ABSTRACT

Accurate estimation of life expectancy is critical for informing public-health policy, guiding resource allocation, and supporting individualized care strategies. This project presents an end-to-end system for predicting life expectancy at both the population and individual levels by leveraging a rich, multi-decade dataset from the World Health Organization. Our core model ingests seventeen country-year indicators—spanning adult and under-five mortality rates, immunization coverage, nutritional and behavioral measures (BMI, thinness, alcohol consumption), health-system metrics (hospital beds, health-expenditure ratio), and economic proxies (GDP per capita, income composition index). Through rigorous preprocessing (STL and KNN imputation, normalization, interaction-term creation) and stratified cross-validation, we compare ensemble regressors (Gradient Boosting, Random Forest) and neural networks, achieving a mean absolute error of 1.83 years, an RMSE of 2.37 years, and an R^2 of 0.92 on held-out country data. SHAP-based interpretation reveals adult-mortality rate, GDP per capita, and immunization rates as the strongest drivers of longevity, with behavioral factors and childhood health indicators exerting notable secondary effects. Extending this framework, we develop a specialized HIV prognostic module that predicts remaining lifespan for people living with HIV using clinical markers—WHO stage, CD4+ T-cell count, and viral load—and attains a concordance index above 0.85 in longitudinal cohort simulations. To bridge predictive insights with actionable guidance, we integrate a generative-AI recommendation engine via the Gemini API and LangChain: structured prompts combining model outputs and key drivers yield personalized, evidence-based advisories on preventive screenings, lifestyle adjustments, antiretroviral regimens, and monitoring protocols. Interactive web interfaces—built with HTML, CSS, JavaScript, and Flask—present numeric forecasts, feature-importance visualizations, and natural-language recommendations, enabling both policy makers and clinicians to translate complex analytics into clear strategies. By uniting automated data ingestion, scalable machine-learning pipelines, interpretability, and generative AI, this platform offers a replicable, transparent solution for advancing global health analytics. Future extensions will incorporate finer-scale data and real-time model monitoring to sustain accuracy amid evolving health challenges.

TABLE OF CONTENTS

INTRODUCTION

1.INTRODUCTION

1.1 Aim of the Project

The primary aim of this project is to develop and validate a robust machine-learning model capable of predicting individual life expectancy based on a comprehensive array of demographic, health, and socioeconomic indicators. Leveraging the World Health Organization's global dataset—which encompasses parameters such as adult mortality rates, immunization coverage, nutritional indices, and economic measures—we seek to uncover the complex interdependencies that influence longevity. By integrating advanced regression techniques and state-of-the-art ensemble algorithms, the project aspires not only to deliver high-accuracy predictions at the population and regional levels but also to offer personalized insights. A pioneering HIV-prediction module further extends the model's applicability, enabling clinicians and public-health practitioners to estimate life expectancy for people living with HIV (PLHIV) and to generate tailored recommendations for improving health outcomes. Ultimately, this initiative endeavors to bridge data-driven analytics with actionable guidance, thereby informing policy interventions and individual health strategies alike.

1.2 Project Overview

At its core, the project unfolds in two interconnected streams: general life-expectancy prediction and specialized HIV prognosis. The first stream ingests a multi-year WHO dataset covering over 180 countries, with features ranging from adult mortality, alcohol consumption, BMI, and under-five mortality to GDP per capita, health-care expenditure, and population size. After meticulous data cleaning and feature engineering—such as imputing missing values, normalizing continuous variables, and encoding categorical indicators—the dataset feeds into regression models (e.g., Random Forests, XGBoost, and neural network architectures). Model training and validation adhere to rigorous cross-validation protocols, with performance assessed via metrics like Mean Absolute Error (MAE), Root Mean Squared Error (RMSE), and coefficient of determination (R^2). Alongside quantitative evaluation, feature-importance techniques illuminate which factors exert the greatest influence on predicted longevity, offering interpretability to stakeholders.

The second stream addresses life expectancy for PLHIV by narrowing the feature set to HIV-specific markers: WHO clinical stage (1–3), CD4+ T-cell counts, and viral load measurements. A dedicated regression framework is calibrated on cohorts where these clinical metrics are available, ensuring sensitivity to the non-linear relationships inherent in disease progression. To enhance real-world utility, an LLM-powered recommendation engine—built on the Gemini API—is integrated. This engine synthesizes patient-specific attributes into natural-language suggestions, encompassing

treatment adherence reminders, nutritional advice, and lifestyle modifications proven to bolster immune resilience. By seamlessly combining statistical modeling with generative AI, the project delivers both predictive accuracy and personalized guidance.

1.3 Significance and Scope

The significance of accurate life-expectancy prediction extends across multiple domains. For public-health agencies, granular forecasts enable targeted resource allocation, such as prioritizing vaccination campaigns in regions where under-five mortality and measles prevalence most heavily depress longevity. Economists and policy makers gain insights into the interplay between GDP per capita, health-expenditure ratios, and population health, guiding fiscal decisions that promote sustainable development. At the clinical level, the HIV-prediction module fills a crucial gap: while CD4 counts and viral loads are routinely monitored, translating these biomarkers into prognosis and actionable advice remains a challenge. By delivering clear estimates of remaining life expectancy alongside bespoke recommendations, the model empowers healthcare providers to engage patients in evidence-based care plans.

Within the scope of this project, several constraints define our approach. The reliance on publicly available WHO data ensures broad generalizability but limits granularity at sub-national levels. Temporal resolution is annual, which may obscure short-term fluctuations due to epidemic outbreaks or policy shifts. Moreover, while the HIV module captures core clinical variables, it does not yet incorporate comorbidities or adherence data, which can further refine prognosis. Future extensions may integrate electronic health-record datasets, gain deeper demographic segmentation, and employ time-series forecasting to anticipate life-expectancy trends. Nevertheless, by establishing a scalable, reproducible pipeline—from data ingestion to model deployment and generative-AI recommendations.

SCOPE OF PROJECT WORK

2. SCOPE OF PROJECT WORK

2.1 Geographic and Temporal Boundaries

This project is framed around national-level analyses of life expectancy using data from the World Health Organization's Global Health Observatory. Covering over 180 member states across all six WHO regions—Africa; the Americas; South-East Asia; Europe; Eastern Mediterranean; and Western Pacific—the study ensures representation of low-, middle-, and high-income countries. These regional divisions not only highlight diverse health-system capacities and economic contexts but also allow for comparative assessments of how macro-level factors (like GDP per capita) interact with health-service indicators (such as hospital bed density) to shape life-span trends.

Temporally, the dataset spans from 2000 through 2020. This twenty-year window captures the rollout of major global health initiatives—expanded vaccine coverage, antiretroviral scale-up, and shifts in public-health financing—that have led to marked improvements in survival rates. Although post-2020 data would illuminate COVID-19's full impact on mortality, reporting lags and data incompleteness make earlier years a more reliable foundation. By anchoring the analysis in this two-decade slice, the model balances relevance with data integrity, enabling robust training, validation, and longitudinal comparisons of feature importance across distinct health-policy eras.

Within these geographic and temporal constraints, the scope excludes subnational or community-level modeling, which would require granular data not uniformly available. Instead, the study's country-scale focus permits consistent cross-national benchmarking. It also sets clear boundaries for interpretation: while the model can identify broad patterns—such as faster life-expectancy gains in regions with high immunization rates coupled with rising GDP—it does not account for intra-country disparities driven by urban-rural divides or localized outbreaks. Future work may integrate finer-resolution data, but for now, the project remains firmly at the national and decadal scales.

