

Traditional Vs Modern Approaches to Life Expectancy Prediction

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ABSTRACT: Demographers, planners in health care, and actuaries have long depended on life expectancy predictions. This paper compares traditional methods, such as Lee-Carter and Gompertz-Makeham, with new frameworks, such as those developed by the Big Life Project, the Global Burden of Disease, and the UK Biobank, through machine learning. Traditional models are noted for being easy to understand, reliable over time, and familiar to most economists. On the other hand, they are getting less able to adjust to the many dimensions, individuality, and changing aspects of the current health challenges patients face.

These current strategies use big data from biomedical fields, AI, and new technologies to individually predict how long patients may live. This information is used in these models to help them make more flexible and appropriate predictions. In addition to making medical care safer and more precise, modern models bring difficulties linked to bias in algorithms, problems with understanding their results, protection of patient data, and the necessary computing power.

This paper compares different paradigms using several measures, pointing out their advantages and disadvantages, as well as the areas in which they overlap. Combining the old demographic approach with the predictive power of machine learning could be the best direction for analysis.

The article highlights that to overcome the ethical, technical, and broader usage issues of current models, it is important to properly adapt them, make their design clear, and involve everyone in data management. When life expectancy prediction is handled sensibly and offered to all fairly, it could revolutionize health care by helping us see important trends, improve health policies, assist doctors in making choices, and guide people to understand their future.

KEYWORDS: Personalized Longevity Forecasting, Hybrid Life Expectancy Models, Explainable AI in Mortality Prediction, MPoRT (Big Life) Risk Model, Dynamic Risk Stratification in Health

I. INTRODUCTION

A. *Background and Significance of Life Expectancy Prediction*

Forecasting life expectancy is important in both demography, public health planning, and statistics. It shows the estimated years an individual can live, depending on risks involved, and helps evaluate how people and the country are doing health-wise, economically, and through the health system. Previously, experts used data on the deaths of many people to create life expectancy models that explained the overall population's health. At the same time, because many health influences include genetics, the environment, and factors linked to how we live and communicate, advanced and flexible approaches are essential.

For years, the Lee-Carter and Gompertz-Makeham models have been used to accurately estimate future mortality rates in demographics. People value these models for being mathematically excellent and accurate over many years. Even so, recently, it has become clear that their shortcomings affect modern epidemiology and individual healthcare. The main problem is that they cannot easily use detailed information from electronic health records, sensors from wearable devices, and DNA profiles.

Because more data is now available in healthcare and epidemiology studies are becoming digital, life expectancy modeling has become more advanced. Big Life (Canada), the GBD study, and the UK Biobank use advanced datasets and machine learning techniques to better track the health changes in individual patients.

They provide information not only further into the future, but also in a more detailed and meaningful way to people, specific groups, and policy teams.

B. *Objectives of the Comparative Review*

In this article, I will examine and compare traditional predictive approaches with modern integrated systems. More importantly, the study wants to:

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- Assess the basis for traditional models such as Lee-Carter and Gompertz-Makeham in terms of their mathematics and methods.
- Check the way modern predictive models are constructed, including GBD, MPoRT (Big Life), and models created using UK BioBank data.
- Analyze and compare the abilities, beneficial features, and weaknesses of both traditional and modern approaches for accuracy, understanding, processing many data sources, and individualization.
- Analyze how artificial intelligence and machine learning are helping to better and more accurately predict a person's life expectancy.

C. *Scope and Structure of the Article*

It considers both the familiar statistical methods and the more recent approaches based on AI that are applied in modeling life expectancy. It includes many fields such as actuarial science, demography, computational health informatics, and public health. The article is divided into smaller sections called sub-main sections.

- Studies and explores traditional demographic models, focusing on their past and present role.
- Describes recent methods that merge social, medical, behavioral, and genetic factors.
- Explores how machine learning and artificial intelligence improve the ability to predict outcomes.
- IT examines the advantages, disadvantages, and examples of use for each industrial organization model.
- Outlines the current problems and prospects in hybrid and scalable prediction approaches.

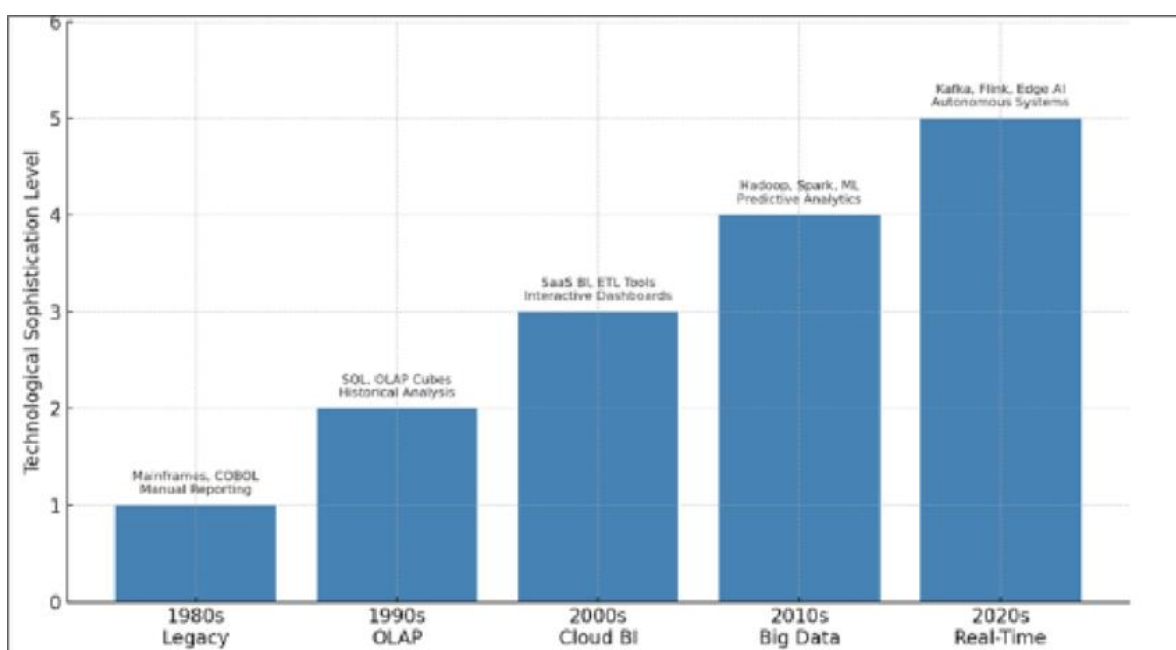


Figure 1. Conceptual diagram of traditional vs. modern approaches to life expectancy modeling

Table I . Summary of Key Life Expectancy Models Discussed

Model	Origin	Type	Data Sources	Output Scope	Personalization
Lee-Carter	1992	Traditional	Mortality rates	National forecasts	Low
Gompertz-Makeham	1825–1860	Traditional	Age-specific death rates	Population-level curves	Low
Big Life (MPoRT)	2010s	Integrated	Social, medical, behavioral	Individualized risk	High

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GBD	1990s–present	Global epidemiological	Medical + burden metrics	Regional/national DALY	Medium
UK Biobank	2006–present	Genomic + ML-based	Genetic, EHR, lifestyle	Personalized health span	High

II. TRADITIONAL APPROACHES TO LIFE EXPECTANCY PREDICTION

A. Overview of Classical Demographic Models

Demography and actuarial science were used to build the formal approach to predicting life expectancy. Because data from public health was restricted to vital records and national census reports, these statistics tended to describe the entire population rather than just individuals. They mainly focused on tracking continuous patterns in mortality among large groups and forecasting so that national planning in pensions, social security, and annuities could be improved.

