



# LEVERAGING MULTIOMICS DATA FOR PERSONALIZED LUNG CANCER PROGNOSIS THROUGH INTEGRATED HEALTH PROFILES

24-25J-211

## NSCLC360





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The background of the slide features a stylized, semi-transparent illustration of human lungs. Scattered throughout the lung area are several spherical virus particles, each covered in red and blue spikes, resembling coronaviruses. The overall color palette is a mix of light blues, greys, and the reds/blues of the virus particles.

INTRODUCTION

RESEARCH QUESTION

SYSTEM DIAGRAM

COMPONENTS

# Introduction

## What is Prognosis?

**Prognosis** refers the understanding of a likely course and outcome of a disease based on the current health status, disease characteristics and response to treatment.

## What is NSCLC?

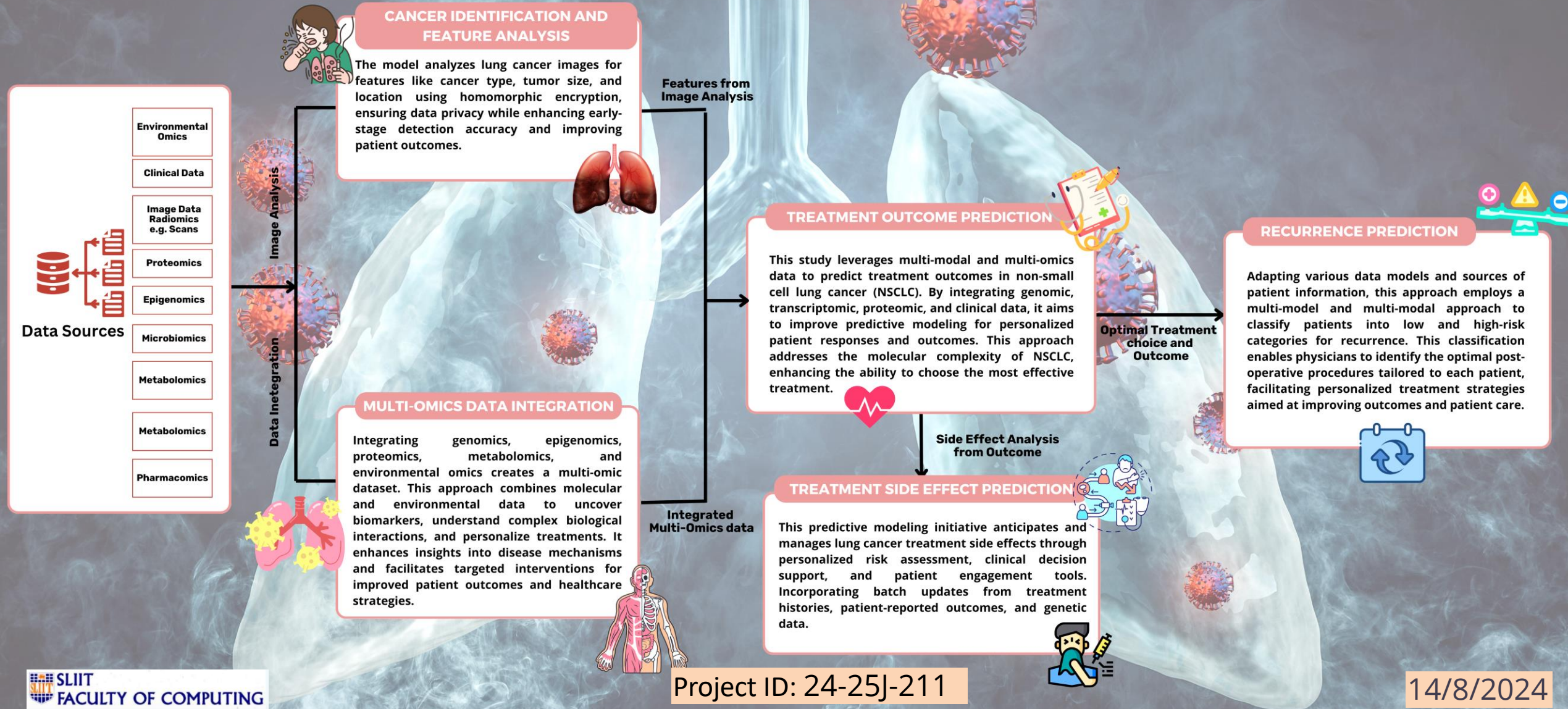
**Non-Small Cell Lung Cancer (NSCLC)** is a particularly deadly form of lung cancer, primarily because it often remains asymptomatic until it has reached an advanced stage. The treatment options for NSCLC vary based on the stage of the cancer and the individual characteristics of the patient.