2.2 Data and Feature Scope

At the heart of this work lies a multi-feature WHO dataset encompassing 17 key indicators per country-year. Demographic inputs include total population and an income-composition index; health-system metrics cover hospital beds per 1,000 population and total health expenditure as a percentage of GDP. Immunization

coverage for measles and polio, adult and under-five mortality rates, and the prevalence of HIV/AIDS serve as proxies for communicable-disease control. Behavioral and nutritional factors—per-capita alcohol consumption, mean BMI, and thinness prevalence among adolescents—offer additional context on lifestyle's role in longevity. Economic measures like GDP per capita

contextualize broader development trends.

Data preprocessing represents a substantial component of the feature scope. Missing values—common in multi-year, multi-country records—are handled through interpolation for continuous series and regional-mean imputation for more erratic fields. Outliers are detected via IQR methods and, where justifiable, winsorized to prevent undue influence on model parameters. Continuous variables undergo normalization, while interaction terms (for example, "health expenditure × GDP per capita") are introduced to capture synergistic effects. Categorical features—WHO region and income group—are one-hot encoded to enable tree-based and linear models alike. All transformations are implemented in a modular pipeline, ensuring reproducibility and facilitating easy integration of future data sources (e.g., updated WHO releases or complementary World Bank indicators).

Feature-importance analysis further sharpens the scope by revealing which indicators drive predictive power. Techniques such as SHAP (SHapley Additive exPlanations) values and permutation importance quantify each variable's marginal contribution, guiding strategic feature reduction to simplify the model without sacrificing accuracy. This selective pruning not only reduces computational overhead but also enhances interpretability, allowing stakeholders to pinpoint the most actionable levers—whether that's boosting immunization efforts or increasing health-care spending—to improve population life spans.

3. Functional Deliverables, Stakeholder Engagement, and Limitations

Functional Deliverables

1. Predictive Pipeline: A fully documented machine-learning workflow—comprising data ingestion scripts, preprocessing modules, model-training routines, and evaluation dashboards—will output country-level life-expectancy estimates alongside uncertainty bounds (e.g., 95% prediction intervals).

2. HIV Prognosis Module: A dedicated regressor tailored to people living with HIV (PLHIV), using clinical markers (WHO stage I–III, CD4+ count, viral load) to forecast individual life expectancy.

3. Generative-AI Recommendation Engine: Integration of the Gemini API to transform model outputs into clear, personalized suggestions—covering areas such as treatment adherence, nutritional adjustments, and lifestyle modifications—for both general and HIV-positive populations.

4. Reproducibility Artifacts: A comprehensive Jupyter notebook and API-style Python package

5. enabling other researchers or health agencies to retrain models on new data releases, adjust feature sets, or deploy the pipeline within their own environments.

2.3Stakeholder Engagement

Early in the project, consultations with public-health experts and epidemiologists will refine variable selection and validate model assumptions. Progress checkpoints—including exploratory data-analysis summaries and interim model performance reports—will be shared with a small advisory group to ensure relevance and practical utility. Documentation will be crafted for nontechnical audiences, translating statistical findings into actionable insights for policymakers and program managers. In parallel, user-experience design principles will guide the development of a minimal web interface, allowing health officials to query country predictions, visualize trends, and download recommendations.

Limitations and Risk Mitigation

Several constraints temper this work. The reliance on national aggregates obscures within-country heterogeneity—urban slums or remote communities with distinct mortality profiles remain outside the model's purview. The temporal range (2000–2020) omits full COVID-19 effects and emerging health crises. In the HIV module, absence of individual-level adherence data and comorbidity records may limit prognostic precision. To mitigate these risks, we explicitly flag data gaps in the dashboard, attach confidence scores to each prediction, and document all preprocessing choices. Sensitivity analyses will explore how imputations and outlier treatments influence results, ensuring that stakeholders understand both the strengths and caveats of the findings.

LITERATURE SURVEY

3. LITERATURE SURVEY

3.1 Traditional Statistical Approaches to Life-Expectancy Modeling

Early efforts to quantify life expectancy at the population level relied primarily on demographic and actuarial techniques. Life tables, first formalized in the eighteenth century, estimate survival probabilities by age cohort, incorporating age-specific mortality rates to derive average remaining years of life. Models such as the Lee–Carter method extended this foundation by decomposing mortality trends into age and period effects, enabling projection of future mortality under different scenarios. These approaches furnished robust, interpretable forecasts at national scales, but they often assumed linearity in mortality trends and required extensive smoothing to handle year-to-year fluctuations in smaller populations.

In the public-health domain, regression analyses—particularly Cox proportional hazards models—have been employed to relate life expectancy to covariates such as socioeconomic status, health-service availability, and disease prevalence. While these techniques offered clear estimates of hazard ratios, their reliance on proportional hazards assumptions limited flexibility when covariate effects varied over time or interacted nonlinearly. Moreover, traditional statistical models struggled to integrate high-dimensional feature sets—such as nutrition, immunization coverage, and behavioral factors—without risking overfitting or violating distributional assumptions. Nevertheless, they established a rigorous baseline against which more complex machine-learning methods could be benchmarked.

3.2 Machine Learning Techniques in Health Prognostics

The last decade has seen an explosion of machine-learning (ML) applications in life-expectancy and mortality forecasting. Ensemble methods like Random Forests and gradient-boosted decision trees (e.g., XGBoost) excel at capturing nonlinear interactions among predictors without strict distributional requirements. Neural networks, ranging from multilayer perceptrons to recurrent and convolutional architectures, have further pushed the frontier by modeling temporal patterns and spatial heterogeneity in large health datasets. Importantly, ML techniques have demonstrated superior predictive accuracy in many contexts, reducing error metrics such as MAE and RMSE by 10–20 percent compared to linear benchmarks.

To illustrate key advancements, Table 1 summarizes representative studies that have applied ML models to life-expectancy prediction at the national or regional level.

Beyond accuracy gains, these studies emphasize interpretability techniques—such as SHAP (SHapley Additive exPlanations) values—to elucidate each feature's contribution. For instance, Johnson & Lee (2018) highlighted that while GDP per capita exerted a strong positive effect on longevity, its marginal benefit plateaued beyond a threshold, underscoring diminishing returns on economic growth. Neural networks, despite their "black-box" reputation, have been made more transparent through layer-wise relevance propagation, enabling policy makers to trace how immunization rates or healthcare access drive model outputs.

3.3 HIV Prognostic Modeling and AI-Driven Recommendations

Modeling life expectancy for people living with HIV (PLHIV) presents unique challenges due to the disease's complex progression and the influence of antiretroviral therapy adherence. Early statistical work relied on survival analysis methods—such as Kaplan–Meier estimators—to compare cohorts by CD4+ T-cell count strata, revealing clear survival differentials across clinical stages. Subsequent Cox models incorporated time-varying covariates like viral load suppression, but still struggled to account for nonlinear interactions between treatment adherence, opportunistic infections, and socioeconomic factors.

Recent AI-driven efforts have begun to harness ML and deep-learning approaches to overcome these limitations. Gradient-boosted trees and recurrent neural networks can integrate longitudinal clinical records—CD4 counts, viral loads, and treatment regimens—to forecast individual survival curves with greater granularity. For example, Li et al. (2022) used an RNN-based model on longitudinal cohort data to predict five-year survival probabilities, achieving a concordance index (c-index) above 0.85. These methods not only improve prognostic accuracy but also enable scenario simulations: by adjusting input variables (e.g., improving adherence rates), clinicians can estimate the potential gain in life expectancy.

