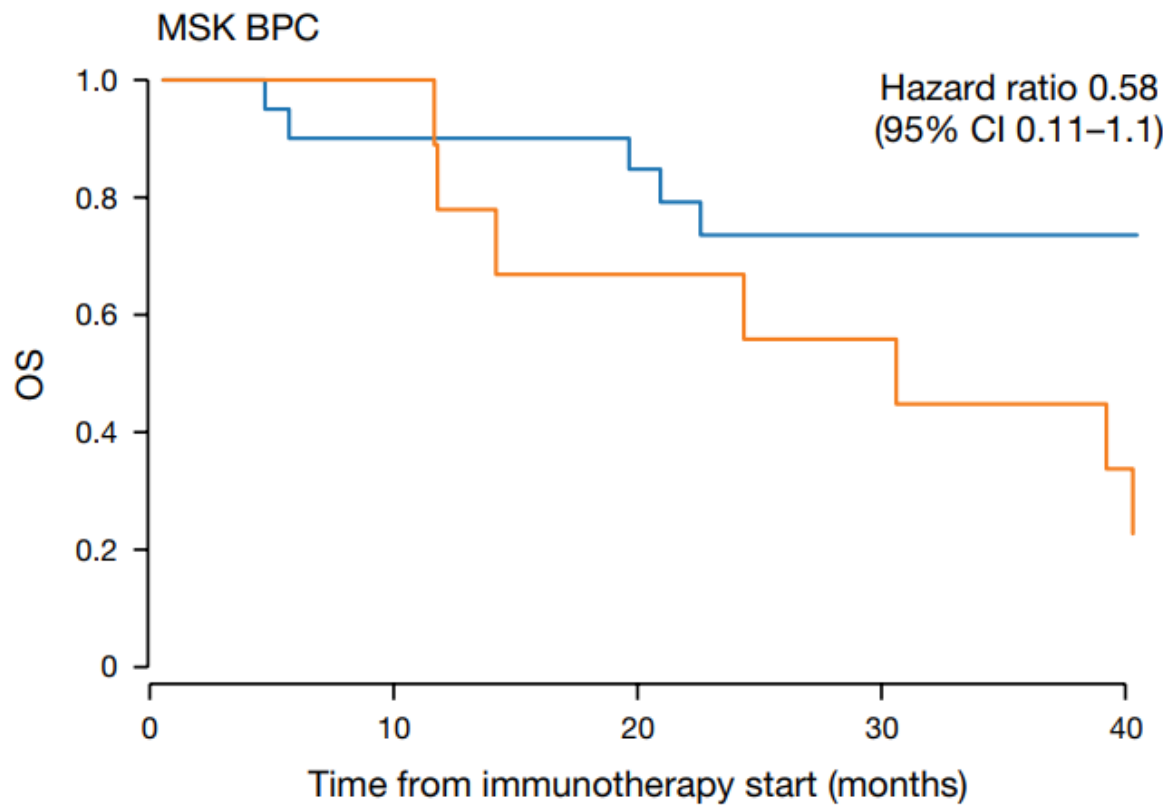
of care for many patients because of their potential to guide therapy. Combining real-world data (RWD) has enormous potential to aid in prediction of tumour trajectories.

The separation of hospital, academic and commercial entities responsible for genomic sequencing, radiology, histopathology and electronic health record data is a hurdle to integrative analysis¹⁰. Several studies have begun to overcome these silos (for example, through the integration of tumour sequencing with treatment data to uncover genomic modifiers of response¹¹, or the integration of billing codes to uncover mutations associated with specific organ sites of metastasis¹²).

“...The digitization of health records and growing availability of tumour DNA sequencing provide an opportunity to study the determinants of cancer outcomes with unprecedented richness...”

“...enables discovery of clinicogenomic relationships not apparent in smaller datasets. Leveraging MSK-CHORD to train machine learning models to predict overall survival...”