# Research Questions?

- How can multimodal machine learning models improve early lung cancer detection and treatment while ensuring medical data privacy?
- How can a quantitative approach leveraging omics data enhance prognostic analysis in non-small cell lung cancer?
- How can we accurately predict NSCLC side effects using patient-specific data and advanced modeling to optimize treatment outcomes?
- How can deep learning models predict NSCLC recurrence by integrating imaging, genomic, proteomic, and clinical data?

# System Diagram





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Advanced Deep Learning for Early Lung Cancer  
Detection and Feature Extraction



# Research Question

**How can advanced machine learning models, through multimodal analysis and data integration, improve the early detection and treatment of lung cancer while ensuring the privacy of medical data?**



# Specific Sub-Objectives

- **Design a model to classify NSCLC features from multimodal imaging data**
- **Optimize the model to enhance NSCLC detection accuracy by reducing false positives and negatives.**
- **Integrate homomorphic encryption to secure medical data while preserving the model's accuracy.**

# System Diagram

CT/PET Images



Train ML Model

Homomorphic encryption



Clinical Data



Human Body

Tumor size

Tumor location

stage

type



# References

- A. Nam, J. G., Kim, J. E., Yoon, S. H., Lee, S., Kim, N. H., Kim, H. Y., ... & Goo, J. M. (2021). Lung cancer screening with deep learning: The DLAD system. *Radiology*.
- B. Lambin, P., Rios-Velazquez, E., Leijenaar, R., Carvalho, S., van Stiphout, R. G., Granton, P., ... & Dekker, A. (2012). Radiomics: The bridge between medical imaging and personalized medicine. *Nature Reviews Clinical Oncology*, 9(12), 749-762.
- C. Ardila, D., Kiraly, A. P., Bharadwaj, S., Choi, B., Reicher, J. J., Peng, L., ... & Shetty, S. (2019). Artificial intelligence in lung cancer diagnosis: Challenges and opportunities. *Nature Medicine*, 25(6), 1019-1025.
- D. Hesamifard, E., Takabi, H., Ghasemi, M., & Jones, C. (2017). Privacy-preserving machine learning as a service using homomorphic encryption. *Proceedings of the 2017 ACM Workshop on Artificial Intelligence and Security*, 36-45.

# Research Gap

Aspect Research	Deep Learning for Lung Cancer Detection	Feature Extraction in Lung Cancer	Homomorphic Encryption in Healthcare	AI Integration in Lung Cancer Detection	NSCLC 360
Research A	✓	✗	✗	✓	✓
Research B	✗	✓	✗	✗	✓
Research C	✗	✗	✓	✗	✓
Research D	✓	✓	✗	✓	✓



# Methodology—Technologies & Techniques

## *Technologies*

- Python language
- Python libraries
- Tensorflow
- VS Code
- Dicom Image viewer

## *Techniques*

- Machine Learning
- Deep Learning
- Optimization

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A New Quantitative Approach for Enhancing Prognostic  
Analysis in Non-Small Cell Lung Cancer



# Research Question

The background of the slide features a stylized illustration of human lungs in a light blue/teal color. Several red, spherical virus-like particles with spikes are scattered around the lungs. Wisps of white smoke or steam are rising from the bottom, suggesting the inhalation of pollutants or pathogens.

**How can a new quantitative approach leveraging omics data enhance prognostic analysis in non-small cell lung cancer?**

# Specific Sub-Objectives

- **Identifying Potential Prognostic Biomarkers**
- **Identifying the Treatment Efficacy**
- **Creating a Prognostic Model**



# References

## Research A

Juan Carlos Restrepo, Dueñas, D., Corredor, Z. and Liscano, Y. (2023). Advances in Genomic Data and Biomarkers: Revolutionizing NSCLC Diagnosis and Treatment. *Cancers*, [online] 15(13), pp.3474-3474. doi:<https://doi.org/10.3390/cancers15133474>.

## Research B

Koh YW, Han JH, Haam S, Lee HW. Prediction of Responsiveness to PD-L1/PD-1 Inhibitors Using miRNA Profiles Associated With PD-L1 Expression in Lung Adenocarcinoma and Squamous Cell Carcinoma. *Anticancer Res*. 2024 May;44(5):2081-2089. doi: 10.21873/anticancer.17012. PMID: 38677736.