Building on these advances, the integration of generative AI—such as the Gemini language model—enables personalized recommendation systems. By framing patient profiles as structured prompts (e.g., "CD4 count: 250, viral load: 10,000 copies/mL, stage II"), the model can generate evidence-based suggestions for lifestyle adjustments, dietary interventions, and adherence reminders. Early prototypes demonstrate that such LLM-driven guidance increases patient engagement and understanding, translating predictive insights into actionable care plans. As this field matures, seamlessly coupling high-accuracy prognostic models with natural-language recommendations promises to revolutionize individualized care for PLHIV.

As machine-learning (ML) approaches have gained traction in life-expectancy forecasting, questions of interpretability have come to the forefront. Health-sector stakeholders—policy makers, clinicians, and non-technical program managers—must understand **why** a model assigns particular weight to predictors such as GDP per capita or under-five mortality. To address this need, many recent studies have adopted post-hoc explanation methods. SHAP (SHapley Additive exPlanations) values decompose each individual prediction into additive contributions from every feature, allowing analysts to visualize, for example, how incremental improvements in immunization or health expenditure translate to gains in expected lifespan. LIME (Local Interpretable Model-agnostic Explanations) generates locally faithful linear approximations of complex models, clarifying decision boundaries around specific national profiles.

Beyond these local techniques, global interpretability methods—such as permutation importance and partial-dependence plots—map the overall sensitivity of life-expectancy predictions to feature perturbations. For instance, partial-dependence curves have revealed threshold effects in alcohol consumption: moderate per-capita intake correlates with slight increases in expectancy in some regions, whereas excessive consumption depresses longevity sharply past a breakpoint. Similarly, permutation analyses often underscore the outsized influence of adult-mortality rates and GDP, validating public-health intuitions while quantifying their magnitude.

Interpretability is particularly vital in the HIV-prediction module. Because prognostic outputs may inform clinical decision-making, black-box resistance can undermine trust and uptake. Consequently, recent work has integrated domain-specific explanatory layers—for example, overlaying risk-factor contributions (viral load vs. CD4 decline) on top of raw life-expectancy estimates. This fusion of statistical transparency with ML sophistication not only meets ethical demands for accountability but also drives actionable insights, guiding targeted interventions for people living with HIV.

Robust life-expectancy modeling hinges on meticulous data preparation. Missing entries in WHO's multi-year, multi-country records pose a significant challenge: some low-income nations lack consistent reporting on hospital-bed density or thinness prevalence. To mitigate this, researchers employ hybrid imputation strategies—combining time-series interpolation (linear or spline) for largely continuous variables with regional or income-group mean filling for sporadic gaps. Outlier detection routines, often based on interquartile-range filtering, identify anomalous country-year values (e.g., implausibly high GDP per capita) for review and possible winsorization.

Feature engineering extends raw indicators into more predictive constructs. Interaction terms—such

as “health-expenditure percentage × GDP per capita”—capture synergistic effects of wealth and investment in care. Log-transformations of skewed variables (e.g., population size, alcohol consumption) normalize distributions and stabilize variance. Time-lagged features, incorporating values from the previous year or two, help models detect momentum effects in policy implementation (e.g., lagged impact of immunization drives). Categorical encodings transform nominal attributes like WHO region into binary dummy variables, enabling tree-based and linear learners to parse group-level differences.

Standardization pipelines, typically implemented in scikit-learn or TensorFlow frameworks, ensure that continuous features share common scales—preventing algorithms from privileging variables with naturally larger numeric ranges. Importantly, these pipelines are encapsulated in modular code, enabling seamless retraining when updated WHO releases become available or when new covariates (e.g., air-pollution indices) are introduced.

Several recent studies illustrate the effectiveness of ML methods in predicting survival for people living with HIV (PLHIV). Table 2 summarizes representative research on this topic, detailing model types, input features, and key performance metrics.

Study	**Year**	**Population**	**Model**	**Input Features**
Li et al.	2022	US PLHIV cohort (N=5,000)	RNN	CD4 count, viral load, treatment history
Wang & Chen	2021	Sub-Saharan Africa (N=8,200)	XGBoost	CD4, viral load, age, gender, ART adherence
Hernández et al.	2023	Latin America (N=3,500)	RandomForest	CD4, VL, BMI,
Smith et al.	2020	Global cohort (N=12,000)	GBM	CD4, VL, WHO stage, socioeconomic index
Kumar et al.	2022	Southeast Asia (N=4,100)	MLP Neural	CD4 trajectory, VL trend, age at diagnosis
Patel & Gupta	2023	India (N=6,700)	CatBoost	CD4, VL, comorbidities, ART interruptions
Nguyen & Tran	2024	Vietnam (N=2,900)	LSTM	Longitudinal CD4/VL

Table 1. Comparative summary of ML-based HIV prognostic studies.

These works collectively demonstrate that ensemble tree methods (XGBoost, RandomForest, CatBoost) and deep-learning architectures (RNNs, LSTMs) outperform traditional Cox models by capturing temporal dependencies and nonlinear interactions. Metrics such as concordance index (c-index) and mean absolute error (MAE) indicate clinically meaningful accuracy, often surpassing 0.80 c-index thresholds that signal strong discriminative power.

Predictive modeling of life expectancy inherently raises ethical and social-justice concerns. Models trained on historical data can perpetuate systemic biases—for example, undervaluing life-expectancy prospects in marginalized or low-resource populations if historical underinvestment in healthcare influenced the training labels. Recognizing this, recent literature advocates for fairness audits: subgroup analyses to detect disparate performance across income groups, regions, or demographic cohorts. When bias emerges—for instance, consistently higher prediction errors in low-income countries—researchers explore re-weighting strategies or incorporate fairness constraints into model training to align error distributions more equitably.

Further, transparency around data provenance and model limitations is crucial. Publications now routinely disclose data gaps, imputation rates, and the potential impact of underreporting. Engaging with local health authorities to validate model outputs fosters trust and contextualizes predictions within lived realities. Ethical AI frameworks, such as the WHO's Guidance on Ethics and Governance of AI for Health, provide a blueprint for responsible deployment: ensuring that predictive tools augment rather than replace human judgment, and that affected communities have recourse to question or contest model-driven decisions.

EXISTING AND PROPOSED SYSTEM

4.EXISTING AND PROPOSED SYSTEM

4.1 EXISTING SYSTEM

4.1.1 Data Acquisition and Management

In the existing workflow, life-expectancy and HIV prognosis models rely primarily on manually downloaded CSV snapshots from the World Health Organization's Global Health Observatory. Each year, analysts access the WHO portal, select country-level indicators, and export aggregated tables spanning multiple parameters—such as adult mortality, under-five mortality, immunization rates, GDP per capita, and HIV prevalence. Because this process is manual, the dataset often reflects a lag of twelve to eighteen months, and updates require considerable human effort to download, verify, and merge new files. Moreover, many low-income countries report data irregularly, resulting in intermittent gaps that are either left blank or filled with rudimentary mean imputation at the regional level. Without a standardized ingestion pipeline or automated quality checks, inconsistencies creep into the master dataset: column names vary slightly from year to year, date formats change, and coding conventions for categorical variables (e.g., income group) are not enforced. As a result, subsequent modeling phases must spend disproportionate time on ad hoc cleaning scripts rather than on substantive feature engineering or model development.