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At risk

PDL1 ⁺	20	18	15	9	1
PDL1 ⁻	9	9	6	5	2

At risk

	421	341	222	155	105
	323	231	137	88	52

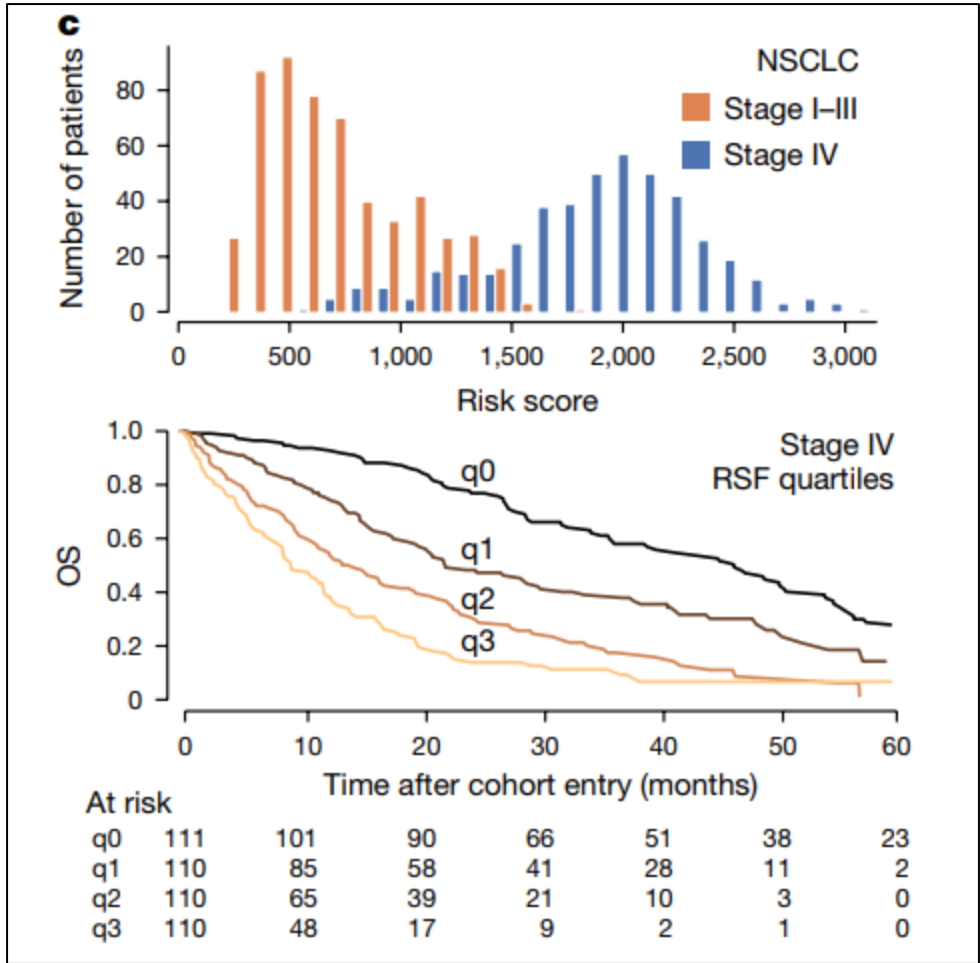




Fig. 4 | Analysis of time to metastatic site colonization. a, Time to metastatic site colonization among patients with LUAD, hormone-receptor-positive breast cancer, CRC with MSS, pancreatic adenocarcinoma (pancreas) and prostate cancer. Cohorts included the manually curated BPC and NLP-derived MSK-CHORD cohorts. **b**, Hazard ratios (colour), number of patients with alteration before site colonization (size) and statistical significance (Benjamini-Hochberg

false discovery rate of 0.01, black outline) within MSK-CHORD. Analyses are adjusted for prior treatment, stage and histologic subtype. Only genes with at least one significant association in at least one cancer type (Benjamini-Hochberg $q < 0.01$) are shown. The inset depicts Kaplan-Meier curves of the cancer type and metastatic site highlighted in the grey rectangle stratified by *RB1* status. WT, wild type.



Machine-learning driven strategies for adapting immunotherapy in metastatic NSCLC

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A list of authors and their affiliations appears at the end of the paper

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Check for updates

Immune checkpoint inhibitors (ICIs), either as monotherapy (ICI-Mono) or combined with chemotherapy (ICI-Chemo), improves survival in advanced non-small cell lung cancer (NSCLC). However, prospective guidance for choosing between these options remains limited, and single-feature biomarkers like PD-L1 prove inadequate. We develop a machine learning model using clinicogenomic data from four cohorts (MD Anderson $n = 750$; Mayo Clinic $n = 80$; Dana-Farber $n = 1077$; Stand Up To Cancer $n = 393$) to predict individual benefit from adding chemotherapy. Benefit scores are calculated using five distinct functions derived from 28 genomic and 6 clinical features. Our integrated model, A-STEP (Attention-based Scoring for Treatment Effect Prediction), estimates heterogeneous treatment effects and achieves the largest reduction in 3-month progression risk, improving weighted risk reduction by 13–23% over stand-alone models. A-STEP recommends treatment changes for over 50% of patients, most often favoring ICI-Chemo. In simulation on external cohort, patients treated in accordance with A-STEP recommendations show improved 2-year progression-free survival (HR = 0.60 for ICI-Mono treatment arm; HR = 0.58 for ICI-Chemo treatment arm). Predictive features include FBXW7, APC, and PD-L1. In this study, we demonstrate how machine learning can fill critical gaps in immunotherapy selection for NSCLC, by modeling treatment heterogeneity with real-world clinicogenomic data, driving precision medicine beyond conventional biomarker boundaries.

The increase in therapeutic options for patients with metastatic non-small cell lung cancer (NSCLC) has created the need for criteria to help providers select the therapy that carries the highest likelihood of benefit for an individual patient¹. While single-feature biomarkers have been identified for numerous targeted therapies, due to the tight correlation between therapeutic efficacy and the presence of certain genomic mutations, such biomarkers have been elusive for immune checkpoint inhibitors (ICIs), which provide long-term disease control to only a minority of all-comers². The absence of biomarkers has been further complicated by the development of combination strategies, leading to the approval of multiple first-line combinations of ICI plus chemotherapy (ICI-Chemo)^{3–5} in addition to ICI monotherapies

(ICI-Mono)^{6,7}, without prospective, randomized data to define which patients benefit most from ICI-Chemo vs ICI-Mono⁸. While more research is needed to define the biology underlying ICI sensitivity, one possible reason for the absence of robust biomarkers is the biologic complexity of the tumor-immune axis and potentially non-linear relationships between treatment response and tumor intrinsic and immune features. This biological complexity suggests the need for more sophisticated models that can incorporate and weight multiple variables.