## Research C

Alamri S et al, Disease prognosis and therapeutic strategies in patients with advanced non-small cell lung cancer (NSCLC): a 6-year epidemiological study between 2015-2021. *Transl Cancer Res*. 2024 Feb 29;13(2):762-770. doi: 10.21037/tcr-23-1816

## Research D

TGarinet S, Wang P, Mansuet-Lupo A, Fournel L, Wislez M, Blons H. Updated Prognostic Factors in Localized NSCLC. *Cancers (Basel)*. 2022 Mar 9;14(6):1400. doi: 10.3390/cancers14061400. PMID: 35326552; PMCID: PMC8945995.



# Research Gap

## Research A

By concentrating only on the presence or absence of biomarkers, the study misses out on quantitative data that could provide more nuanced insights. The levels or expression gradients of biomarkers can be critical in understanding disease progression, treatment response, and patient stratification.

## Research B

This study focuses on a single biomarker's expression, rather than a holistic approach looking at multiple biomarkers

## Research C

The study is conducted in Riyadh, Saudi Arabia, which may limit the generalizability of the findings to other populations with different genetic backgrounds, environmental exposures, and healthcare systems. Expanding the study to include diverse geographical regions would strengthen the findings and allow for comparisons between different populations.

## Research D

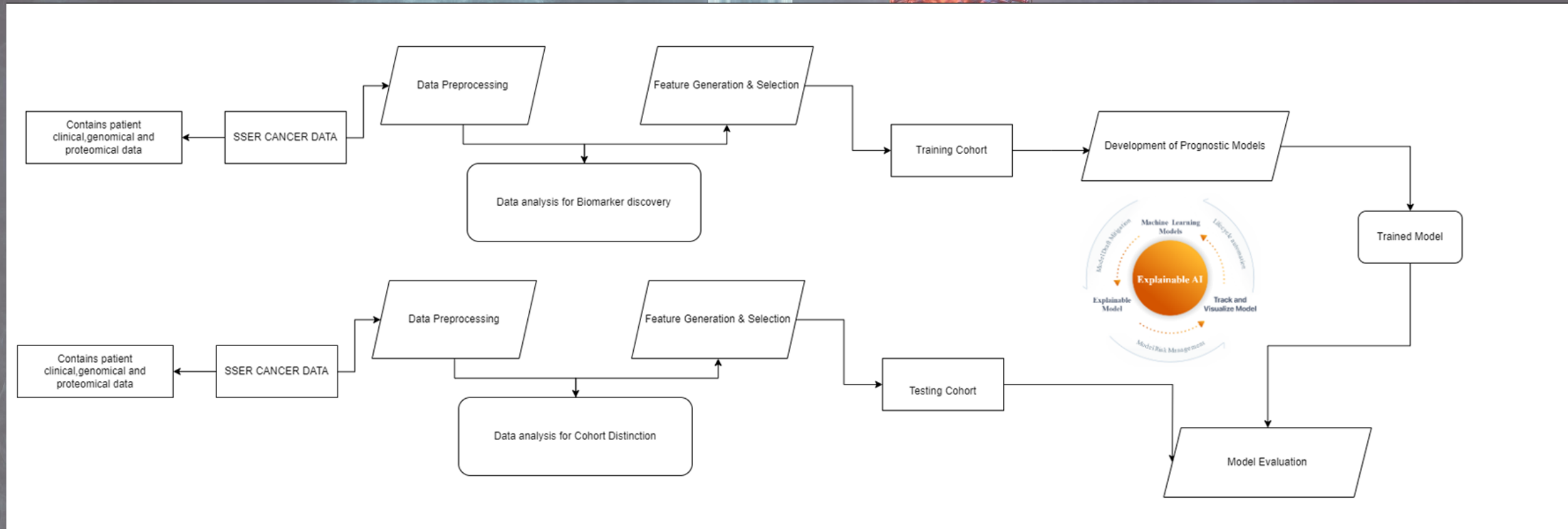
Lack of detailed discussion on the prognostic role of tumor microenvironment (TME) factors in resected NSCLC



# Research Gap

Aspect Research	Improved Outcomes	Data Bias	Optimization	Black Box Nature
Research A	✗	✗	✗	✓
Research B	✓	✗	✗	✗
Research C	✓	✓	✓	✗
Research D	✓	✗	✓	✗