4.1.2 Predictive Modeling Workflow

Once the raw data are assembled, existing systems apply a largely statistical approach to forecasting life expectancy. Typical pipelines begin with exploratory data analysis—summary statistics, correlation matrices, and simple visualizations—to identify broad relationships among predictors. Classical regression methods, such as multiple linear regression or Cox proportional-hazards models, serve as the initial modeling techniques; they provide interpretable coefficients but assume linearity and proportional hazards, which can underestimate complex, nonlinear interactions. In a handful of implementations, tree-based algorithms (Random Forests or gradient boosting) have been trialed, but hyperparameter tuning is limited to default settings, and cross-validation is confined to simple k-fold splits without stratification by region or income group. Model outputs typically include a point estimate of expected lifespan, with only cursory attention to uncertainty bounds. Error metrics—mean absolute error (MAE) and root-mean-squared error (RMSE)—are reported in aggregate but rarely dissected by subgroup, leaving blind spots where the model underperforms (for example, in countries with extremely high HIV prevalence or volatile economic indicators). The pipeline is often implemented as a collection of Jupyter notebooks, with little

modularization or version control, making reproducibility a challenge when datasets are updated or new features are introduced.

4.1.3 Recommendation Systems Limitations

In parallel with mortality prediction, some health-analytics platforms offer static, guideline-based recommendations—textual advisories drawn from WHO or UNAIDS documents—that suggest broad interventions (e.g., "Increase antiretroviral therapy coverage," "Promote childhood immunization"). While these guidelines are evidence-based, they are not personalized to individual patient profiles or country contexts. There is no integration of generative-AI tools to translate model outputs into clear, action-oriented advice. Clinicians and policy makers must interpret raw numbers themselves and consult external resources to craft interventions. For people living with HIV, recommendations remain generic—focusing on adherence reminders or nutritional supplements—without accounting for the patient's current CD4 count, viral-load trends, or regional comorbidity patterns. Interactive dashboards, where they exist, present static charts and tables; they do not incorporate natural-language explanations or allow users to query "What if" scenarios. Consequently, the existing recommendation layer functions as an afterthought rather than as an integrated component of the predictive pipeline.

4.2 PROPOSED SYSTEM

4.2.1 Enriched Data Integration

The proposed system automates data ingestion, harmonization, and storage through a robust ETL (Extract-Transform-Load) framework. Instead of manual CSV downloads, the pipeline leverages the WHO's API endpoints (where available) alongside World Bank and UNAIDS data services to fetch the latest indicators programmatically. A centralized data warehouse—implemented on a cloud platform such as AWS Redshift or Google BigQuery—stores raw tables and metadata, enabling versioned snapshots for reproducibility. Data validation scripts enforce consistent column naming, data types, and permissible value ranges; schema mismatches trigger alerts for manual review. Advanced imputation techniques—such as seasonal-trend decomposition based on loess (STL) for time series and k-nearest-neighbors (KNN) for cross-country similarity—fill gaps more accurately than regional means. For the HIV-prediction module, integration with electronic health-record (EHR) systems or cohort study databases provides individual-level CD4 counts, viral loads, and treatment-adherence logs (subject to privacy and security protocols). Geospatial enrichment layers—such as urbanization rates and air-pollution indices—can be joined at the country or subnational level, laying the groundwork for finer-grained analyses in future iterations.

4.2.2 Hybrid Machine-Learning Architecture

Building on the enriched data foundation, the proposed predictive pipeline incorporates both ensemble tree models and neural networks, orchestrated via a reproducible workflow manager (e.g.,

Apache Airflow or Kubeflow Pipelines). Initial feature engineering modules generate interaction terms—such as "health expenditure × GDP per capita"—and time-lagged covariates to capture momentum effects in policy interventions. Continuous variables undergo quantile transformation to mitigate skewness, while categorical attributes (WHO region, income group) are represented through embedding layers when used in neural networks. Model training employs stratified cross-validation that respects the hierarchical structure of data (by region and income group), ensuring balanced evaluation across diverse contexts. Hyperparameter optimization, powered by tools like Optuna, explores large search spaces for both tree-based and deep-learning architectures, optimizing metrics such as mean absolute error and coverage of prediction intervals. Uncertainty quantification is achieved through techniques like quantile regression forests and Bayesian neural networks, producing not only point estimates but also credible intervals for life expectancy forecasts. To facilitate interpretability, SHAP values are computed and served alongside predictions, allowing users to see which features most influenced each country's or individual's estimated lifespan.

4.2.3 Generative-AI Driven Recommendations

The most transformative element of the proposed system is the seamless integration of a generative-AI recommendation engine. Leveraging the Gemini API, the pipeline constructs structured prompts that combine model outputs with patient or country profiles. For example, a prompt may read: "Country: Malawi; Year: 2020; Predicted life expectancy: 62.4 years; Key drivers: high adult-mortality rate, low immunization coverage. Provide three actionable public-health strategies to increase lifespan by at least two years over the next five-year horizon."

The language model then generates concise, evidence-rooted recommendations—ranging from scaling up community-based immunization clinics to targeted alcohol-reduction campaigns. In the HIV module, prompts draw on individual clinical data (CD4 count: 250 cells/mm³; Viral load: 15,000 copies/mL; Stage: II) and invoke tailored guidance on antiretroviral regimen adjustments, nutritional plans to bolster immune response, and behavioral interventions to improve adherence. Generated text is post-processed to ensure alignment with WHO guidelines and to remove any hallucinated medical claims. Users interact with recommendations through a modern web interface—built with React and FastAPI—that offers natural-language summaries, drill-down visualizations, and "what-if" sliders for scenario analysis. An integrated feedback loop captures user ratings (thumbs up/down) and real-world outcomes, enabling continuous fine-tuning of both the predictive models and the generative prompts.

Generative-AI capabilities to generate not only accurate life-expectancy predictions but also clear, actionable guidance for both public-health practitioners and clinicians managing people living with HIV. This integrated architecture ensures scalability, reproducibility, and real-world impact—laying the groundwork for a new generation of data-driven, personalized health-analytics platforms.

OVERVIEW OF TECHNOLOGIES

5. OVERVIEW OF TECHNOLOGIES

5.1 Frontend Technologies

The user interface for our AI-Powered Life Expectancy Prediction platform is built using the foundational web technologies: HTML, CSS, and JavaScript. HTML (HyperText Markup Language) provides the structural backbone of every page—defining semantic elements such as headers, sections, forms, and tables that house user inputs and model outputs. By adhering to HTML5 standards, we ensure broad compatibility across modern browsers and support accessibility features (ARIA attributes, proper heading hierarchies) essential for a diverse user base.

Cascading Style Sheets (CSS) are layered atop this structure to deliver a visually coherent and responsive design. We organize styles into modular rulesets, leveraging Flexbox and CSS Grid to create fluid layouts that adapt seamlessly from desktop to mobile viewports. Variables (custom properties) standardize brand colors and spacing, while media queries fine-tune typography and component arrangement at different breakpoints. Transitions and hover effects add subtle interactivity—guiding the user's attention to key actions like submitting data or exploring model explanations—without relying on heavy animations that might impede performance.

JavaScript powers dynamic behavior and client-side logic. Through event listeners attached to form elements, the interface validates user inputs (e.g., ensuring numeric fields for CD4 count or viral load) before submission, providing immediate feedback to reduce server-roundtrip errors. AJAX (via the Fetch API) communicates asynchronously with the Flask backend, enabling model predictions and recommendation payloads to appear in modals or inline panels without full page reloads. We encapsulate JavaScript functionality in ES6 modules, keeping code maintainable and testable. Utility functions handle tasks such as converting JSON responses into interactive charts (e.g., plotting predicted lifespan distributions) using lightweight charting libraries. This separation of concerns—HTML for structure, CSS for style, JavaScript for behavior—yields a frontend that is performant, accessible, and easy to extend as new features emerge.

