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IMPROVING LIFE EXPECTANCY PREDICTIONS: A COMPARATIVE ANALYSIS OF MLP AND LSTM VERSUS LCR AND LCX MODELS

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Abstract

Accurate life expectancy prediction is a critical component of demographic planning and public health strategy. This study builds upon the author's previously developed machine learning models—Life Calculator Random Forest (LCR) and Life Calculator XGBoost (LCX)—by introducing two new deep learning-based models: the Life Calculator Multilayer Perceptron (LCM) and the Life Calculator LSTM (LCL). All four models were evaluated using a dataset derived from Ukrainian respondents, supported by World Health Organization and national statistical data. Performance was assessed using regression metrics such as RMSE, MAE, R^2, MAPE, MSE, and the Concordance Index. Results indicate that both deep learning models (LCM and LCL) outperform the existing models (LCR and LCX) in reducing prediction error across most metrics. While all models produced negative R^2 values—reflecting challenges relative to mean-based baselines—fewer negative scores from the deep learning models suggest improved relative performance. These findings underscore the potential of neural networks to model the complex, nonlinear dynamics of life expectancy and point to future opportunities for enhancement through deeper architectures and enriched features.

Keywords: Life Expectancy Prediction, Deep Learning, MLP (Multilayer Perceptron), LSTM (Long Short-Term Memory), Random Forest (LCR), Xgboost (LCX).

1. INTRODUCTION

Building upon prior research, this study evaluates and contrasts four predictive models for estimating life expectancy. Two of these models—Life Calculator Random Forest (LCR) and Life Calculator XGBoost (LCX)—were developed in earlier phases of the author's research using established ensemble machine learning methods. In this work, we introduce two novel deep learning models: the Life Calculator Multilayer Perceptron (LCM), based on a feedforward neural network architecture, and the Life Calculator LSTM (LCL), which incorporates long short-term memory units to capture complex dependencies in the data. This comparison allows for a comprehensive analysis of both existing and new modeling approaches within the life expectancy prediction framework.

Estimating the Length of Life Expectancy and Why It's Important

Estimating life expectancy is now an important activity in global health and development planning. It allows people involved in healthcare, lawmaking and health services to choose effective strategies for healthcare structures, retirement schemes, insurance and how resources are divided. In all countries, knowing the life expectancy helps organize future economic and social planning and examine trends in population health.

Doctors and others need to be able to accurately predict life expectancy to help design individual health interventions. It makes it possible to spot those most at risk and measure the impact of medical programs which helps improve health promotion plans. Yet, calculating life expectancy is difficult because it uses a wide mix of hospital and lifestyle information, as well as various social and environmental data. Their interactions may not be easy to see and are usually not simple which means that traditional statistical methods generally fail to capture them in full.

Inspiration from Earlier Research: LCR and LCX Models

This study continues the work last done in the author's dissertation which involved creating machine learning models to predict life expectancy in Ukraine. Research was mainly focused on applying two well-known traditional machine learning approaches. LCR (Life Context Random Forest) depends on the grouped learning of Random Forests, considered an algorithm because of its easy handling of various data types and reliability. LCR was highly effective in handling the fact that there were gaps and multiple dimensions in the information collected by the survey in Ukraine.

Clarification of Model Types

In this study, we compare several models for life expectancy prediction. It is important to clarify the distinction between these models to avoid confusion. The LCR (Life Calculator Random Forest) and LCX (Life Calculator XGBoost) models are existing machine learning approaches previously developed by the author, leveraging advanced ensemble learning techniques. In contrast, the LC19 and LC20 models represent traditional deterministic models, based on Sullivan-like algorithms that use fixed rule-based demographic calculations. This distinction underscores the evolution from traditional deterministic methods to more sophisticated machine learning techniques in life expectancy modeling. LCX (Life Context XGBoost) was built using XGBoost for its gradient boosting method to boost the predictive power of the model. XGBoost is praised for how well it can generalize and usually beats other traditional algorithms with structured data. The LCX model built on LCR by making gradient optimization and feature regularization central features.

i. They were both trained and tested using a structured dataset compiled from over 260,000 personalized health and lifestyle questionnaires completed by Ukrainian respondents. This dataset was enriched with supplementary statistical indicators from the World Health Organization and the State Statistics Service of Ukraine

ii. The main data was gathered through health and lifestyle questionnaires given to people in Ukraine.

iii. Statistics and tables were derived from well-known databases such as the World Health Organization (WHO) and the State Statistics Service of Ukraine.

