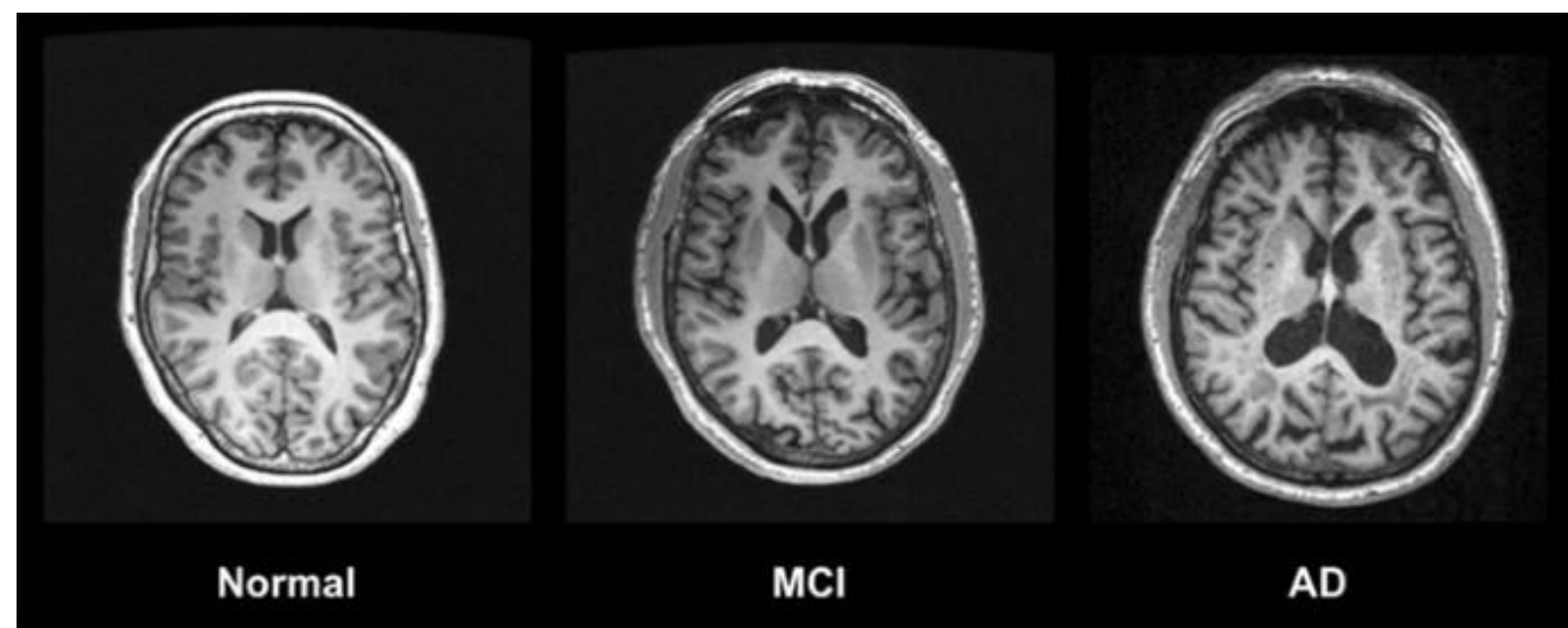


Integrating Multi-Omics and Survival Analysis for Alzheimer's Disease Risk Prediction and Progression Modeling

HARNE, Aastha Mukund (B.Eng. Computer and Data Engineering)
Supervisor: Prof. Kei Hang Katie Chan

Background



Alzheimer's Disease (AD) affects over **55 million** individuals globally and is the leading cause of dementia.

It progresses through 3 stages:

Cognitive Normal (CN) → Mild Cognitive Impairment (MCI) → Dementia

OBJECTIVE: Develop a predictive framework integrating multi-omics features and survival analysis to enhance early-stage AD risk prediction and model disease progression.