# Methodology — System Diagram





# Methodology—Technologies & Techniques

## *Technologies*

- **Python**
- **NumPy**
- **Tenserflow**
- **Weights&Biases**
- **Google Colab**

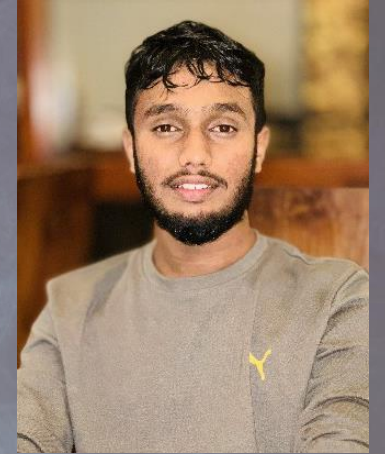
## *Techniques*

- **Machine Learning**
- **Deep Learning**
- **Explainable AI**
- **Optimization**

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**Advanced Deep Learning for Non-Small Cell Lung  
Cancer Side Effect Prediction**





# Research Question

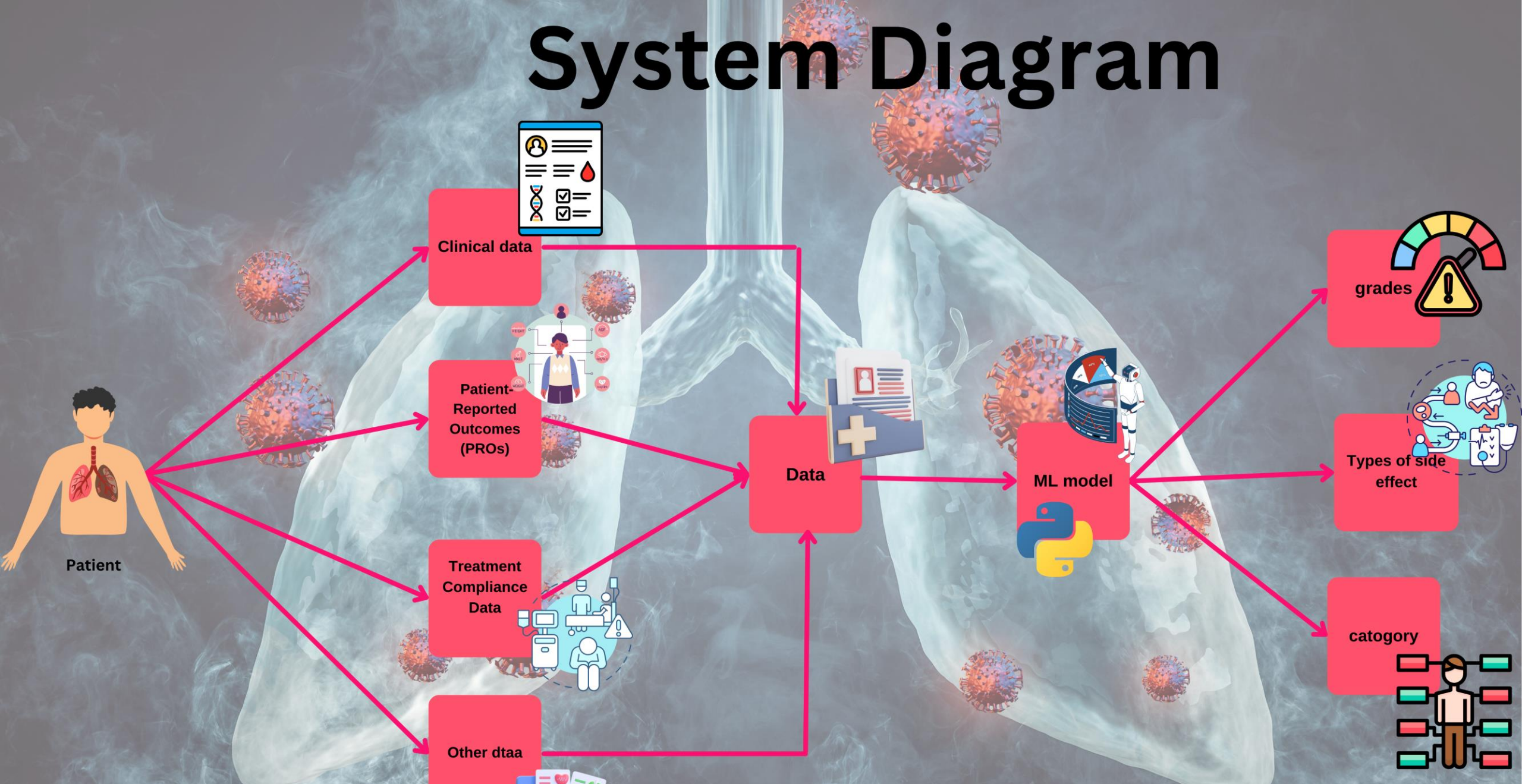
**How can we accurately predict side effects in non-small cell lung cancer (NSCLC) leveraging patient and treatment specific data and advanced modeling techniques, to optimize treatment strategies and improve overall patient outcomes?**