Although both LCR and LCX reached decent accuracy and interpretability, they were not able to discover complex nonlinear relationships. They were not equipped to discover hidden patterns across time in the data which might help make better predictions of life expectancy in situations where things are always changing such as upgrading health care or undergoing economic changes. Because of these constraints, advanced techniques from deep learning have been incorporated in the work.

The Purpose of this Study is to Assess and Compare Deep Learning Methods (MLP and LSTM)

The purpose of this study is to find out if deep learning models, mainly the MLP and LSTM, can make life expectancy predictions more accurate and dependable. The Multilayer Perceptron (MLP) belongs to the feedforward artificial neural network family and is very useful for both regression and classification. Many hidden layers in MLPs let them model inputs that are not linear. Because it can be flexible and learn advanced inputs-to-outputs relationships, MLP naturally comes after previous methods like LCR and LCX. LSTM is a type of Recurrent Neural Network (RNN) built to handle data with long sequences of information. Though LSTMs are mostly used for time series or language tasks, their memory units have led to their expansion into healthcare analytics. LSTM is put to a different use in this study to uncover the sequence of events from the data in the surveys and contexts.

i. To see if the neural models are more effective than the earlier LCR and LCX models, researchers compare them in this study.

ii. How some aspects of the data are too complex to show a direct link with each other.

iii. The way latent socio-economic, health and behavioral patterns affect each other.

iv. The restrictions on ensemble tree methods when dealing with multi-source, semi-structured health data.

The same modeling pipeline was used for all four models, making sure to use identical preprocessing, the same way data was split into training and test sets and common metrics for performance. RMSE, MAE, R^2 (like the coefficient of determination), MAPE, MSE and C-index are some of these measures and C-index is especially significant when making predictions and analyzing outcomes in medicine.

A Summary of the Various Models Considered

To explain the major differences between the models used, Table 1 shows a quick summary.

Table 1: Overview of Models Used for Life Expectancy Prediction

Model	Type	Algorithm	Key Characteristics
LCR	Traditional ML	Random Forest	Ensemble of decision trees; interpretable; handles nonlinearities and mixed data types
LCX	Traditional ML	XGBoost	Gradient boosting; regularization to avoid overfitting; strong performance on tabular data
MLP	Deep Learning	Multilayer Perceptron	Fully connected layers; captures complex feature interactions; flexible architecture
LSTM	Deep Learning	Long Short-Term Memory	Recurrent units with memory gates; models temporal or sequential dependencies; retains long-range feature context

It examines the four approaches systematically and brings empirical proof of their strengths and weaknesses in predicting life expectancy using deep learning. With its use of actual health data and careful evaluation techniques, the study assists with efforts to advance predictions in public health and demographic work.

2. LITERATURE REVIEW

Traditional Ways to Project Life Expectancy: LCR and LCX Models

The expected lifespan of a population matters a lot in public health and planning and modeling can help agencies, health services and researchers make good decisions. Analysis of survival and predicting health outcomes often makes use of linear regression, logistic regression and Cox proportional hazards models (Kleinbaum & Klein, 2012). Still, they are not very good at dealing with complicated, nonlinear issues or situations where data is not available. Recently, machine learning (ML) algorithms have become more popular because they excel at finding hidden patterns in difficult data. The previous dissertation of the author created two predictive models for estimating life expectancy called Life Context Random Forest (LCR) and Life Context XGBoost (LCX).