Fundamentally, these models use statistics such as per-age death rates, life tables for individuals born in a given year, and average life expectancy. Typically, these inputs are examined based on frameworks that expect mortality to increase slowly as a person grows older and as time goes on. Due to their practicality and strength, these models are used by national and international groups and the insurance industry and continue to support long-term estimates of mortality.

For many years, actuarial practices and studies about mortality have greatly benefited from the Lee-Carter model and the Gompertz-Makeham model. In the early 1990s, the Lee-Carter model was introduced, allowing for forecasting changes in mortality by including a time-changing index. The Gompertz-Makeham model, introduced early in the 19th century, portrays aging by using a biological approach to mortality increase and considering that some deaths occur independently of aging.

Though the models played a key role as references in their time, we now see that they no longer meet the needs of modern public health well. Specifically, these models don't take into account a person's genes, way of life, and socioeconomic status, and they assume that death rates are the same for all demographic groups. These reasons mean they are not well equipped for tasks where risks can be reassessed or life expectancy is individually estimated.

Still, there is no doubt that classical demographic models are very important. They make things clear, are easy to replicate, ensure the institution continues, and form the basis for comparing newer and more complex models. Where precise health data is missing, typical mathematical models are still seen as helpful and appropriate for predicting life expectancy. Since they are easy to use, they are often taught, used in making policies, and chosen for places where how results are interpreted is as vital as their accuracy. After classical models were developed, hybrid and machine learning models followed, working to improve them by using many different types of data and versatile algorithms. We will discuss further how, with modern approaches, instead of considering everyone averaged together, different people are individually projected in their potential to live.

B. The Lee-Carter Model

i. Historical Background and Formulation

Lee and Carter's 1992 paper on the Lee-Carter model changed the way people study demographic forecasting. Prior to development, most techniques used for projects in mortality relied either on set rules or the smoothing of data, and these methods did not have a formal way to account for uncertainties. The Lee-Carter model was useful as it offered a way to estimate mortality with randomness and allowed for assessing the accuracy of these estimates, great help for planning in areas such as social security, pensions, and insurance.

The model was created to address the need to account for both historic trends and differences in mortality depending on age. Actuarial models from the past were unable to address both of these trends at the same time, especially as many people started living longer and dying at various stages.

ii. Mathematical Structure

By following this equation, the model can be defined:

$$\ln(m_{x,t}) = a_x + b_x k_t + \epsilon_{x,t}$$

Where:

- In year t , $m_{x,t}$ represents the rate at which people die at age x .
- a_x is used to describe the typical age-related death rate over time.
- b_x reflects the vulnerability to general shifts in mortality at age x
- k_t measures the changing level of deaths in a given year

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- The error term, called ϵ_t , is expected to follow a normal distribution with a mean of zero.

Usually, researchers estimate parameters using SVD and then predict future values of k_t through popular time series models, like ARIMA.

iii. Strengths and Limitations

Strengths:

- Excellent to predict how people's life spans will change over the long term.
- The approach is simple to understand and explain.
- Evidence from deaths in the past supports it.

Limitations:

- Points out that all age groups share the same pattern of life expectancy rates (through k_t).
- It is not able to take into account characteristics such as health, habits, or the physical environment.
- This tool cannot be used to estimate an individual's life expectancy.

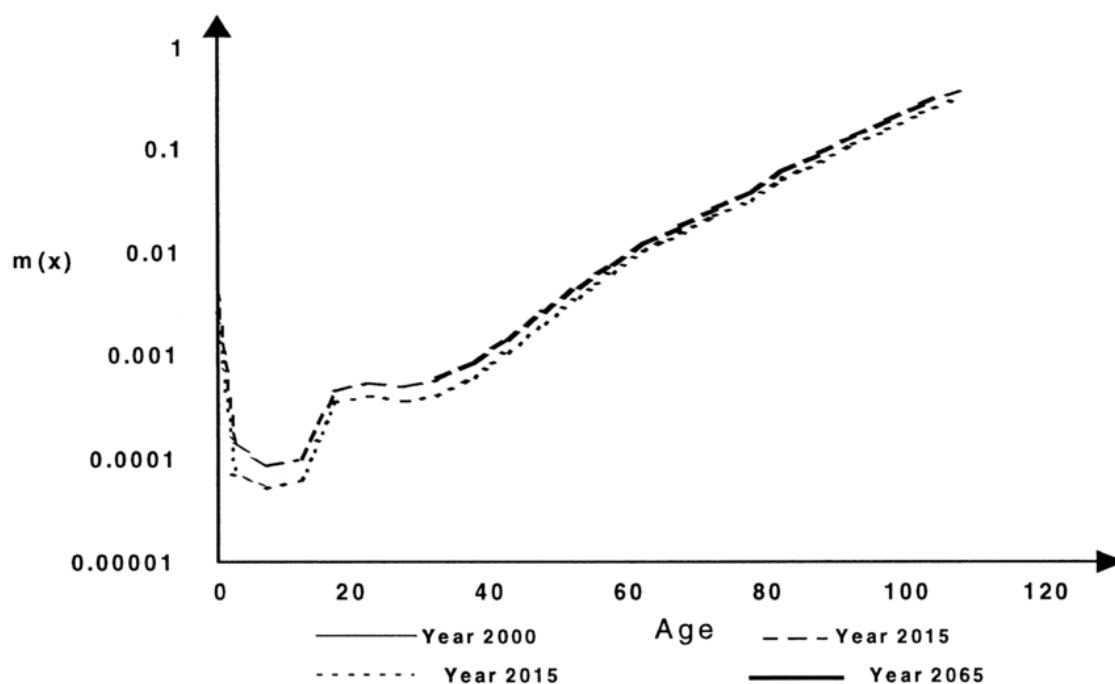


Figure 2. Age-specific mortality curves generated by the Lee-Carter model for different k_t values

C. The Gompertz-Makeham Model

i. Historical Background and Formula

Mortality features were first expressed as the Gompertz-Makeham model, and it is still considered vital in actuarial science and demographic modeling. In 1825, Benjamin Gompertz introduced the model to show the exponential rise in mortality with age. In 1860, William Makeham included an extra component to represent outside mortality risks that affect all individuals equally. As a result of this improvement, the model can now explain why some people die young and how environmental hazards can impact deaths.