# Specific Sub-Objectives

- To identify key factors influencing side effects through feature engineering and analysis.
- Enhance the of side effect prediction with the potential Data collected  
....
- Enhance the built machine learning models



# System Diagram



# Methodology – Requirements

## Personnel Requirements

- **Expertise in data science, machine learning, and clinical research. Strong communication and collaboration skills to work effectively with medical professionals.**

## Functional Requirements

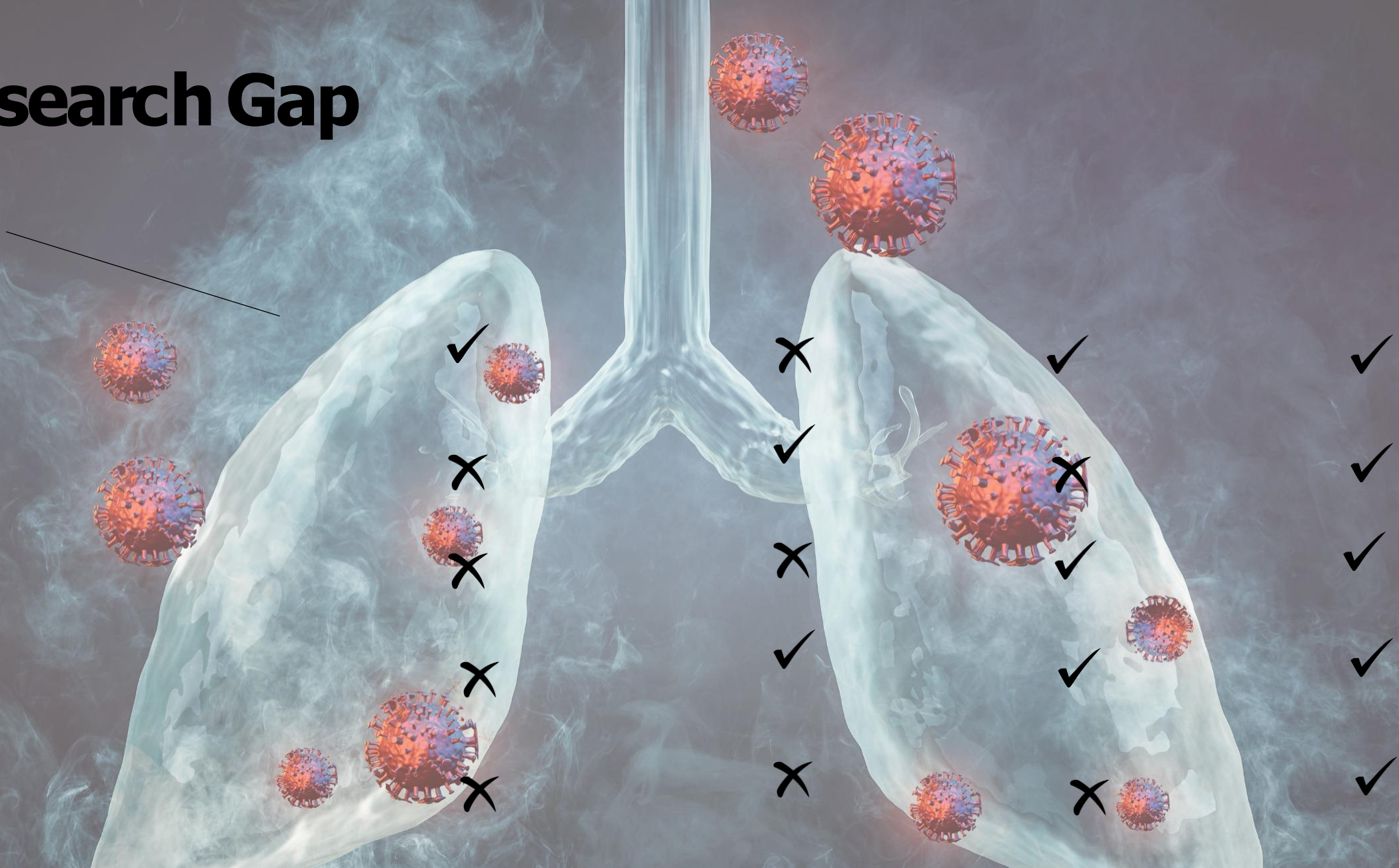
- **Data Collection**
- **Model Training**
- **Side effect prediction**
- **User interface**
- **Report generation**