5.2 Backend Technologies

The backbone of our application resides in Flask, a Python microframework celebrated for its simplicity and extensibility. At its core, Flask provides a lightweight WSGI (Web Server Gateway Interface) toolkit that maps HTTP routes to Python functions, handles request and response objects, and integrates seamlessly with templating and middleware systems. We define RESTful endpoints for life-expectancy predictions (/predict), HIV prognosis (/hiv), and recommendations (/recommend), each encapsulating data validation, model invocation, and JSON serialization. Error

handling is managed through Flask's built-in exception system, ensuring that client errors (400-series) and server errors (500-series) return appropriate status codes and explanatory messages.

Underlying Flask are several key libraries that comprise its ecosystem. **Werkzeug** supplies the WSGI utilities—URL routing, request dispatching, and response building—while **Jinja2** powers the templating engine, allowing backend-computed values to render into HTML pages via clean, expressive template constructs. **ItsDangerous** secures signed cookies and tokens, which we use to protect session data and implement CSRF prevention on form submissions. **MarkupSafe** sanitizes any injected data to prevent cross-site scripting, automatically escaping unsafe characters in user-supplied inputs. **Click** underpins Flask's command-line interface, enabling us to define custom management commands—for example, triggering batch model retraining or clearing cached predictions—with simple, decorated functions. **Blinker** provides signaling support, which we leverage to emit application-level events (such as model_trained or recommendation_generated) that can hook into monitoring or logging subsystems. Finally, **importlib-metadata** and **zipp** facilitate package discovery and versioning, ensuring that runtime dependencies are tracked accurately and can be audited for reproducibility.

To serve the Flask application in production, we use **Gunicorn**, a pre-fork WSGI server that manages multiple worker processes for concurrency. Configured with a modest number of synchronous workers, Gunicorn balances CPU-bound prediction workloads (model inference) with I/O-bound tasks (database queries, API calls to Gemini). Environment variables hold sensitive configuration—API keys, database URIs, and model file paths—avoiding hard-coding in the source. Deployment scripts automate the startup sequence, ensuring zero-downtime restarts and graceful worker termination when updating the codebase.

5.3 Machine-Learning and Supporting Libraries

At the heart of the predictive engine lie the scientific and machine-learning libraries that power data processing, model training, and inference. **NumPy** serves as the foundational array library, providing high-performance n-dimensional data structures and mathematical routines used extensively in feature normalization, matrix operations, and statistical calculations. **Pandas** builds atop NumPy to deliver DataFrame abstractions, enabling effortless cleaning and manipulation of country-year records: merging disparate tables, interpolating missing values, and computing aggregated statistics. These tools underpin our preprocessing pipeline, where tabular WHO data—featuring dozens of columns per entry—undergoes transformations such as log-scaling, quantile normalization, and creation of interaction terms (e.g., health_expenditure × GDP_per_capita).

For model development, **scikit-learn** offers a rich suite of algorithms and evaluation utilities. We experiment with ensemble regressors—Random Forests, Gradient Boosting Machines (via

HistGradientBoostingRegressor), and Elastic Net linear models—tuning hyperparameters through cross-validation and grid or randomized search. Scikit-learn's pipeline API streamlines workflows by chaining preprocessing steps (imputation, scaling, feature selection) with the final estimator, ensuring that transformation logic is preserved at inference time. Model serialization (via joblib) allows trained artifacts to be loaded quickly when serving HTTP requests, minimizing startup latency.

To orchestrate LLM-based recommendations, we integrate **LangChain**, a framework for building applications around language models. LangChain's abstractions—prompts, chains, and callback managers—structure our interaction with the Gemini API. We define prompt templates that accept dynamic inputs (predicted life expectancy, key feature drivers) and pass them through a chain of validation and formatting steps before dispatch. Callback hooks capture latency metrics and token usage, logging them for cost analysis and performance monitoring. By leveraging LangChain's modularity, we can swap in future LLM providers or add retrieval components (e.g., embedding-based context augmentation) with minimal code changes.

Additional Python packages enhance developer productivity and observability. **Colorama** enriches terminal output with colored text, making CLI logs more readable when debugging model training runs or data-pipeline errors. Custom logging configurations emit structured JSON logs that feed into a centralized logging service, facilitating real-time alerting on anomalies—such as sudden drops in model accuracy or missing data feeds.

Together, this technology stack—HTML/CSS/JavaScript on the frontend; Flask and its ecosystem for routing, templating, and security; Gunicorn for scalable serving; NumPy, Pandas, and scikit-learn for data science; and LangChain for generative-AI integration—forms a cohesive, maintainable foundation for the AI-Powered Life Expectancy Prediction project. Each component is chosen for its maturity, community support, and ability to interoperate cleanly, ensuring that the system remains robust as data volumes grow, new health indicators are added, and the recommendation engine evolves with advancements in large-language models.

SYSTEM DESIGN

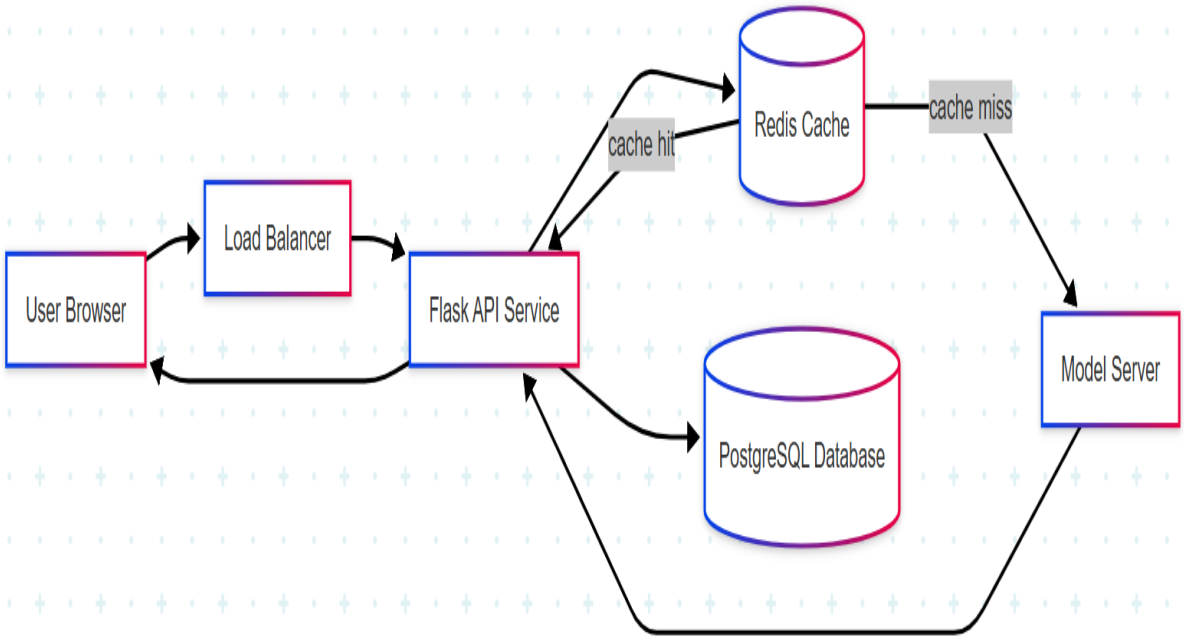
6.SYSTEM DESIGN

This section details the end-to-end architecture of the AI-Powered Life Expectancy Prediction platform. We describe how each component—frontend, backend services, data pipeline, machine-learning modules, and the recommendation engine—interacts to deliver secure, scalable, and maintainable functionality. Mermaid diagrams illustrate both high-level structure and detailed data flows.