The Formula displays the hazard function $\mu(x)$ of death for every age x as the total of all forces stated:

$$\mu(x) = A + Be^{cx}$$

Where:

- A: The constant risk to one's life caused by factors that don't change with age (Makeham term).
- B: The baseline risk of death for people based on their age,
- C: The change in the rate at which mortality increases as people age (Gompertz term).

The model breaks the risk of death into two parts: one is unrelated to age and includes accidents or diseases that might impact anyone; the other is related to aging and involves the effects of aging on the body.

ii. Age-Dependent Risk Modeling

Advancing age is associated with rising mortality rates, according to the Gompertzian term Bec^x . As expected from data and science, the curve that follows leads to reduced immunity and raised risk of illness as we grow older.

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The structure of the model helps to fit data on mortality among both adults and the elderly, as age is a main factor in their risk of death. The ability to isolate this principle in aging allows biogerontology to assess the rates of aging and varied senescence patterns in different communities.

The hazard function can be integrated in practice to determine the survival function $S(x)$, the probability density function of death $f(x)$, and the life expectancy at any age x . Therefore, the model can be easily used in simulations and for actuarial calculations.

iii. Use Cases in Elderly Population Modeling

Many population models for the elderly use the Gompertz-Makeham formula because age plays the main role in causing mortality. Frequently, insurance firms use it to value annuities, work out annual premiums, and predict risk related to living longer. Forecasting mortality patterns for older people is made easier and more accurate with its simple and precise approach.

It affects the planning of policies, as knowing survival predictions for the elderly guides policy changes for pension age, insurance supports, and mental and physical care for adults. Also, the Gompertz slope C in the model can help us understand population health by describing the general rate at which biology ages.

Yet, the model often indicates a higher risk of death in people living much longer, while studies reveal that in extreme old age, the risk of dying tends to be lower. Therefore, when looking at people older than 90, different approaches or adjustments are typically required.

Regardless of this shortcoming, the Gompertz-Makeham model is generally used when there is not much mortality data or where the process needs to be done efficiently. Because each risk is identified separately, it feels natural and works well in many settings for different people.

Table II. Parameter interpretation in the Gompertz-Makeham model

Parameter	Meaning	Effect On Mortality Curve
A	Baseline (Non-Age) Mortality	Vertical Shift Upward
B	Starting Point Of Age-Dependent Risk	Impacts Mortality At Younger Ages
C	Rate Of Mortality Increase With Age	Steepness Of Curve At Older Ages

D. Critical Evaluation of Traditional Models

i. Applicability in National Statistics

National and international demographic forecasters have relied on the Lee-Carter and Gompertz-Makeham models in the past. Due to being simple, easy to read, and reliable, they have become the preferred tools for many national statistical organizations, including the U.S. Social Security Administration, the United Nations Population Division, and Eurostat. The models work best for long-term forecasts of mortality, as they can use open data to provide clear results such as life expectancy and survival rates at retirement.

The Lee-Carter model stands out as it accurately represents the trend of dying with age and can reproduce realistic predicted statistics. The method's description of how mortality is changing through time enables organizations and governments to review changes in mortality and account for possible uncertainties in future population predictions.

Also, the Gompertz-Makeham model remains important in actuarial fields. Due to the ease of using its closed-form survival and hazard functions, it can be used for calculating insurance premiums and pension liabilities, as well as determining annuity prices when focusing on elderly people. Modeling mortality risk based on age makes it easy to study several causes of death in policy making and the financial sectors.

In addition, these models are easy for governments and organizations with minimal resources to use due to their high computational efficiency. When information on health and behavior is scarce, low- and middle-income countries still rely on traditional methods for estimating mortality and making policy choices.

ii. Limitations in Individualized Health Forecasting

Traditional models may be useful, but still have limitations that keep them from being applicable in predicting health for just one individual. What stands out most about these examples is that they were created to describe the way overall mortality changes rather than how individuals die.

For example, the Lee-Carter model suggests that each age group's mortality rate will change with the same mortality index over time (kt). While it manages to show wide mortality changes, this structure cannot highlight differences among groups identified by their sex, race, socioeconomic status, geography, or lifestyles. The outcome is that predictions are not particularly useful for guiding efforts at the local or individual organization level.

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The Gompertz-Makeham model, even with its simplicity and neatness, is just like the other models I mentioned. It believes that the rate of dying rises equally with age in all individuals, regardless of their past habits, present ailments, or genetic background. For this reason, it can't keep up with the current use of wearables, health apps, and EMRs for recording health information. Moreover, the models expect death risk to rise gradually over time rather than being affected by sudden disruptions (like pandemics, wars, or changes in lifestyle) or health behavior. As a result, they find it harder to keep pace with fast-changing situations in the health field.

The approach also fails to consider certain metrics that deal with illness. Earlier frameworks paid no attention to quality of life and disease burden, as they concentrated only on deaths. They reveal little information about outcomes other than death, preventing these measures from being important in many health policies.

Also, standard models do not give accurate results for the precise and detailed prediction needed for health forecasts for each person. This means that using integrated models and AI leads to more flexible and personalized estimates for how long a person will live. Even so, classical models serve as essential references, guides for understanding, and basic standards in comparing different models and policies.

III. MODERN INTEGRATED MODELS AND DIGITAL FRAMEWORKS

A. *Paradigm Shift in Life Expectancy Modeling*

Over recent decades, the method of predicting life expectancy has changed significantly. Biomedical big data, wearables, and progress in machine learning and artificial intelligence (AI) are the main reasons these newer and more personalized systems are preferred. Thanks to these new systems, a wide variety of health factors like genes, biometrics, external exposures, and habits can be used to make more precise and fitting predictions of someone's life span.

The approaches now in use are flexible and can take into account many trends in life insurance, contrary to historical models. They help doctors anticipate deaths, focus on things we can change to improve health, keep tabs on patients' health in real time, and assist with prevention and control in the community. A few of these models are the Big Life Project (MPoRT), the Global Burden of Disease (GBD) study, and the UK Biobank Risk Models.

B. *The Big Life Project and MPoRT Model*

One of the best efforts to model life expectancy using a completely integrated approach is the Big Life Project from Canada. Essentially, MPoRT uses behavioral, social, and clinical risk factors to determine both mortality risk and the life expectancy that somebody loses as a result.