## Non – Functional Requirements

- **Accuracy**
- **Scalability**
- **Security**
- **Performance**
- **Usability**



# Research Gap



# Methodology – Technologies & Techniques



## *Technologies*

- **Python language**
- **Python libraries**
- **Tenserflow**
- **VS Code**
- **Google Colab**

## *Techniques*

- **Machine Learning**
- **Deep Learning**
- **NLP**
- **Optimization**



# References

Mazzocco, T., & Hussain, A. (2011). A side-effects mapping model in patients with lung, colorectal and breast cancer receiving chemotherapy. *2011 IEEE 13th International Conference on e-Health Networking, Applications and Services*. This study provides valuable insights to medical and nursing staff for predicting chemotherapy side effects, enabling them to select appropriate interventions to minimize symptom impact.

Srinivas, T. A. S., Monika, M., Aparna, N., Narasimha Rao, C., & Ramprabhu, J. (2023). A Methodology to Predict the Lung Cancer and its Adverse Effects on Patients from an Advanced Correlation Analysis Method. *2023 International Conference on Intelligent Data Communication Technologies and Internet of Things*.

Fletcher, C., Wilson, C. J., Hutchinson, A., & Grunfeld, E. (2018). The relationship between anticipated response and subsequent experience of cancer treatment-related side effects: A meta-analysis comparing effects before and after treatment exposure. *Cancer Treatment Reviews*.

# IT21331022 | IRFAN N.A.A

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Advanced Deep Learning for Non-Small Cell Lung  
Cancer Recurrence Prediction and Stratification





# Research Question

**How to accurately predict the recurrence in non-small cell lung cancer (NSCLC) by developing advanced deep learning models that can extract key features from imaging data as well as genomic, proteomic and clinical data. And predict the time of cancer recurrence as well as the locality of recurrence.**

# Specific Sub-Objectives

- Identifying features for predicting recurrence of cancer location and time frame
- Fusion Of Data of Multiple Modalities
- Stratifying patients with cancer according to risk of relapse



# References

Aonpong P, Iwamoto Y, Han XH, Lin L, Chen YW. Improved Genotype-Guided Deep Radiomics Signatures for Recurrence Prediction of Non-Small Cell Lung Cancer. Annual Int Conf IEEE Eng Med Biol Soc. 2021 Nov;2021:3561-3564. doi: 10.1109/EMBC46164.2021.9630703. PMID: 34892008.

Janik A, Torrente M, Costabello L, Calvo V, Walsh B, Camps C, Mohamed SK, Ortega AL, Nováček V, Massutí B, Minervini P, Campelo MRG, Del Barco E, Bosch-Barrera J, Menasalvas E, Timilsina M, Provencio M. Machine Learning-Assisted Recurrence Prediction for Patients With Early-Stage Non-Small-Cell Lung Cancer. JCO Clin Cancer Inform. 2023 Jul;7:e2200062. doi: 10.1200/CCI.22.00062. PMID: 37428988; PMCID: PMC10569772.

Christie JR, Daher O, Abdelrazek M, Romine PE, Malthaner RA, Qiabi M, Nayak R, Napel S, Nair VS, Mattonen SA. Predicting recurrence risks in lung cancer patients using multimodal radiomics and random survival forests. J Med Imaging (Bellingham). 2022 Nov;9(6):066001. doi: 10.1117/1.JMI.9.6.066001. Epub 2022 Nov 8. PMID: 36388142; PMCID: PMC9641263.