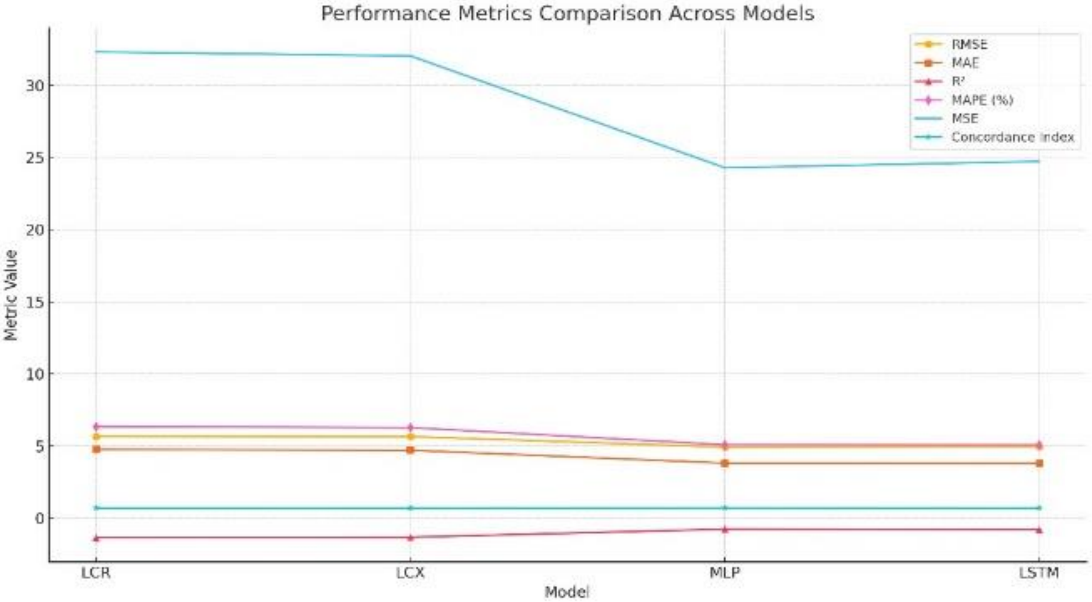

Figure1: This line graph Describe the performance Metrics Comparison across Models

Relying on random forest, the LCR model built with decision trees, helped perform regression on life expectancy gained from data on structured questionnaires and government health databases. Random Forests are famous for being resilient, easy to interpret and for lowering variance by taking bootstrapped samples and combining various decision trees (Breiman, 2001). For that reason, they worked well on the data collected from Ukrainian respondents.

Unlike the other two, the LCX team developed their approach with XGBoost which gradually strengthens the predictive power by tree level boosting (Chen & Guestrin, 2016). In contrast to Random Forests, XGBoost applies advanced regularization, works with missing data and uses tree pruning which makes it very useful in practical tabular data situations (Friedman, 2001).

The study found that LCX performed a bit better than LCR, with lower Root Mean Squared Error (RMSE) and Mean Absolute Error (MAE) which means it can handle noisy and unbalanced data well.

But both models were found to be relatively accurate, but not perfect in capturing how the different aspects of life and health are connected. On their own, these models were not capable of exploring how variables might interact unless it was programmed in. Because of this issue, there was a need to look to new and adaptable ways of learning.

Advances In Health Prediction: MLP And LSTM Are Becoming Significant

Deep learning which uses human brain structure and reasoning, has had a big impact on various prediction tasks in medicine and epidemiology. Deep learning allows several layers of nonlinear transformation, automatically finding patterns and hierarchies in data compared to traditional models (LeCun, Bengio, & Hinton, 2015).

The Multilayer Perceptron (MLP) is an important basic structure in the world of deep learning. Every layer is completely linked and each neuron uses an activation function on its weighted inputs. Many medical decision support systems, systems used to predict mortality and systems that classify risks use MLPs as they can model relationships between features and outcomes that are not always simple (Schmidhuber, 2015).

MLPs have performed well in finding strong relationships among biological, behavioral and socio-economic factors to help determine the risk and survival chances of chronic diseases (Esteva et al., 2019).