Using a Cox proportional hazards model, MPoRT shows that many factors (such as smoking, exercise, education, income, and diseases) contribute to the likelihood of death. These characteristics come from nationwide health studies and are combined with observations on who died, so the data can be used for modeling.

The outcome from MPoRT is useful for individuals since it tells them how much their life could be extended if they modify their risky behaviors. The model is powerful because it is interpretable and personalized, and is available to everyone, from experts to the public, due to the Big Life calculator.

Table III: Example Inputs and Outputs of MPoRT Model

Input Factors	Data Type	Output
Smoking history	Categorical	Life expectancy reduction (in years)
BMI	Continuous	Probability of death in 10 years
Physical activity	Ordinal scale	DALYs lost
Education level	Categorical	Relative risk (hazard ratio)

C. *The Global Burden of Disease (GBD) Framework*

GBD is considered one of the most complete and elaborate attempts to examine and compare health status in various parts of the world and at different times. In the 1990s, the GBD framework was developed, and by now, the Institute for Health Metrics and Evaluation (IHME) at the University of Washington is responsible for leading it. Because of this new approach, life expectancy is now seen as influenced by both the chances of survival and the chances of being sick.

In contrast to other approaches that only account for death, the GBD method looks at how health can be affected by outcomes other than death. This model focuses on the Disability-Adjusted Life Year (DALY), which adds up years lost by death and years suffered with disability.

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i. Use of DALY, YLL, and YLD

The DALY is formed by applying a single index to two components of the burden of disease.

- **Years of Life Lost (YLL):** The component shows the number of years cut short from the life of a person who died prematurely. The calculation consists of multiplying deaths by the average amount of time a person of that age is supposed to live.

$$YLL = N \times L$$

Where:

- The letter N stands for the number of deaths.
- L = number of years someone is expected to live if they reach the age of death
- **Years Lived with Disability (YLD):** They count the years that someone experiences poor medical status because of disease or injury. It considers the high number of health problems and a measure of the severity of each condition.

$$YLD = P \times DW$$

Where:

- P means how common a condition is.
- DW stands for disability weight.

Overall, the total DALY is represented by the sum.

$$DALY = YLL + YLD$$

With this model, health researchers and policymakers can look at how both losing years of life and experiencing disabilities affect the population. While conditions such as depression or disorders affecting bones or joints do not normally shorten life, they are important causes of health loss each year.

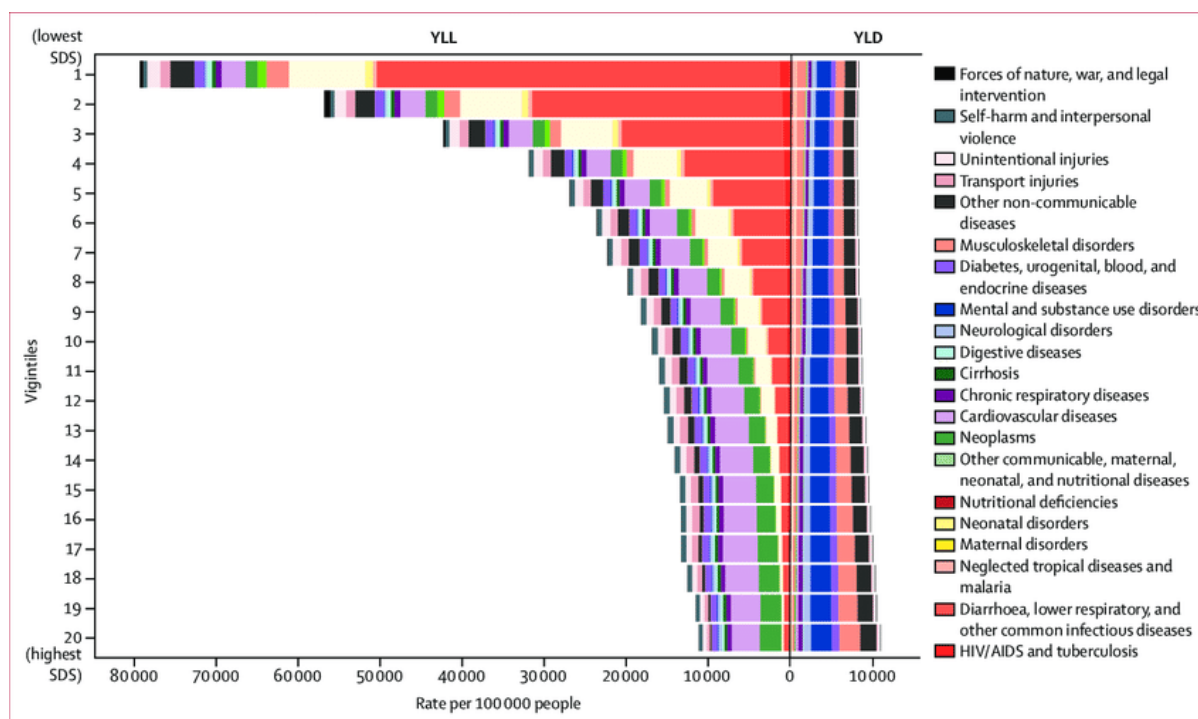


Figure 3: Visualization of YLL, YLD, and DALY Concepts within the GBD Model

ii. Applications in Policy and Global Health Analysis

States, transnational institutions (e.g., WHO and the World Bank), and ministries of health worldwide often rely on the GBD approach to make decisions on health policy and progress. Since the findings are broken down by numerous categories, GBD data help reveal where health support is required the most and what important changes are taking place in the health status of populations.

With GBD data, it becomes possible to estimate lifespan in life expectancy modeling.

- By removing YLD from the total years of life, it is possible to calculate healthy life expectancy (HALE).
- Discovering the best ways to prevent premature death and disability by figuring out what causes such cases
- Monitoring trends for years to discover any new health risks or to measure the success of health interventions.
- Assessing the general health condition of various nations on the same scale.

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For instance, a country with an extended life expectancy but many cases of chronic illness might therefore be experiencing the “expansion of morbidity.” Because of GBD data, it is possible to measure the difference between our lifespan and our health span, helping to improve both life expectancy and the quality of life.

The methods of GBD are based on high-level statistics such as Bayesian meta-regression, using ensembles and smoothing data over the time and location of records. With these techniques, shared data from vital registration, household surveys, hospitals, and disease registries can be used harmoniously in more than 200 countries and territories.

In addition, because GBD provides regular updates, it can show the latest shifts in health, including the results of crises such as the COVID-19 pandemic. Thanks to its adaptability, it is among the most useful and significant tools in population studies.

In essence, the Global Burden of Disease model makes a significant difference in life expectancy modeling by looking at longevity beyond being alive. By bringing together statistics on illnesses and deaths, GBD ensures that health forecasts are accurate and relevant. The findings it provides cannot predict one person’s future, but these findings are useful for regional strategies, comparisons between nations, and making decisions in public health.

