Hybrid Deep Learning Approaches for Mortality Prediction in Non-Hodgkin Lymphoma: A Comparative Analysis

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Introduction

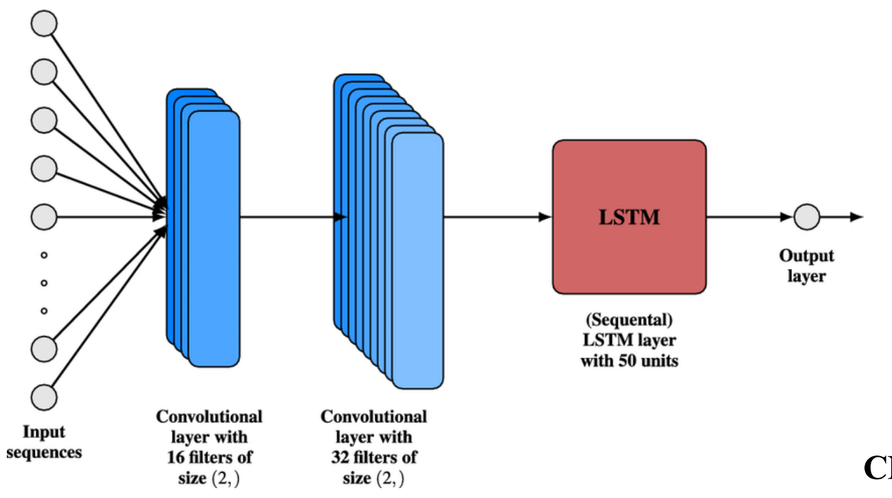
- Non-Hodgkin Lymphoma (NHL) comprises a heterogeneous group of lymphoid malignancies with substantial variability.
- Recent advances in artificial intelligence have introduced hybrid deep learning architectures that combine the strengths of temporal and nonlinear modeling, offering potential improvements in predictive analytics for population-level cancer outcomes.

Objectives

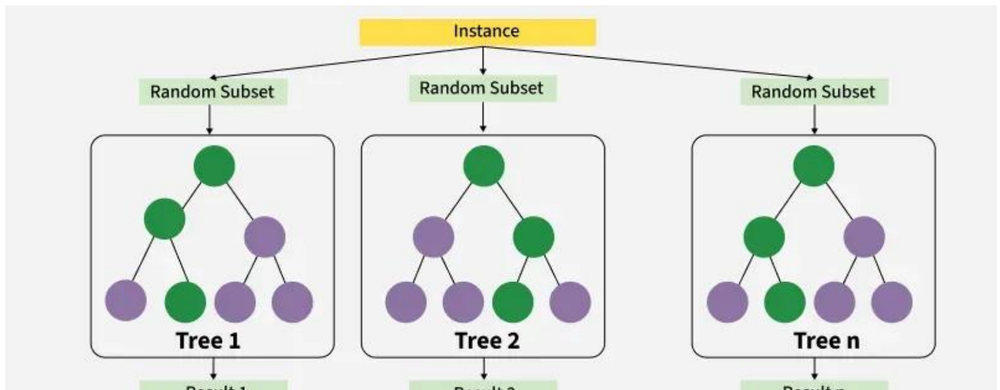
To compare the predictive performance of multiple hybrid deep learning models in estimating NHL mortality using demographic and temporal features.

Methods

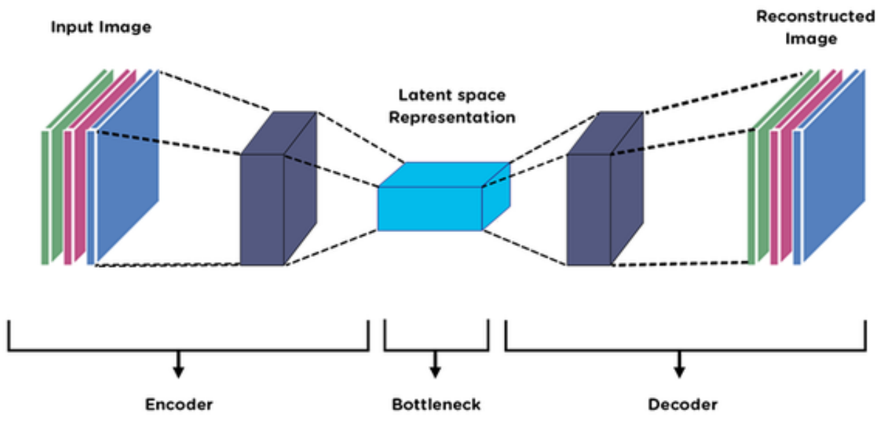
- Mortality data from the CDC WONDER database (1999–2021) were extracted, encompassing state, year, age group, sex, and ethnicity.
- Four hybrid models were developed: CNN-LSTM, XGBoost, Transformer-XGBoost, and Autoencoder-XGBoost.
- The dataset was divided into training (80%) and testing (20%) subsets.
- Model performance was assessed using Root Mean Square Error (RMSE), Mean Absolute Error (MAE), and the Coefficient of Determination (R^2).