# Research Gap

Aspect	Integration of diverse data sources	Novel Biomarkers	Genearalizability	Personalization	Black Box Nature
Research A	✓	✗	✗	✗	✗
Research B	✓	✓	✗	✗	✗
Research C	✗	✗	✗	✗	✗



# Methodology – Technologies & Techniques

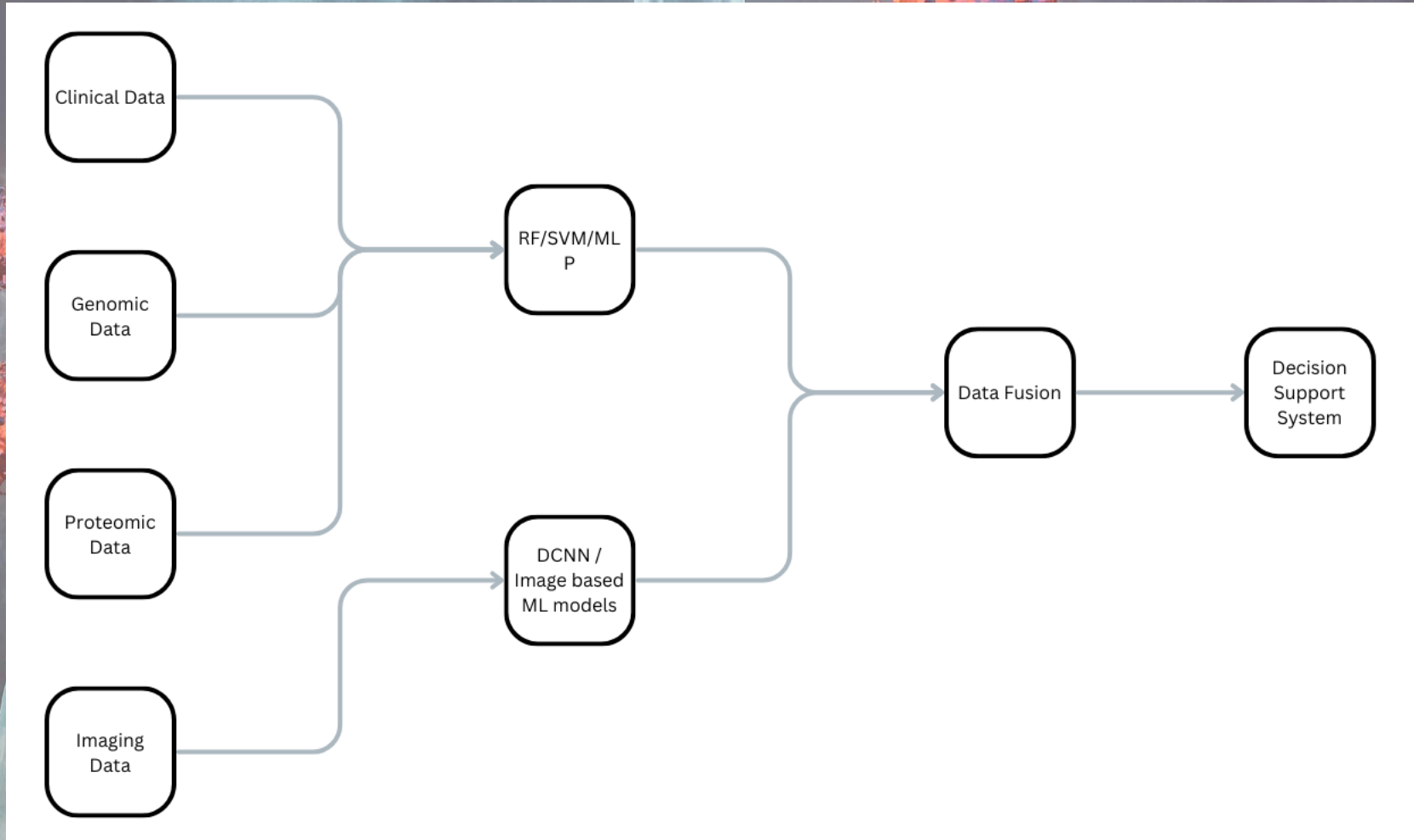
## *Technologies*

- **Python language**
- **Python libraries**
- **Tensorflow**
- **VS Code**
- **Google Colab**