D. UK Biobank Risk Models

The UK Biobank plays a key role in the development of current life expectancy models. The database was started in 2006 and focuses on research by collecting genetic, health, behavioral, and lifestyle information from participants aged 40 to 69. Being one of the most extensive population health datasets worldwide, the UK Biobank has allowed scientists to develop detailed models for figuring out a person’s risks, helping with precision health, discoveries in longevity, and predictions about life expectancy.

Unlike the majority of common life expectancy models, those built using the UK Biobank include large amounts of detailed and multilevel information. As well as vital information and medical files, this covers genetic analysis, blood results, imaging (MRI, ultrasound, ECG), body measurements, health sensor information, and survey responses on social status, how people lead their lives, and emotional health.

i. Use of Genetic, Biometric, Lifestyle, and Wearable Data

A major advantage of the UK Biobank dataset is that it allows researchers to examine how genes and health problems are related by using statistics and AI. A person’s genetic risk for cardiovascular disease, cancer, or diabetes, among other long-term diseases, can be estimated with the use of polygenic risk scores from GWAS.

Genomics can be improved by using biometric and lifestyle data to better show how our lifestyle, genes, and the environment interact. When both individuals share a certain genetic risk profile, those with less negative BMI, are more physically active, avoid alcohol, have a healthy sleep schedule, and have less dangerous work exposure may live longer. The detailed analysis of risk factors allows the UK Biobank models to offer solutions that are both precise and suited to each user.

Using real-time information from sensor devices further increases how active the situation can be. More and more, tools that monitor heart rate variation, activity, stability during movement, and sleep time are being connected to models that improve whenever a person’s health changes. This means that estimates are updated based on any behavior changes or new medical events that occur.

ii. Machine Learning Techniques: Random Forest, XGBoost, Neural Networks

With data from so many different individuals, it is necessary to rely on advanced ML algorithms for modeling risk. It is often difficult to capture these types of patterns using the usual statistical analyses, such as linear regression and Cox proportional hazards.

Researchers have applied several ML techniques on UK Biobank data to study life expectancy.

- **RF or Random Forest:** Combines multiple decision trees and uses their collective decisions as the answer. RF models perform well in cases where the data are a mix of types, missing entries are found, and there are interactions among the predictors. The results make it simple for researchers to understand the impacts of different variables on mortality or durability.
- **XGBoost (Extreme Gradient Boosting):** A method that is highly efficient and performs well when training on tabular data. SVMs make it possible to add hundreds of features and can handle data that includes little or no reliable information. Many times, survival time or the risk of death within a selected period is estimated with XGBoost when conducting longevity studies.
- **Neural Networks (NN):** These include Multilayer Perceptrons (MLPs) for table data and Convolutional Neural Networks (CNNs) for health images such as brain scans or pictures from the eyes. They can find complicated and abstract patterns in the information and are able to learn from inputs that are not organized, for example, images from medical studies and raw signals from the body.
- **RNNs and (LSTM):** Useful for processing time-series information collected from wearables or used in hospitals. They track changes in health throughout a person’s life and use this to adjust their estimates of life expectancy.

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Table IV: Comparison of ML models used in UK Biobank longevity predictions

Model Type	Strength	Limitation	Application
Random Forest	Handles nonlinearity, interpretable	Less efficient with deep time series	Risk factor ranking
XGBoost	High accuracy, fast, robust	Requires careful tuning	Life expectancy scoring
MLP	Learns complex patterns	Less transparent	Combined lifestyle + genetic risk
LSTM	Good for sequential data	Requires large data volumes	Time-varying mortality risk

Applying these models has helped in estimating mortality as well as how quickly someone ages, when they get diseases, and their general health. Researchers found that using a combination of medical records, habits, and genes is better at predicting the mortality of middle-aged and elderly adults than old-fashioned methods.

Even so, there are some issues that models like these face. Normal requirements are a strong computer, running experiments multiple times, and preventing unfair prejudice in data when using results outside the UK. Besides, tools such as SHAP (Shapley Additive Explanations) and LIME help clarify ML models, yet there is still doubt from both medical professionals and decision-makers because these models are still rather complex.

All in all, the power of combining big data from the life sciences and machine learning has helped the UK Biobank create life expectancy models that are extremely detailed, flexible, and accurate. They help improve science by making it possible for public health to provide precise interventions supported by real-time and individual health data. While it is still not easy to apply this method to a large number of individuals, the techniques tested on the UK Biobank provide an example to follow for future efforts.

IV. MACHINE LEARNING AND AI IN LIFE EXPECTANCY MODELING

A. *From Statistical Estimation to Predictive Intelligence*

In the past, linear regression and classical survival analysis have provided the main support for calculating life expectancy. Typically, the approaches are built on lines of thought based on linearity, cumulative effects, and a fixed set of features. They are clear and simple to understand, yet often fail when looking at data that is both complex and high-dimensional. They particularly find it hard to incorporate the unusual and complex relationships that play a role in determining longevity in everyday situations. Nowadays, ML and AI make it possible to focus on predictions taken from data, rather than from pre-built models. Instead of deciding on the function in advance, machines work through big data and discover details that could be difficult to spot in traditional modeling. For life expectancy models, this approach fits since the outcome depends on many factors such as health history, present and past genes, daily habits, environmental risks, and economic background.

Extracting the underlying patterns from a range of high-dimensional and heterogeneous data is one of the biggest advantages of ML and AI in this context. Such models can represent relations between variables that are both complex and changing throughout the years. In addition, AI-powered algorithms are flexible and can handle new information with little or no need for manual handling.

Adaptation enables AI to provide a degree of customization missing from regular systems. Rather than giving a single life expectancy forecast for the population, AI-based systems can offer real-time results for each person. As someone's health situation changes, the model adjusts the risk and updates the predicted results. Now, healthcare and public health planners can benefit greatly from the advances in using predictive data and smart forecasts.

Essentially, ML and AI have improved life expectancy modeling by making results more accurate and able to reflect individual cases. They choose not to use unchanging beliefs, instead looking for a way to better understand and predict human lifespan.

B. *Supervised Machine Learning Models for Risk Estimation*

Predicting life expectancy means relying on machine learning approaches that can model mortality and health outcomes using information labeled from data. Here, the input is given and the output is known, such as the length of survival or whether someone passed away. Processing huge biomedical data, the models learn how various factors are related and can use that learning to make projections for undiagnosed cases. People often use Random Forests, as well as Gradient Boosting Machines, which have an optimized form called XGBoost. Processed with a large data volume, these machines can be used in real-world studies of lifespan.

Random Forests are collections of decision trees that are each built using a different set of training data. Neural networks can model both the nonlinear and interactive parts of a problem and are still able to apply their learning to different situations. Handling different types of information in data and being able to cope with missed values is beneficial for long-term and medical studies. Additionally, Random Forests assist in seeing which factors have the biggest impact on early mortality or healthy aging.