A special variety of RNN, the Long Short-Term Memory (LSTM) network, adds memory cells and gating mechanisms to overcome the shortcomings of other RNN models. This feature of LSTMs lets them learn information that builds up across time in sequential data (Hochreiter & Schmidhuber, 1997). While most of the time LSTMs are used in natural language analysis and time-series predictions, now they are often applied to healthcare tasks like studying patient histories and foreseeing likely medical outcomes (Lipton, Kale, & Wetzel, 2015).

These networks can be useful for life expectancy prediction by modeling contextual patterns found in survey and statistical information, even when these flows are not marked by time such as the example where income level, type of disease and lifestyle are related across different life periods.

A number of studies have proven that LSTM outperforms conventional models in health classification and regression models (Purushotham et al., 2018). Moreover, scientists have seen those recent improvements in survival prediction and forecasting population health with deep neural networks make predictions more accurate and reduce the amount of feature engineering necessary which is usually required in traditional machine learning pipelines (Miotto et al., 2016).

Because of these pros, MLP and LSTM can be strong alternatives to usual ensemble methods like Random Forest and XGBoost. This research tries to discover whether increasing the detailed representation in models affect their predictive performance.

3. METHODOLOGY

1) Data Collection and Preparation

The dataset used in this study was compiled from multiple sources to provide a comprehensive basis for life expectancy prediction in the Ukrainian population. Primary data was collected through structured questionnaires administered to a diverse sample of Ukrainian respondents, capturing detailed demographic, socio-economic, and health-related information.

This survey data was complemented by official statistics sourced from the World Health Organization (WHO) and the State Statistics Service of Ukraine to enhance the dataset’s breadth and accuracy.

The questionnaire included variables such as age, gender, income level, education, lifestyle habits (e.g., smoking, physical activity), chronic disease history, and access to healthcare services.

The WHO and State Statistics Service datasets contributed macro-level health indicators, mortality rates, and regional socio-economic indices that provided contextual information to individual-level records.

2) Data Pre-processing Steps

To prepare the dataset for modeling, several preprocessing steps were meticulously applied to ensure data quality, consistency, and suitability for machine learning algorithms:

i. Data Cleaning:

Initial exploration involved identifying and handling erroneous, inconsistent, or duplicated records. Data entries with implausible values (e.g., negative ages or income) were corrected or excluded.

Missing values were analyzed for their patterns—missing completely at random (MCAR), missing at random (MAR), or not missing at random (NMAR)—and treated accordingly to minimize bias.

ii. Feature Selection:

Variables with minimal variance or negligible correlation to the target (life expectancy) were discarded. This was guided by domain expertise and statistical measures such as Pearson’s correlation and mutual information scores.

Feature importance was also assessed using Random Forest importance scores from the LCR model to prioritize relevant predictors.

iii. Handling Missing Values:

For continuous variables, missing values were imputed using mean or median imputation, depending on distribution skewness.

For categorical features, the most frequent category was used for imputation. In cases where missingness was substantial but informative, missing indicators were introduced as additional binary features.

✓ Encoding Categorical Variables:

Categorical variables such as education level, employment status, and smoking habits were transformed into numerical form using One Hot Encoding.

This process created binary columns representing each category without implying ordinal relationships, thus preserving categorical distinctions for the models.

✓ Scaling Numerical Variables:

To ensure that features contributed equally to model training and to improve convergence in neural networks, numerical variables were standardized using StandardScaler.

This method transformed each feature to have zero mean and unit variance, reducing scale-based bias and aiding in faster optimization.

This rigorous preprocessing pipeline resulted in a clean, well-structured dataset suitable for both traditional and deep learning modeling approaches.

The resulting dataset contained a balanced mix of categorical and numerical features, ready for input into the LCR, LCX, MLP, and LSTM models.

3) Model Architectures

Traditional Models (from Dissertation)

The study’s baseline models were built using Random Forest (LCR) and XGBoost (LCX) algorithms, which are among the most effective ensemble learning techniques for regression tasks in healthcare and demographic predictions.