Machine learning⁹ and statistical-based¹⁰ modeling represent powerful tools to improve outcome prediction in oncology by modeling the heterogeneity in treatment effects^{11,12}. Several

“... In this study, we demonstrate how machine learning can fill critical gaps in immunotherapy selection for NSCLC, by modeling treatment heterogeneity with real-world clinicogenomic data, driving precision medicine beyond conventional biomarker boundaries.”



DIAGNOSTIC
MEDICINE
CONSORTIUM

Presents....



ZETA STORM

VALIDATE. AUTOMATE. CREATE.

DMC's Candidate Service Model **Exemplar**

- Clinical Trial Matching and *Prediction* Service
 - An exemplar that targets specific malignancy classes with known bad outcomes:
 - NSCLC
 - Cholangiocarcinoma
 - Leverages the **ZetaΣtorm** engine that was born out of the initial effort to develop the AKI/CKD population modeling tool demonstrated yesterday
 - Leverages the use of cutting-edge, multiplexed data sets in tandem with time-series based hidden Markov models
 - Built by a single pathologist – **not** by a team of bio-informaticists with an added team of programmers in tow

SURGICAL PATHOLOGY REPORT

Patient Name: John Doe **Date of Service:** 01/10/2022
Medical Record Number: 12345678 **Physician:** Dr. Smith

SPECIMEN: Liver, Tumor Resection

DIAGNOSIS: **Cholangiocarcinoma** (Intrahepatic)

- Moderately differentiated adenocarcinoma.
- Tumor size: 3.5 cm in greatest dimension.
- Lymphovascular invasion: Present.
- Perineural invasion: Present.
- Margins: Negative for malignancy.

IMMUNOHISTOCHEMISTRY:

- CK7: Positive
- CK19: Positive
- CEA: Focal Positive
- CA 19-9: Positive
- p53: Wild Type
- Ki-67: 20%

MOLECULAR STUDIES:

- **Next-Generation Sequencing (NGS) Panel:**
 - **FGFR2:** Fusion Detected (FGFR2-BICC1)
 - **IDH1:** R132C Mutation
 - **KRAS:** Wild Type
 - **TP53:** Wild Type
 - **Microsatellite Instability (MSI):** Stable
 - **PD-L1 Expression:** Negative (CPS < 1%)

Pathologist: Dr. Karen Lee

Report Date: 01/12/2022

Thus, revisiting yesterday's presentation, the exemplar that DMC has developed leverages the notion that lab data, and in this case, the molecular-enriched surgical pathology report, can and should become the initiation point for the selection of the most appropriate therapies or clinical trials, using cutting-edge statistical modeling and highly optimized user interfaces, based on best-practice user experience (UX) engineering.

DMC's service model becomes the vehicle by which such sophisticated tools are democratized to the greatest possible plurality of patients, health practices, and IVD entities.

Surgical Pathology Report

Patient Name: Jane Doe
DOB: 05/12/1965
Specimen #: BX-2023-456

Medical Record #: 12345678
DOB: 05/12/1965

DIAGNOSIS

Cholangiocarcinoma (Bile Duct Cancer)

Histologic Grade: Moderately Differentiated (Grade 2)

Staging: T2 N1 M0

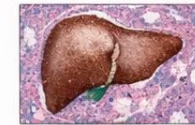
MOLECULAR FINDINGS

- ▶ *Whole Genome Sequencing Analysis*
- ▶ **Mutations Identified:** **KRAS** (G12D), **TP53** (R248W), **FGFR2 Fusion**
- ▶ *High-Dimensional Multiplex Data Integration*

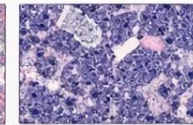
PROGNOSTIC INSIGHTS

- ▶ **Estimated Time to Metastasis:** 8-12 Months

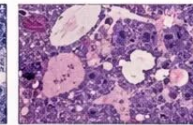
- ▶ *Predicted Sites of Metastasis*



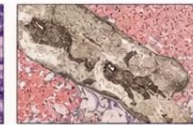
Liver



Lung



Lymph Nodes



Bone

CLINICAL TRIAL OPPORTUNITIES

Trial ID	Target Therapy	Eligibility	Odds Ratio of Success
CT-101	FGFR2 Inhibitor	Eligible	72%
TRK-202	KRAS Inhibitor	Eligible	58%
P53-305	P53 Reactivator	Eligible	45%
IMM-410	Immunotherapy	Eligible	33%

COMMENTS

HMM Analysis suggests earliest metastasis to liver. Recommend prompt consideration of **FGFR2-targeted** clinical trial CT-101 due to highest success probability.