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When analyzing data from the UK Biobank and Framingham Heart Study, Random Forests have been proven to be more effective than Cox models at predicting how long a person will live if they have multiple types of risk factors.

Preparing predictions becomes more advanced with models such as Gradient Boosting Machines and XGBoost. In each step, these algorithms build a decision tree that improves on the remaining errors made in the earlier tree. The reason XGBoost is often preferred in structured data is that it achieves very accurate predictions. It has numerous uses in longevity science: estimating the age at death and when someone might fall ill, and also anticipating how lifestyle and genes might shorten a person's healthy life span. Because it is scalable and efficient, it can analyze large data on different factors without needing precise ideas about relationships between those factors.

Besides research, they have been used in public health strategies for handling emergencies. XGBoost technology was applied to develop dashboards that helped assess the risk for the population during the COVID-19 pandemic by considering clinical, behavioral, and demographic data. Supervised learning contributes to higher relevance in clinical support and policy planning because it adjusts to new data, discovers nonlinear relationships, and allows for assessing a patient's individual risk. The use of Random Forests and Gradient Boosting has made AI-driven life expectancy prediction possible and effective.

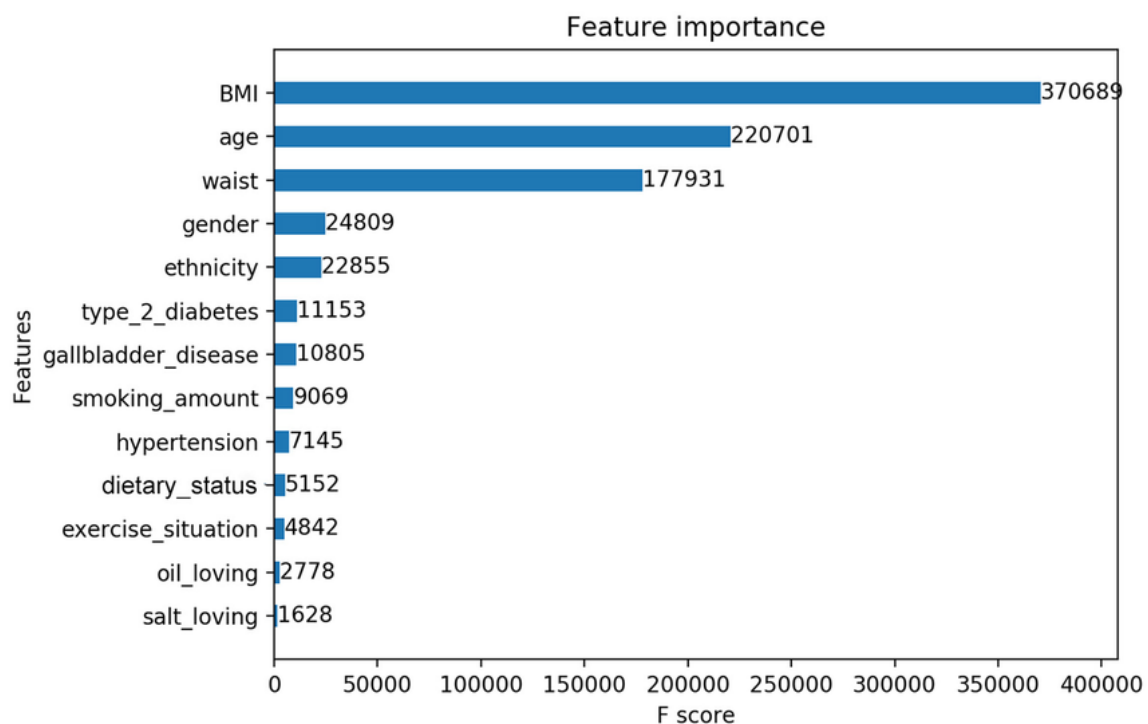


Figure 4: Feature Importance Plot from XGBoost Model Predicting Life Expectancy.

C. Neural Networks and Deep Learning

Because traditional models are limited by complex data, building life expectancy models is now possible because of neural networks and other deep learning approaches. While tree algorithms do well with organized data sets, neural networks outperform them when the data comes from biosensors, medical imaging, genomics, and continuous monitors. Since they can learn difficult relationships on their own, apart from any manual feature design, they function well in predicting health outcomes. They are now mostly used with data from wearables and records to help calculate life expectancy changes if any new facts become available.

MLPs, used in deep learning, feature layers of artificial neurons that take input from items such as blood pressure, glucose values, cholesterol, and genetic risks and calculate the possible outcomes, like risk of death or how long someone is expected to live. In situations where there are many variable factors and they strongly affect each other, MLPs are most useful. Since their introduction, they have helped generate longevity calculators that consider both medical and lifestyle features of patients. Usually, these models rely on big datasets and can make very accurate predictions. Still, because their workings are not easily seen, they can be difficult to explain, unlike decision trees that display the significance of different variables.

Recurrent Neural Networks (RNNs) and their updated version, named Long Short-Term Memory networks, are very useful when working with time-series health data. They work by processing information in sequence and storing past data to identify changes in a patient's health. LSTM models have proved effective in handling ongoing biometric data such as sleep patterns, heart activity,

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physical exercise, and compliance with medication. Thanks to their adaptable predictions, they can be applied to current health data for real-time purposes. They have been used in healthcare systems to detect emerging threats of heart diseases and strokes, to guard against lowering life expectancy if not managed on time. With more health monitoring being used, these models now play a bigger role in helping predict the longevity of each person.

D. *Explainability and Interpretability: From Black Box to Glass Box*

We must be concerned about understanding these models when applying them to life expectancy prediction. Cox regression and other traditional models have well-structured coefficients and assumptions that anyone in healthcare can understand. However, many modern AI models, including those based on deep learning, are considered hard to explore since it's unclear how decisions are made internally. Since healthcare professionals cannot always understand or justify these predictions, their acceptance is often reduced. For predictions about health, it is equally important to understand the reasoning behind them as it is to get the most accurate answers.

Thanks to these tools, it is easier to understand how complex models function. SHAP (SHapley Additive exPlanations) is one of the most well-known approaches, since it credits each input variable with a part of the prediction based on collaborative game theory. It is possible to understand which variables impact the model the most and also to look at individual predictions. LIME (Local Interpretable Model-Agnostic Explanations) is another frequently employed tool to build small models around specific predictions and measure how changing single features restates the prediction. They can be applied without relying on any specific type of AI and reveal valuable facts about how AI works.