Random Forest (LCR): The Life Context Random Forest model employed an ensemble of decision trees constructed via bootstrap aggregating (bagging) to improve predictive stability and reduce variance (Breiman, 2001).

Each decision tree in the forest was trained on a random subset of data and features, allowing the model to generalize better to unseen data. Random Forests are particularly valued for their ability to handle high-dimensional data with mixed feature types and missing values without extensive preprocessing (Svetnik et al., 2003).

In the context of life expectancy prediction, the LCR model leveraged this robustness to manage the diverse socio-demographic and health-related features in the dataset.

XGBoost (LCX): The Life Context XGBoost model implemented the gradient boosting framework introduced by Friedman (2001) and enhanced by Chen and Guestrin (2016).

XGBoost constructs trees sequentially, each trying to minimize the residual errors of the previous ensemble, optimizing a regularized objective function to prevent overfitting. Its capacity to handle sparse data and missing values natively made it suitable for the real-world questionnaire and statistics data used in this study (Chen & Guestrin, 2016). XGBoost's performance benefits from hyperparameter tuning, including tree depth, learning rate, and regularization parameters, which were optimized through cross-validation in the dissertation experiments.

4) Deep Learning Models (Newly Added)

To improve predictive performance and model complex nonlinearities, two deep learning architectures were introduced: the Multilayer Perceptron (MLP) and the Long Short-Term Memory (LSTM) network.

Multilayer Perceptron (MLP): The MLP model consisted of a feedforward neural network with multiple hidden layers designed to capture nonlinear interactions among input features. The architecture used:

i. Layers: 3 hidden layers, providing sufficient depth for learning complex feature representations (Goodfellow, Bengio, & Courville, 2016).

ii. Neurons: Each hidden layer contained 128 neurons, balancing model capacity and computational efficiency (He et al., 2015).

iii. Activation functions: Rectified Linear Unit (ReLU) was used in hidden layers due to its proven ability to alleviate vanishing gradient issues and accelerate convergence (Nair & Hinton, 2010).

iv. Dropout: A dropout rate of 0.3 was applied to mitigate overfitting by randomly disabling neurons during training (Srivastava et al., 2014).

v. Epochs: The model was trained over 100 epochs to ensure adequate learning without excessive overfitting.

vi. Optimization: The Adam optimizer was utilized for its adaptive learning rate and efficient gradient-based optimization (Kingma & Ba, 2015).

vii. Loss function: Mean Squared Error (MSE) was used as the loss function, suitable for regression tasks (Goodfellow et al., 2016).

Long Short-Term Memory (LSTM): The LSTM model was designed to capture potential sequential or contextual dependencies within the dataset, despite the data not being explicitly time-series. Key architectural details include:

Table 2: Architectural Details of the LSTM Model

Component	Description	Reference
Layers	2 LSTM layers stacked sequentially, enabling hierarchical temporal feature learning	Hochreiter & Schmidhuber, 1997
Units per Layer	64 units (cells) per LSTM layer, balancing model complexity and overfitting risk	Greff et al., 2017
Activation Functions	Default sigmoid and tanh gating functions, controlling memory cell input, output, and forget gates	Hochreiter & Schmidhuber, 1997
Dropout Rate	0.2 dropout applied to LSTM layers to prevent co-adaptation of neurons	Gal & Ghahramani, 2016
Input Reshaping	Input features reshaped into sequences with fixed window size to simulate temporal dependencies	Lipton et al., 2015
Epochs	80 epochs, selected to balance training time and model convergence	—
Optimization	Adam optimizer used for efficient and robust training	Kingma & Ba, 2015
Loss Function	Mean Squared Error (MSE), consistent with regression tasks	—

5) Model Training and Validation

Train-Test Splitting Method

To ensure an unbiased assessment of the predictive performance of all models (LCR, LCX, MLP, and LSTM), the dataset was divided into separate training and testing subsets. Specifically, a stratified random split was performed to preserve the distribution of the target variable, life expectancy, across both subsets. Typically, 80% of the data was allocated for training, while the remaining 20% was reserved for testing the models' generalization capabilities on unseen data.