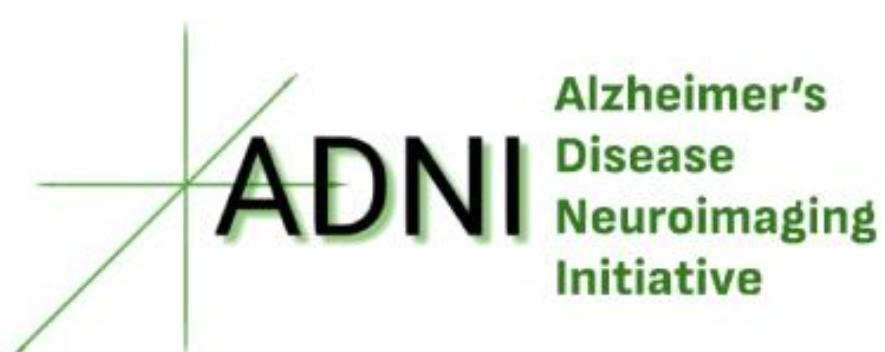
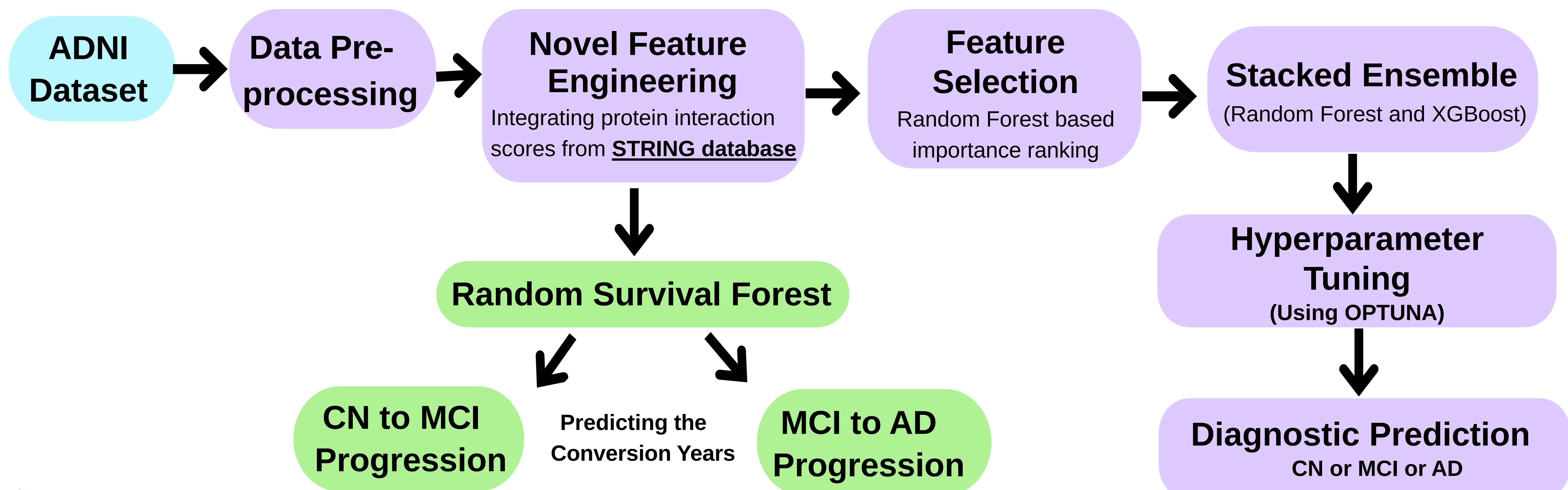
Current Challenges

Late Diagnosis limits treatment effectiveness

Unpredictable Progression within the stages

Current models neglect protein interactions

Methodology



Clinical, imaging, and biomarker data



Interaction scores between biomarkers (ABETA, TAU, APOE4) and adjusted to every patient's data enhancing prediction.

CN-MCI and MCI-AD Multistage Progression Prediction:

Survival models predict the probability that an individual will transition to the next disease stage (MCI or Dementia) within a specified number of years.

Results

1. Enhanced Prediction Model Performance

92.5%

Test set Accuracy

Classification Report			
	Precision	recall	F1-score
CN	0.94	0.88	0.91
MCI	0.89	0.93	0.91
AD	0.95	0.94	0.95

2. Multi-State Progression Prediction

- CN to MCI Prediction: **Test C-index of 0.863**
- MCI to Dementia Prediction: **Test C-index of 0.842.**

Future Applications

- Clinical Decision Support:** Integration into early risk assessment tools for Alzheimer's Disease.
- Personalized Forecasting:** Protein interaction-based features enable individualized disease progression modeling.
- Research Advancement:** Highlights the critical role of protein interactions in Alzheimer's pathology, guiding future biomarker discovery.