Besides these, PDPs help display the impact that small changes in a variable have on the main outcome when other aspects are unchanged. As an illustration, PDPs may explain what effect changing your smoking, exercise, or weight habits can have on how many years you are likely to live. Armed with SHAP and LIME, these effects can highlight which factors within a black-box model lead a patient to be predicted as being at risk. Sharing information openly is vital for getting users and practitioners to trust AI, which can then develop from being 'black box' engines to systems that show how their decisions were made. While AI is being used more in healthcare, its predictive models must continue to be understandable, useful, and supportive to individuals.

Table V: Comparison of Predictive Methods in Life Expectancy Modeling

Method	Strengths	Limitations	Use Case
Random Forest XGBoost	Robust, interpretable, handles mixed data	Slower on large data, black-box feel	Risk stratification from EHRs
	High accuracy, efficient, handles missing data	Hyperparameter tuning needed	Individual longevity scoring
MLP	Captures nonlinearities, scalable	Low interpretability	Lifestyle-based lifespan prediction
LSTM	Excellent for sequences, adaptive	Computationally intensive	Wearable-driven dynamic forecasts

E. *Ethical, Technical, and Practical Considerations*

Even though using machine learning and artificial intelligence for life expectancy modeling seems promising, introducing them in healthcare and public health processes can lead to several major ethical, technical, and operational concerns. We should pay special attention to these issues to keep predictive health care from reducing health equity, the quality of data, or trust among patients and doctors. When it comes to ethical challenges, bias and fairness are the most significant issues. Historical data in AI often shows patterns of existing inequalities around race, society, gender, or location. Untreated, biases might mean predictions about life expectancy are often wrong for particular groups of people. As a result, models may perform poorly and contribute to health injustice that is not easy to spot and remedy.

Data privacy is also an important subject. To predict life span, models use a lot of information about individuals, including their medical records, genes, habits, and data from devices used for monitoring their health. The law in Europe requires the GDPR, and in the United States, the HIPAA, while dealing with personal data in the health sector. People using AI should be aware of how their data will be used, provide permission for its use, and keep control over who can access their information. Protecting data, making sure there is no identifying information, and overseeing ethics are important for people to trust AI used in longevity.

Functionally speaking, a major issue is keeping conclusions generalizable. Some AI models are built using the health records of specific populations, like the UK Biobank, meaning they miss important details about others. Without making any changes, applying these models can lead to weak outcomes in different areas or cultures. To test the model's reliability for different cases,

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strong testing, validation, and specific settings are vital. For AI to be used widely in the healthcare industry, it must be easily incorporated into current medical procedures. It means that electronic health records work with these tools, the interface is straightforward for health workers, and the information can be applied easily in practice. When integration fails, the most precise models can still be overlooked in practice.

V. COMPARATIVE EVALUATION AND IMPLICATIONS

A. *Evaluation Criteria: Accuracy, Interpretability, Personalization, Scalability*

Comparing traditional and modern ways of modeling life expectancy must focus on important performance characteristics. They are primarily evaluated based on their predictive accuracy, how easy it is to understand them, whether they can be adjusted for each user, and how many users they can serve. There is a functional connection in the dimensions that supports the use of the model in research, medical care, and policymaking.

Accuracy means that the model can predict mortality correctly. Long-term population projections using Lee-Carter and Gompertz-Makeham are quite reliable, but when you have detailed information on individuals, models powered by machine learning usually do better. A model is interpretable when its predictions are easy for humans to see how and why they are made. Classical models have an advantage over many deep learning models because of their easy-to-understand equations.

Personalization is related to how much the model can differentiate between people's risks, instead of only considering groups. Today's models can handle lifestyle data, risks from genes, and current health readings. The ability of a model to adjust to large and varied groups is what we call scalability. Traditional approaches use fewer resources and can be installed anywhere, but modern systems are heavier to run, but are adaptable in different situations depending on how they are configured.

Table VI: Dimension-by-Dimension Comparison of Traditional vs Modern Models

Evaluation Dimension	Traditional Models (Lee-Carter, Gompertz-Makeham)	Modern Models (ML/AI-based)
Accuracy	Moderate, best for population trends	High, especially with individual data
Interpretability	High (transparent formulae and parameters)	Low to moderate (requires explainability tools)
Personalization	Low (generalized estimates)	High (individualized forecasting)
Scalability	High for national use	High with sufficient infrastructure

B. *Strengths and Weaknesses of Traditional vs Modern Models*

People use the traditional models because they are uncomplicated, strong, and straightforward to apply. Basically, they need just a few data items, such as average lifespan and mortality rates, to produce results that can guide decisions on pensions, insurance, and health policy. For this reason, they are very valuable where limited resources and data are an issue. Still, the main disadvantage of both approaches is that they are not flexible. They fail to address people's changing habits and variations in health within groups.

They do this by combining information from electronic health records, wearable devices, genomics, and a review of daily routines. Such complex patterns cannot be easily discovered by other methods, so experts in psychiatry use their findings early to prevent risks and support patients' needs. However, these models can have problems: performance decreases when essential data is not available or skewed, they often fit the study group's unique characteristics too tightly, and since their inner workings cannot be explained easily, this prevents them from even being used in healthcare.

As a result, researchers face the choice between how much they can explain an AI system and how well it learns, and also between covering every case and customizing for individuals. Using a combination of traditional models and modern AI in one structure seems very promising for achieving a balance between them.

C. *Implications for Public Health, Clinical Decision-Making, and Policy*

There are major consequences when comparing the differences between older and newer models of healthcare and policy. Using modern approaches in public health, it becomes easier to find early signs of health trends in the population, discover areas with the most premature deaths, and set suitable health interventions. AI's real-time capabilities help monitor changes, whether during a pandemic or when managing patients with long-lasting diseases.

In the medical field, AI-based models are helpful by offering personalized screening for risks, aiding doctors in treatment planning and prognoses, and helping to communicate with patients. Yet, because information on how these predictions work is not always

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available, clinicians might not feel certain using such tools in critical situations. Hence, for explainability to be part of medical integration, it must be more than just a technical aspect.

Many policymakers depend on traditional actuarial models for their long-range planning and forecasting activities. Since they are user-friendly and clear, they assist in meeting accountability and regulation requirements. Nevertheless, it is important that policy frameworks in health planning use AI models and put in place clear standards to ensure they are ethical, authentic, and understood by all.

D. Cultural and Population-Specific Considerations (e.g., Ukrainian Dataset Relevance)

Applying modern models of length of life can be challenging because they are not easy to use in a variety of cultural and medical settings. Health information collected from the UK Biobank mostly reflects experiences and needs from wealthy, mainly Western populations, and not necessarily from populations in other regions. If you do not localize these models, the results may be totally different from what the actual situation is.