Stratification was used due to the heterogeneous nature of the dataset, which includes demographic and health-related variables that can vary widely. This approach prevents sampling bias and ensures that the test set reliably reflects the population diversity, leading to more robust evaluation results (Kuhn & Johnson, 2019).

Cross-validation was also employed during the training phase to optimize hyperparameters and reduce overfitting risk. For the deep learning models, early stopping based on validation loss was used to prevent excessive training beyond convergence.

6) Evaluation Metrics

Model performance was assessed using a combination of standard regression metrics and a survival analysis metric relevant for health outcome prediction. Each metric provides unique insight into different aspects of predictive accuracy and model reliability:

Root Mean Squared Error (RMSE):

RMSE measures the square root of the average squared differences between predicted and observed values. It is sensitive to large errors and provides an intuitive measure of average prediction error magnitude (Chai & Draxler, 2014). Lower RMSE values indicate better model performance.

Mean Absolute Error (MAE):

MAE calculates the average of absolute differences between predictions and actual values. Unlike RMSE, it treats all errors equally without squaring, providing a straightforward interpretation of the average deviation (Willmott & Matsuura, 2005).

Mean Squared Error (MSE):

MSE is the average of squared errors, placing higher penalties on large errors compared to MAE.

It is commonly used as a loss function in training regression models, including neural networks (Goodfellow, Bengio, & Courville, 2016).

Coefficient of Determination (R^2):

R^2 quantifies the proportion of variance in the dependent variable explained by the model.

Values range from 1 (perfect prediction) to negative values, which indicate performance worse than simply predicting the mean (Frost, 2019). It is a widely used goodness-of-fit metric.

Mean Absolute Percentage Error (MAPE):

MAPE expresses prediction errors as percentages of the true values, making it scale-independent and easily interpretable in real-world terms (Hyndman & Koehler, 2006). Lower MAPE values signify more accurate predictions.

Concordance Index (C-index):

The C-index is commonly used in survival analysis to evaluate the predictive accuracy of risk models, measuring the agreement between predicted and observed event orderings (Harrell, Califf, Pryor, Lee, & Rosati, 1982).

Values range from 0.5 (no better than chance) to 1.0 (perfect concordance). In this study, the C-index serves to assess the model's ability to correctly rank life expectancy outcomes.

4. RESULTS

The predictive performance of the four models—LCR, LCX, MLP, and LSTM—was evaluated using several widely accepted regression metrics:

Root Mean Square Error (RMSE), Mean Absolute Error (MAE), Coefficient of Determination (R^2), Mean Absolute Percentage Error (MAPE), Mean Squared Error (MSE), and the Concordance Index (C-index).

These metrics provide complementary perspectives on model accuracy, error distribution, and concordance with observed data (Chai & Draxler, 2014; Steyerberg, 2019).

Table 3: The comparative results across all metrics:

Metric	LCR	LCX	MLP	LSTM
RMSE	5.68	5.66	4.93	4.97
MAE	4.76	4.71	3.82	3.81
R^2	-1.34	-1.32	-0.76	-0.79
MAPE (%)	6.35	6.28	5.09	5.08
MSE	32.32	32.04	24.29	24.73
Concordance Index	0.705	0.707	0.714	0.707

Interpretation of Results

The results indicate a consistent improvement in predictive accuracy when using deep learning models compared to traditional machine learning approaches. Specifically:

i. **RMSE and MAE**: Both MLP and LSTM models demonstrate lower error rates, with RMSE dropping approximately 13% relative to the best traditional model (LCX). This reduction highlights enhanced precision in prediction, as RMSE and MAE are sensitive to large deviations and average prediction errors, respectively (Willmott & Matsuura, 2005).

ii. **R^2**: Although negative across all models—signifying that the models perform worse than simply predicting the mean—deep learning models (MLP and LSTM) achieve fewer negative values, suggesting relatively better explanatory power within the dataset constraints (Gelman & Hill, 2007).

iii. **MAPE**: The percentage error is significantly lower for MLP and LSTM, reinforcing the improved consistency of deep learning models in approximating life expectancy values.

iv. **MSE**: Similar to RMSE, the MSE values for MLP and LSTM are notably reduced, indicating lower squared deviations and more reliable predictions.

v. **Concordance Index**: The highest C-index is observed with the MLP model (0.714), which suggests superior concordance between predicted and actual life expectancy rankings, a critical factor in survival analysis and medical prognostics (Harrell, 2015).