## *Technique*

- **Machine Learning**
- **Deep Learning**
- **DICOM Image Formatting**

# Methodology—System Diagram

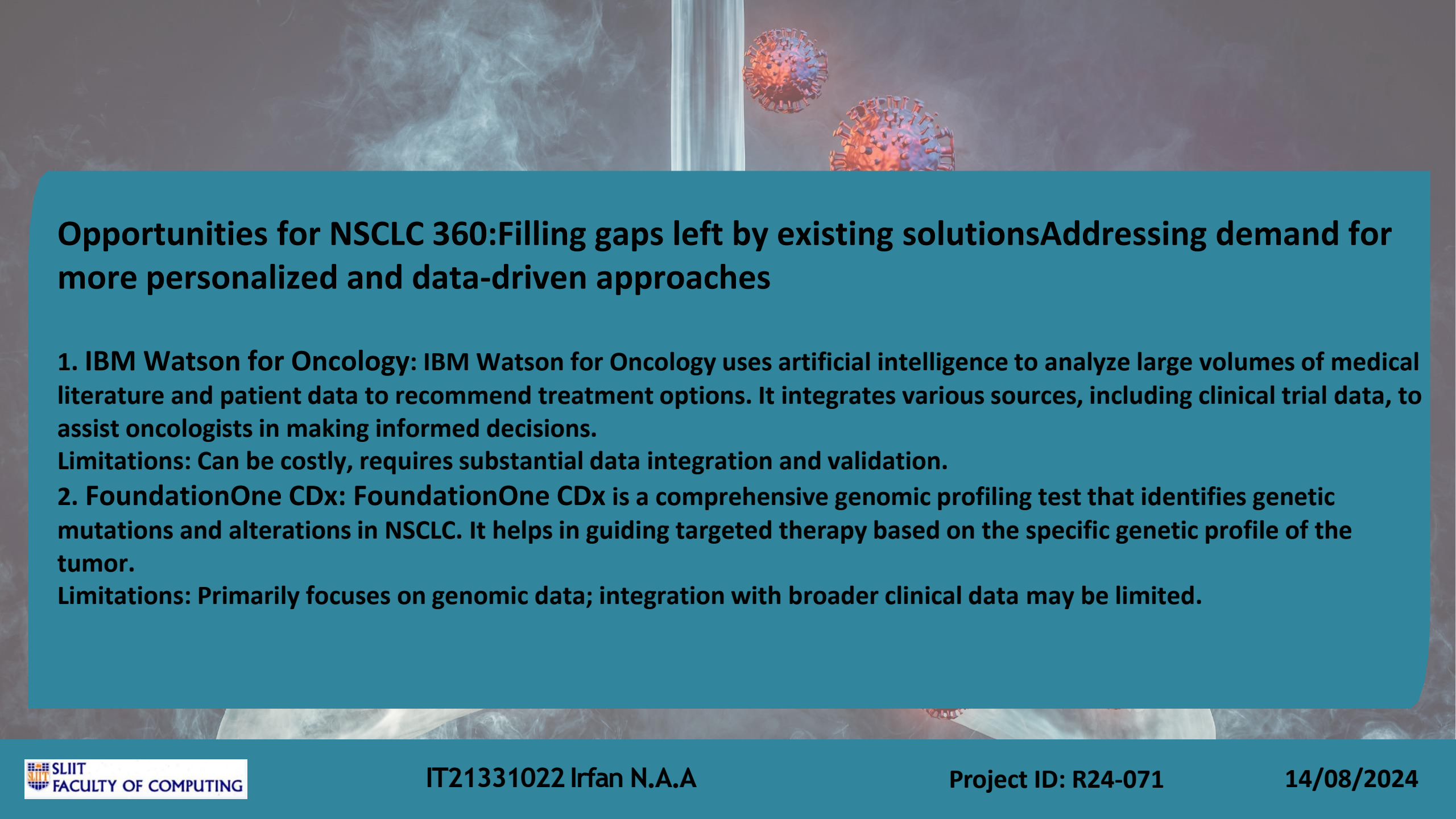




# Contribution to the domain/Commercialization



- Complexities in personalized treatment
- Gaps in integrating multi-omics data
- Challenges in predicting outcomes and recurrence



## **Opportunities for NSCLC 360: Filling gaps left by existing solutions Addressing demand for more personalized and data-driven approaches**

**1. IBM Watson for Oncology:** IBM Watson for Oncology uses artificial intelligence to analyze large volumes of medical literature and patient data to recommend treatment options. It integrates various sources, including clinical trial data, to assist oncologists in making informed decisions.

**Limitations:** Can be costly, requires substantial data integration and validation.

**2. FoundationOne CDx:** FoundationOne CDx is a comprehensive genomic profiling test that identifies genetic mutations and alterations in NSCLC. It helps in guiding targeted therapy based on the specific genetic profile of the tumor.

**Limitations:** Primarily focuses on genomic data; integration with broader clinical data may be limited.





**THANK YOU**