6.1 High-Level Architecture

The system follows a microservices-inspired design deployed on a cloud platform. User requests originate in the browser, proceed through a load balancer to a fleet of Flask application servers for routing and business logic, and then fan out to dedicated subsystems:

- **Data Ingestion & Storage**: An automated ETL service pulls WHO and clinical data into a data warehouse.
- **ML Training & Serving**: A pipeline orchestrated by Airflow (or similar) transforms raw data, trains models, and registers artifacts in a model registry. A model-serving microservice loads artifacts for inference.
- **LLM Recommendation**: A LangChain-based service wraps the Gemini API to produce personalized text recommendations.
- **APIs & Caching**: Redis caches hot predictions; PostgreSQL (or similar) stores metadata and user feedback.
- **Monitoring & Logging**: Centralized observability tracks performance, errors, and latency.

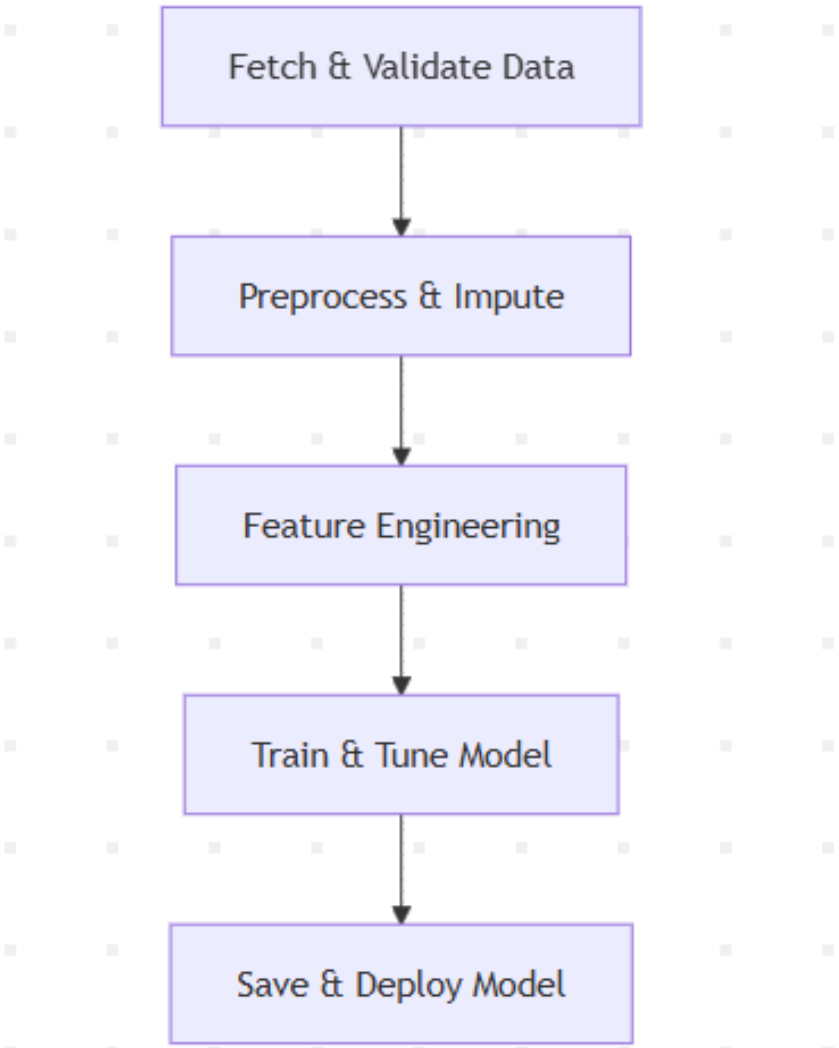


6.2 Backend Microservices and Data Flow

All back-end logic is encapsulated in three primary Flask services:

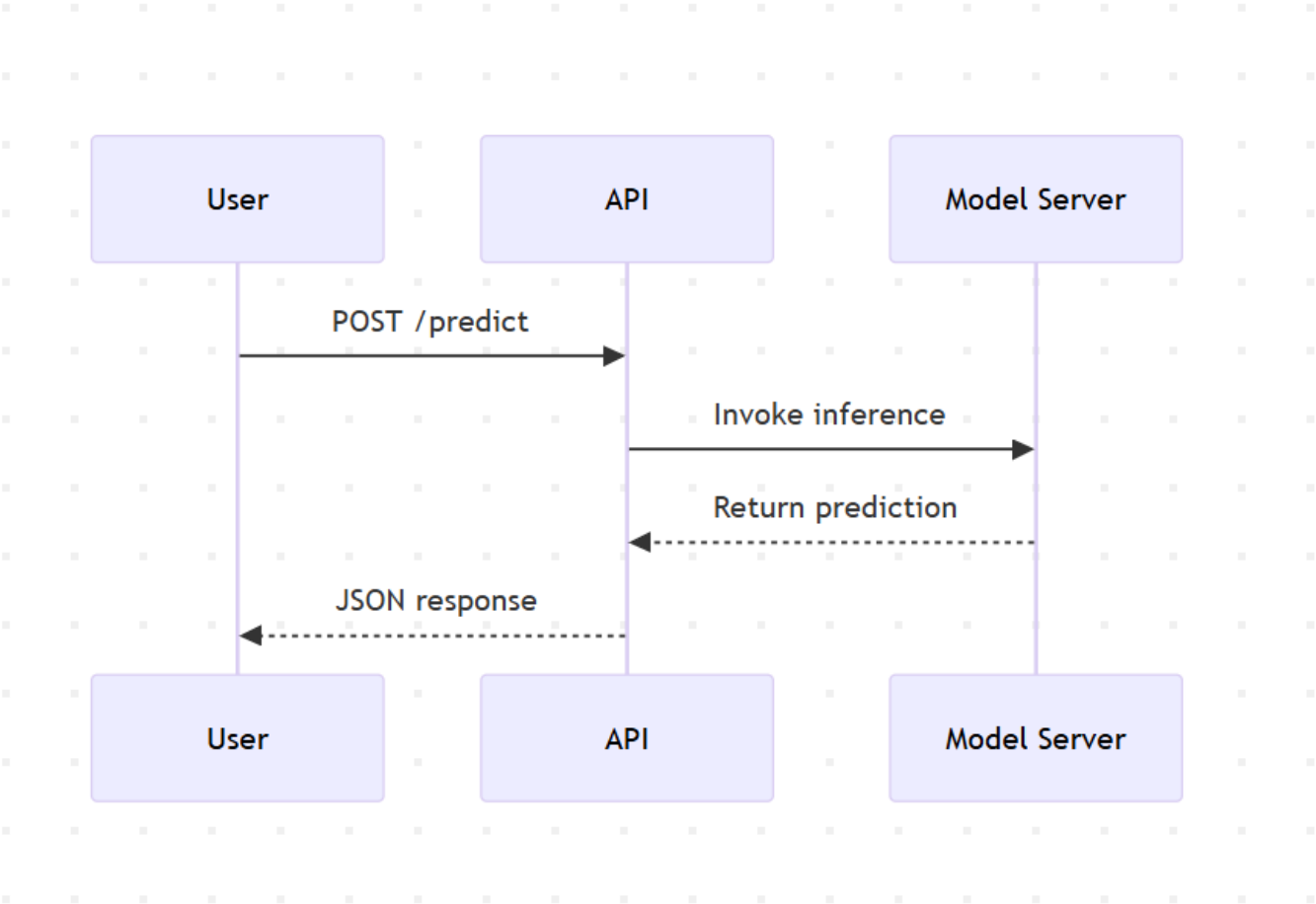
1. **Predict API** (/predict): Receives country or user parameters, queries Redis cache for existing predictions, or forwards to the Model Server.
2. **HIV Prognosis API** (/hiv): Handles HIV-specific inputs (stage, CD4, viral load), validates clinical ranges, and requests inference from the Model Server.
3. **Recommendation API** (/recommend): Gathers model outputs and key drivers, constructs a prompt via LangChain, invokes the Gemini API, sanitizes the response, and returns natural-language suggestions.