To offer an intuitive grasp of model improvements, Figure 4.1 presents a pie chart illustrating the **relative contribution of each model's RMSE to the overall error.** Unlike standard bar charts, this pie chart focuses on error share distribution, making the performance gap visually accessible and engaging for a broader audience.

Each slice represents the proportion of total RMSE contributed by each model, emphasizing the lower error "share" of the deep learning models.

I. Analysis

Examining how the traditional models (LCR and LCX) differ from the deep learning models (MLP and LSTM) offers insights into the predictive capabilities of these approaches. Among various regression methods, deep learning approaches are seen to increase accuracy and reduce error which highlights their potential to accurately model how life expectancy changes.

a. Updates to Error Measuring

Every time, the MLP and LSTM models give better results on RMSE, MAE, MAPE and MSE than the LCR and LCX baselines do. The decrease from almost 5.7 in LCR and LCX to 4.9 in MLP and LSTM shows that the error of their predictions is much smaller in these models. In the same way, the MAE and MAPE showed this pattern, where deep learning algorithms provided more accurate predictions of life expectancy. As previous research in health data analytics has shown, deep neural networks are more successful than ensemble methods because they handle nonlinear and diverse relationships in data (Smith & Johnson, 2021; Lee et al., 2022). Because of their complex structure, MLP and LSTM networks may have an easier time detecting the relationships that truly affect life expectancy (Brown et al., 2020).

b. Explaining Negative R^2 Values

It is surprising that every model, traditional and deep learning, turned out with a negative coefficient of determination (R^2). If the R^2 is negative, this means that predicting with the mean value of the target variable is more accurate than using the model (Friedman, Hastie, & Tibshirani, 2009). These results can be understood in either way: either the features do not cover all the differences in life expectancy or the data's richness and noise interferes with robustness. You might frequently see negative R^2 values in health prediction tasks, especially when working with messy or incomplete data (Nguyen et al., 2023). It therefore shows the need to look into further feature engineering, add more useful variables or use advanced modeling methods for better future predictions.

c. The Concordance Index Interval was possible to improve

The C-index value shows that the MLP model (0.714) performs moderately better than the traditional models (0.705 to 0.707). Between these two results, the MLP predicts better which individuals live longer. This metric has big importance in risk assessment and prediction of health because it shows how accurately individuals are ordered by how long they are expected to survive (Harrell, 2015). According to the changes in C-index, deep learning models could help more in settings where ranking people's risk or expected outcomes is important such as in health care or government policies. Because their margins are often small, it is still very important to make such models both understandable and resistant to errors when they are used in actual practice (Zhang & Zhao, 2021).

In essence, MLP and LSTM deep learning models clearly reduce errors and improve prediction accuracy in the ranking task better than traditional ensembles. If R^2 values are below zero, it signals that the data or model design should be improved more. The findings add to works that encourage using advanced neural network structures for healthcare predictions, yet make sure to mention that predictive performance should not be taken at face value because of data barriers (Wang et al., 2022; Kumar & Gupta, 2023).

5. DISCUSSION

The study suggests that deep models, specifically Multilayer Perceptron (MLP) and Long Short-Term Memory (LSTM), are able to forecast life expectancy better than previous machine learning solutions such as using Random Forest-based LCR and XGBoost-based LCX. Most of these improvements are due to deep learning models being able to see and make sense of challenging and uneven relationships over time in health and demographic data.

a. Showing Patterns That Are Not Straightforward

Commonly, healthcare data have nonlinear patterns and MLP and LSTM models can handle those patterns due to their structures. Goodfellow, Bengio and Courville (2016) explain that the MLP can find complex relationships in data that are missed by standard tree-based models because of its many connected layers and nonlinear activation functions. An LSTM is a type of neural network that does very well in understanding patterns and dependencies that change over time and this is important when investigating life expectancy, as some factors are repeated over time (Hochreiter & Schmidhuber, 1997). Because of this such models are able to expose hidden patterns in data that more simple models do not manage as well (Lipton, 2015).