For this reason, it is vital to build datasets about Ukrainian populations and other similar Eastern European areas. Several unique dangers play a role in shaping the health issues found in Ukraine after it left the Soviet Union, including unequal access to care, war-related problems, risks tied to industry, and a lack of funding for its health services. Models focused on Ukrainian data can better represent what is happening in the population, so their longevity predictions are likely to be more accurate.

The point demonstrates how important context is when designing a model. The development and characteristics of mortality risks are affected by culture, the environment, and differences among health systems. Consequently, global models allow for more people, but local models are more precise, so the future of life expectancy prediction will come from combining them.

VI. CHALLENGES AND FUTURE DIRECTIONS

A. Data Privacy, Ethics, and Bias in AI-Driven Life Prediction

Because machine learning and artificial intelligence are now included in modeling life expectancy, the topic of ethics is becoming more complicated. It is especially important to focus on data privacy and security, as people's health data may be sensitive. AI models must generally access detailed datasets that consist of medical backgrounds, genetics, measurements, and behavioral patterns. Therefore, people are worried about who owns the data, whether they are properly informed, and the risks of accidentally sharing confidential medical data. Complying with standards set by the General Data Protection Regulation (GDPR) and the Health Insurance Portability and Accountability Act (HIPAA) is required by law and also matters to ensure people's rights are protected.

Equally concerning is the issue of algorithmic bias. If the training data for AI models has biases related to race, income, gender, or location, these biases might be passed on to those models. Modeling life expectancy mainly from people in the West may cause decisions and the division of resources to be biased toward Western countries. Fairness can be achieved by including different people in training datasets, checking for bias in each step, and using techniques to address it at the development stage. Without these measures in place, predicting each person's lifespan could end up worsening the inequality found in healthcare.

B. Integration with Wearable Tech, EHR, and Real-Time Data Streams

Now that health data can be collected in real time through wearables, mobile apps, and other remote devices, it is possible to update our predictions of how long people will live. Currently, wearing a smart watch or fitness tracker records information on heart rate variability, sleep patterns, physical activity, and stress, each of which is associated with a person's long-term well-being. AI models can respond more flexibly to risks by using the input from this data to predict changes in patients' bodies.

Moreover, with Electronic Health Records (EHRs), healthcare providers can see the entire history of a patient's health. AI systems can forecast life expectancy by gathering structured data from medical history and, with the use of sensors, track how a patient's health changes. However, integration is not without its barriers. Some technical issues in AI are standardizing data, connecting different systems, and ensuring proper data transfer. On the organizational side, clinicians must be educated and reassured to ensure they accept the use of AI in their work.

C. Potential for Global Adaptation and Crisis Response

Applying AI life expectancy models in global health and crises could be very useful in the future. When pandemics, natural disasters, conflicts, and emergencies happen, fast and accurate health forecasts are needed to allocate resources, provide early notice, and organize people by their risk of catching diseases. AI technology allows for the rapid detection of vulnerable sections of the population that may be at risk of sudden mortality.

COVID-19 highlighted that it is important for forecasting to be both agile and adaptable. AI models processed updates in case data and mortality to project surges in various regions, increased hospital needs, and the impact on people who were indirectly affected

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by problems in hospitals. Added to this, in places like Ukraine affected by war, adaptations to life expectancy models can consider factors such as traumatic experiences, disruptions to usual living, reduced access to medical help, and the disorganization of the economy.

At the same time, adapting models on a global scale involves setting them up with data from the local epidemiological picture, culture, and medical facilities. Because of this, AI systems created outside the country may not produce correct or suitable results. As a result, future tools for modeling life expectancy ought to match quality and relevance by being reliable internationally but specific to different places.

D. *Future of Hybrid Models Combining Demography and AI*

In the future, it is very promising that hybrid models are being developed by combining classical demography's approach with the abilities of artificial intelligence. Instead of relying exclusively on AI, traditional models can be improved by using AI to solve small problems and help explain everything in a way that is easy to follow. So, the Lee-Carter model might be introduced into a machine learning setup, allowing for adjustments in forecasts based on a user's behaviors and measurements.

With hybrid frameworks, people can get the best from each tested strategy. They remain as clear, verifiable, and recognized by institutions as the traditional models, yet now benefit from the flexibility and up-to-date nature of AI. For this field, explainable models are vital since it is necessary for both complying with guidelines and being trusted by the public. In healthcare, they can act as systems that give recommendations using data-refined results.

In the long run, combining these approaches with AI will be more beneficial than using one on its own. Utilizing the strengths of all paradigms, experts make scientific systems that are predictive, ensure equity, remain clear in their decisions, and work well with how human health is changing. Hybrid models will bridge the gap between the traditional practices in science and the use of data and computational intelligence in health care.

VII. CONCLUSION

At first, life expectancy was only estimated with single population numbers, but today, there are dynamic, data-driven, and individualized models. These changes mirror new developments in global health science, technology, and the global need for forecasting tools that are exact, just, relevant to all, and clear.

Here, we have looked at how the traditional Lee-Carter and Gompertz-Makeham models compare with Big Life (MPoRT), the GBD Project, and UK Biobank-based frameworks. They are strong because they are mathematically pleasing, remain stable over long periods, and are easy to understand. Many demographic research and public planning institutions incorporate these theories in their work. Still, because they are simply organized, it becomes difficult for them to respond to modern health shifts, like how risks have become more personal and technology offers us up-to-the-minute health information.

To add, modern models have made great strides by expanding their coverage and increasing their complexity. Using machine learning algorithms, large sets of medical data, and factors associated with behavior, they get a more personalized result and higher accuracy. They offer insight for improvements, highlight aspects we can change to live longer, and are useful for ongoing care. Still, these models may face hurdles such as being hard to understand, difficult to compute, and involving privacy, bias, and transparency concerns.

It is evident from the review that every modeling approach has advantages and disadvantages. The purpose and appropriate fit of each model vary from situation to situation. NATIONAL_LEVEL_WORDING: Traditional models are effective for national-level actuarial plans, but modern AI-based models are preferred for individual planning and treatment in highly digital systems.

The future involves joining these two schools of thought, rather than ignoring one. The most promising method for demography is to blend theoretical stability and flexible intelligence. They assist in gaining the trust of the public and, at the same time, offer analysis that creates tailored treatments for each person.

We should also consider the role these theories play in the world as a whole. Since several epidemiological frameworks have been created in wealthier nations, they should be adjusted and recalibrated in regions where the data and diseases are different. By specializing in life expectancy prediction tools for the Ukrainian population, as you pointed out in your dissertation, you are working toward a sense of inclusive validity.

Life expectancy measure goes beyond just using statistics. It brings together issues of healthcare equity, rightful rules for governing, deciding policy, and empowering individuals. Forecasting a lifespan should not only reflect present health care but also help create better future waves of health. While testing the accuracy is important, it is also vital to determine if the model helps ensure fair and thoughtful decisions, improving the health of individuals and whole communities.

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