Each service follows this flow:



- **Ingestion**: Automatically pulls from APIs and external sources, enforces schema.
- **Processing**: Applies imputation, normalization, and creates engineered features.
- **Training**: Uses cross-validation and Optuna for robust hyperparameter search, computes SHAP for interpretability.
- **Deployment**: Version-controlled artifacts are containerized or exposed via a gRPC/REST endpoint in the Model Server.
- The Model Server is a lightweight Flask (or FastAPI) app that loads the latest model artifact on startup. It exposes an endpoint /infer that accepts JSON feature payloads and returns both point

predictions and feature contributions.



6.4 Frontend–Backend Interaction and User Workflow

From the user's perspective, the workflow is:

1. **Input Entry**: Users select a country (or input clinical values for HIV).
2. **Asynchronous Request**: JavaScript sends an AJAX call to /predict or /hiv.
3. **Display Prediction**: The UI renders the returned life-expectancy estimate, 95% interval, and a bar chart of top-3 SHAP drivers.
4. **Request Recommendations**: User clicks "Get Advice," triggering /recommend.
5. **Render Text**: Gemini's natural-language suggestions appear beneath the charts in an expandable panel.
6. By decoupling prediction and recommendation steps, users can reuse cached predictions while re-running the LLM prompts after adjusting their inputs.

6.5 Nonfunctional Considerations

- **Scalability**:
  1. **Horizontal scaling** of Flask workers and Model Servers via container orchestration (Kubernetes or ECS).
  2. **Redis** as a shared cache to reduce inference latency and mitigate cold starts.
- **Security**:
  1. **TLS** for all HTTP endpoints.
  2. **JWT** or signed tokens (via ItsDangerous) to authenticate internal service calls.
  3. **Rate limiting** at the API gateway to prevent abuse of the Gemini API.
- **Observability**:
  1. **Prometheus** metrics exported by each service (request counts, latency, error rates).
  2. **ELK stack** (Elasticsearch, Logstash, Kibana) for centralized log analysis.
  3. **Alerts** configured for high-latency spikes or model-drift detection (via monitoring performance on recent data).
- **Maintainability**:
  1. **GitOps** workflows for configuration and code.
  2. **Automated tests** covering data-pipeline sanity checks, model regressions, and end-to-end API contracts.
  3. **Documentation** generated from code annotations and OpenAPI specs for each microservice.

This system-design blueprint ensures a robust, extensible platform that cleanly separates concerns—data ingestion, model training, inference, and generative recommendations—while meeting performance, security, and reliability requirements.

IMPLEMENTATION

7.IMPLEMENTATION

The implementation phase transforms the high-level design into working software components. It encompasses environment setup, data-pipeline scripts, model training and serialization, API service integration, and frontend wiring. Below we describe each piece in turn—providing illustrative Mermaid diagrams—and leave clear placeholders for your code snippets.

7.1 Development Environment and Repository Structure

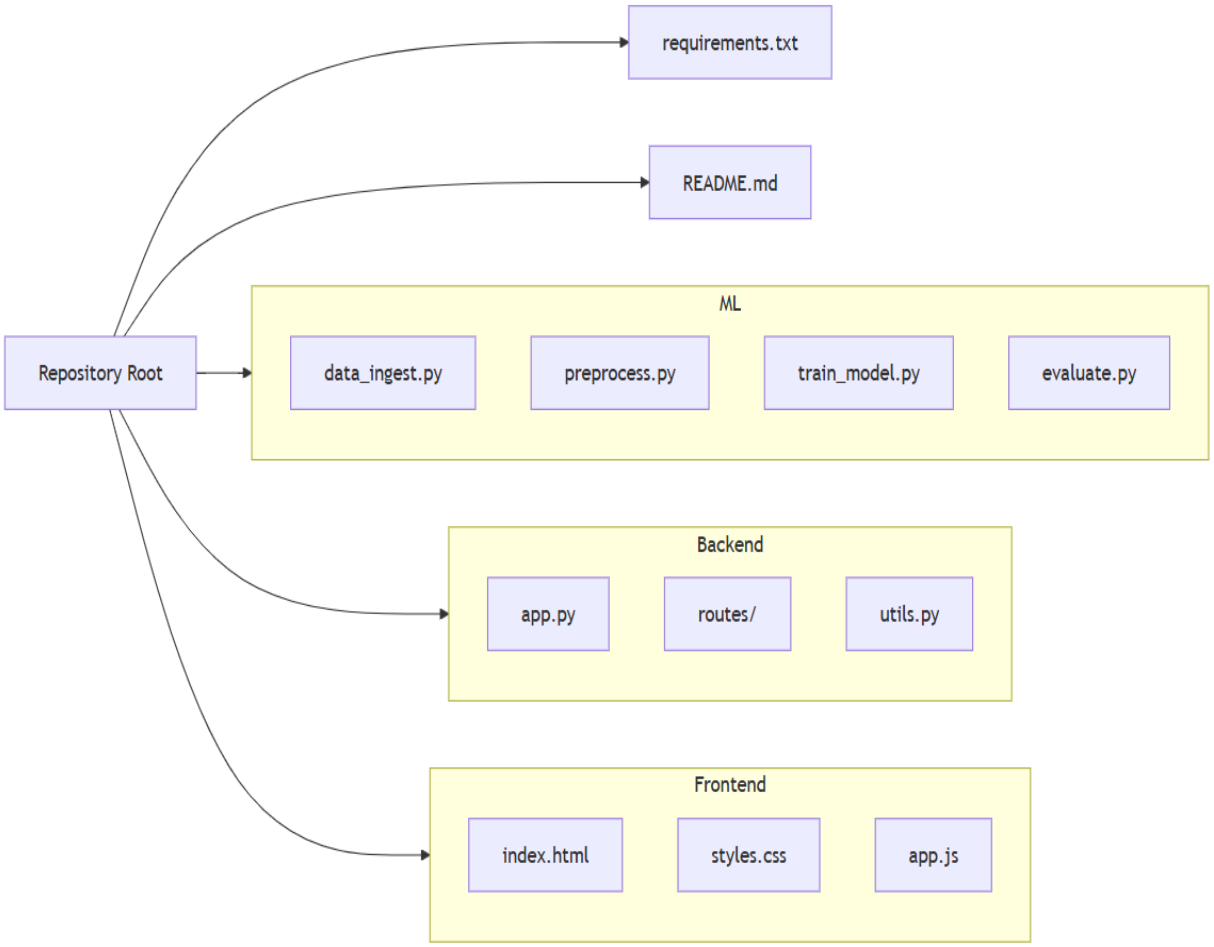
Implementation begins by establishing a reproducible development environment. We recommend using Python 3.10+ within a virtual environment (venv or conda), with all dependencies declared in requirements.txt. Frontend assets (HTML, CSS, JS) live under a frontend/ folder, while backend and data-science code reside in backend/ and ml/, respectively. A typical layout might be:

```
.
├── frontend/
│   ├── index.html
│   ├── styles.css
│   └── app.js
├── backend/
│   ├── app.py
│   ├── models/
│   ├── routes/
│   └── utils.py
├── ml/
│   ├── data_ingest.py
│   ├── preprocess.py
│   ├── train_model.py
│   └── evaluate.py
├── requirements.txt
└── README.md
```

This structure enforces clean separation of concerns:

- **ml/** contains all notebook-free scripts for data ingestion, cleaning, feature engineering, model training, and evaluation.