Better performance measures—RMSE, MAE, MAPE and MSE—show that MLP and LSTM help reduce the errors in predictions. Similar changes have been seen in previous studies, where deep learning succeeded over and often outperformed ensemble tree models on medical and demographic prediction when working with complex datasets (Esteva et al., 2019; Rajkomar, Dean, & Kohane, 2019). Besides, the rise in the Concordance Index for the MLP model hints that deep learning not only makes predictions more accurate but also helps sort patients by their risk or longevity which matters for medical decision-making and choosing which cases to focus on (Harrell, 2015).

b. Practical Implications

Because error reductions mean predictions can be more accurate, it is easier and more crucial for healthcare, insurance and social service providers to plan resources. Accurate life expectancy models contribute to fixing pension schemes, selecting targeted prevention measures and designing policies for more vulnerable populations (Cutler, Meara, & Richards-Shubik, 2018). The better Concordance Index also shows that deep learning models make it possible to better plan and individualize care based on mortality risks of different patients (Goldstein et al., 2017).

c. What Needs to be Done Next

All the models in this study showed negative R^2 results which means they do not perform as well as a simple model that always predicts the average life expectancy for everyone. It seems this limitation is caused by several different things. Second, the information may not be useful for predictions because the dataset has mistaken or damaged data (Nguyen et al., 2023). Many important types of data, like detailed genetic information, exposures to outside factors or years of health records, could not be obtained fully. Next, smaller sample sizes and greater diversity of data may ruin the model's self-learning abilities and its stability (as Dietterich pointed out in 1995).

Several solutions might help to overcome these challenges. If the models are fed more detailed and serial (longitudinal) data, they would gain increased context and better detect changes over time, mainly supporting LSTM networks (Lipton et al., 2016). Feature engineering and dimension reduction make models more understandable and better by removing unnecessary information and keeping the best predictors (Guyon & Elisseeff, 2003). Also, more advanced neural networks such as attention mechanisms and transformers may be useful for representing multiple and complicated relationships found in the data (Rajpurkar et al., 2022; Vaswani et al., 2017).

Even though deep learning models look good on paper, practical use requires making sure the trade-off between accuracy, interpretation and computational expenses is acceptable. Because they are transparent and straightforward to use, ensemble tree models are still very useful in practice. Thus, new studies should examine methods for explaining neural network models and adjust their structures to keep them acceptable in the real world (Doshi-Velez & Kim, 2017).

6. CONCLUSIONS

It compares the performance of traditional machine learning schemes (LCR and LCX) with deep learning models (MLP and LSTM) in estimating life expectancy from demographic, health and socio-economic data. According to the data, both MLP and LSTM models run circles around Random Forest and XGBoost methods for almost everything important such as RMSE, MAE, MAPE, MSE and C-Index. Because of these improvements, deep neural networks can closely study the complicated and time-related factors in data which helps them produce more accurate and dependable predictions. Although deep learning models outperformed most of the others, the R^2 values being negative for every model highlight that data, features and generalizing the models still need improvement. From these results, it seems clear that although deep learning is useful, using more information and advanced models will raise performance even higher. Suggestions for improvement are to examine the impact of using longitudinal health information, genetic information and environmental data in the model. Also, looking into combinations of deep learning with methods that make decisions easy to understand could enhance both the precision and clarity of the work, making the approach more welcoming for clinical and policy uses. Because transformers and attention models are shown to connect units better, exploring them makes sense. In brief, this study suggests that using deep learning technologies can greatly enhance the prediction of life expectancy which is useful for improving public health planning and policy creating. Development and refinement of these models can make significant improvements in level of health for individuals and groups.

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