CNN-LSTM

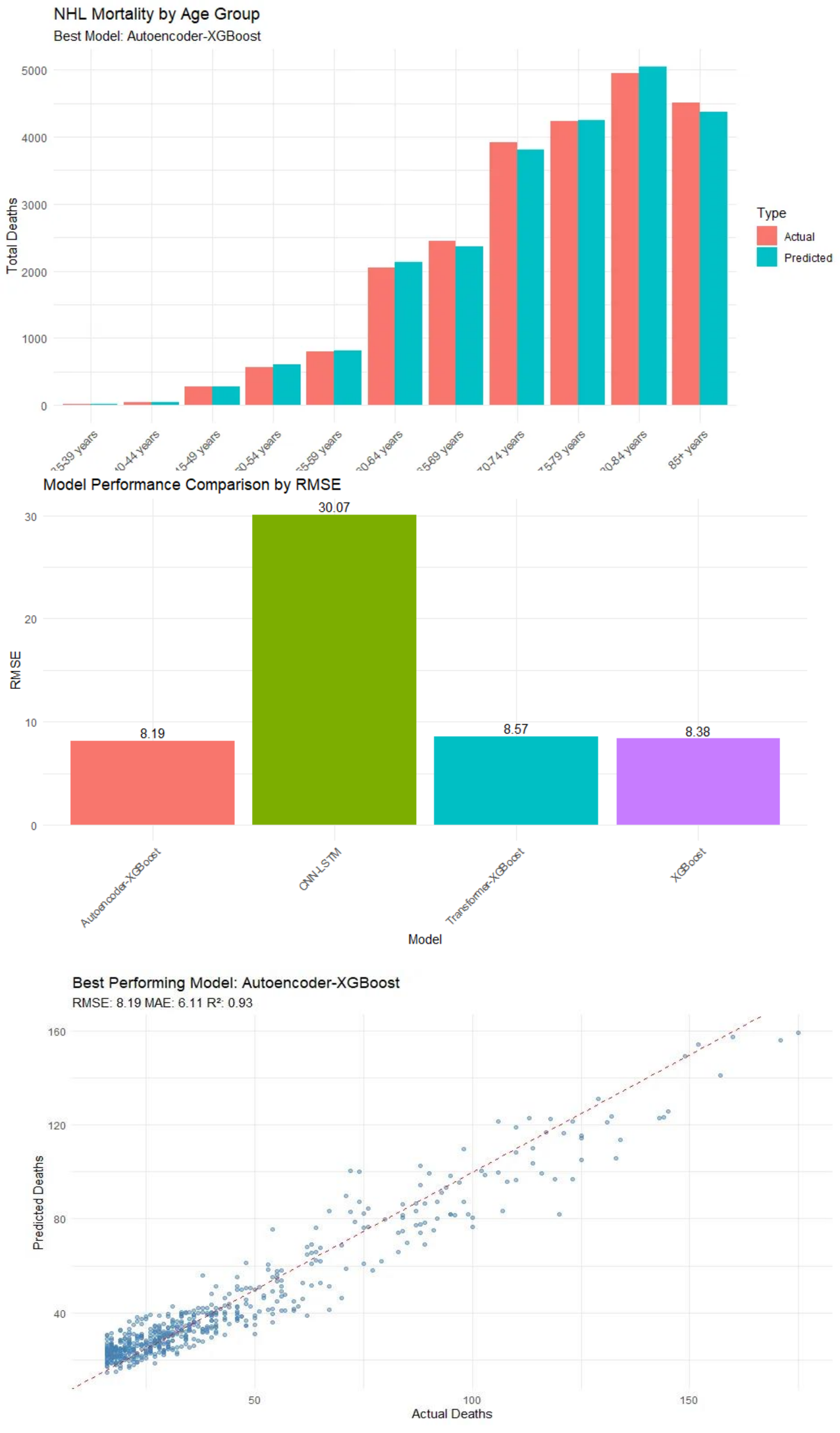


XGBoost



Autoencoder

Results



Summary

The Autoencoder-XGBoost model demonstrated the best performance (RMSE: 8.19, MAE: 6.11, R^2: 0.93), outperforming XGBoost (RMSE: 8.38, R^2: 0.92) and Transformer-XGBoost.

Discussion

- The Autoencoder-XGBoost model achieved the most accurate mortality predictions
- The CNN-LSTM model's underperformance suggests limitations in applying sequence-based deep learning to demographic time series data.
- Limitations- relying on data based on ICD codes limits generalizability.
- Some hybrid deep learning models (especially Autoencoder-XGBoost) can be difficult to interpret for clinical decision-making.

References

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