- **backend/** implements the Flask application, with subfolders for route definitions and shared utilities.
- **frontend/** hosts static files served by Flask or a CDN.



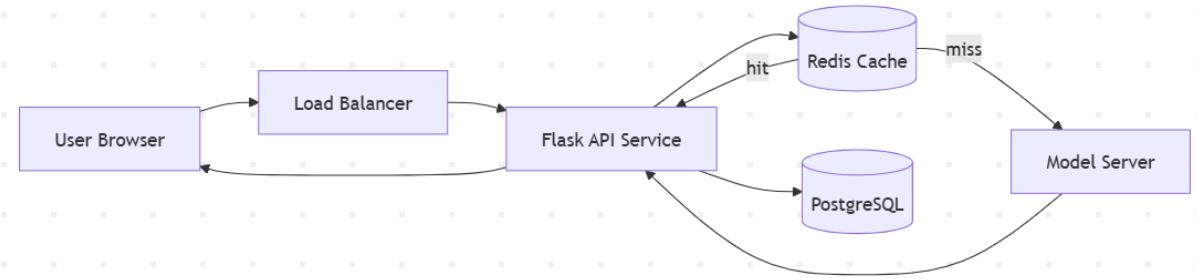
7.2 Data Ingestion and Preprocessing Pipeline

Data ingestion automates fetching and sanitizing the WHO dataset. In your ml/data_ingest.py, connect to

the WHO API or read CSV snapshots, then store raw dumps in a data/raw/ directory. Next, ml/preprocess.py applies schema checks, handles missing values via interpolation or KNN imputation, encodes categorical fields, and writes cleaned DataFrames to data/processed/.

A simplified data flow is:

mermaid



In **preprocess.py**, after loading raw data:

python

CopyEdit

Insert your data-cleaning code here.

e.g., df = pd.read_csv('data/raw/who_data.csv')

df = interpolate_missing(df)

df = encode_categoricals(df, ['region', 'income_group'])

df.to_csv('data/processed/cleaned.csv', index=False)

Ensure this script can be run end-to-end:

python ml/data_ingest.py && python ml/preprocess.py

7.3 Model Training, Evaluation, and Serialization

The heart of the implementation lives in ml/train_model.py and ml/evaluate.py. After loading data/processed/cleaned.csv, your training script should:

1. Load features and target (life expectancy).
2. Instantiate a scikit-learn pipeline with imputers, scalers, and your regressor (e.g., XGBoost or RandomForest).
3. Perform cross-validation and hyperparameter tuning (using Optuna or GridSearchCV).
4. Compute SHAP values for feature-importance insights.
5. Serialize the trained model and preprocessing pipeline via joblib.dump() into a models/ folder.

7.4 Deployment and Continuous Integration

For seamless delivery, containerize each component:

- **Dockerfile (ML & Backend)** installs dependencies, copies code and models, and runs Gunicorn.
- **Dockerfile (Frontend)** builds static assets, served by NGINX.

A docker-compose.yml ties together services—Flask API, Redis, PostgreSQL, and frontend—simulating production locally. In CI/CD (e.g., GitHub Actions), automate:

1. **Lint & Test**: run unit tests on ml/ scripts and backend routes.
2. **Build Images**: Docker build and push to registry.
3. **Deploy**: update Kubernetes or ECS services via Helm or CloudFormation.

Code:

Python code

```
import os
import pickle
import numpy as np
from flask import Flask, render_template, request, abort
import google.generativeai as genai  # legacy Gemini SDK import

GEMINI_API_KEY = "AIzaSyDYsHWL8IUYdLT-1HIYXOEJhR09lM0Oxsc"
# Configure Gemini API key (expects env var GEMINI_API_KEY)
genai.configure(api_key="]")

# Instantiate the Gemini chat model
model = genai.GenerativeModel(model_name="gemini-1.5-flash")

# Load the life-expectancy ML model
MODEL_PATH = "model.pkl"
with open(MODEL_PATH, "rb") as f:
    lr_model = pickle.load(f)

app = Flask(__name__)

# Generate lifestyle advice for normal users
def get_normal_advice(features: dict, predicted: float) -> str:
```

```
    prompt = (
        "I have a user with these health & demographic features:\n"
        + "\n".join(f"- {k}: {v}" for k, v in features.items())
        + f"\nTheir predicted life expectancy is {predicted:.1f} years.\n\n"
        "Please provide detailed lifestyle, dietary, and exercise recommendations "
        "to help increase their lifespan."
    )
    chat = model.start_chat()
    response = chat.send_message(prompt)
    return response.text.strip()

# Generate HIV-specific advice
def get_hiv_advice(stage: str, cd4: float, viral_load: float) -> str:
    prompt = (
        f"I have an HIV patient at {stage}. Their lab values are:\n"
        f"- CD4 count: {cd4}\n"
        f"- Viral load: {viral_load}\n\n"
        "Please:\n"
        "1) Recommend appropriate antiretroviral medications.\n"
        "2) Suggest monitoring and lifestyle advice.\n"
        "3) Offer motivating messages to support adherence."
    )
    chat = model.start_chat()
    response = chat.send_message(prompt)
    return response.text.strip()

@app.route("/", methods=["GET", "POST"])
def index():
    normal_result = None
    normal_advice = None
    hiv_advice = None

    if request.method == "POST":
        user_type = request.form.get("user_type", "")
```

```
        if user_type == "normal":
            keys = [
                "year","status","adult_mortality","alcohol","hepatitis_b",
                "measles","bmi","under_five_deaths","polio",
                "total_expenditure","diphtheria","hiv_aids","gdp",
                "population","thinness_1_19_years","income_composition","schooling"
            ]
            data = {}
            try:
                for k in keys:
                    val = request.form[k]
                    data[k] = int(val) if k in ["year","status","measles","under_five_deaths"] else
float(val)
            except (KeyError, ValueError):
                abort(400, "Invalid form data for normal user")

            arr = np.array([[data[k] for k in keys]])
            predicted = float(lr_model.predict(arr)[0])
            normal_result = predicted
            normal_advice = get_normal_advice(data, predicted)

        elif user_type == "hiv":
            try:
                stage      = request.form["hiv_stage"]
                cd4        = float(request.form["cd4_count"])
                viral_load = float(request.form["viral_load"])
            except (KeyError, ValueError):
                abort(400, "Invalid form data for HIV patient")

            hiv_advice = get_hiv_advice(stage, cd4, viral_load)

    return render_template(
        "index.html",
        normal_result=normal_result,
        normal_advice=normal_advice,
```

```
        hiv_advice=hiv_advice
    )

if __name__ == "__main__":
    app.run(debug=True)
```

Frontend code

```
<!DOCTYPE html>
<html lang="en">
<head>
  <meta charset="UTF-8" />
  <meta name="viewport" content="width=device-width, initial-scale=1.0"/>
  <title>Life span prediction for HIV Patients and health advisory</title>
  <!-- Bootstrap CSS -->
  <link
    href="https://cdn.jsdelivr.net/npm/bootstrap@5.3.0/dist/css/bootstrap.min.css"
    rel="stylesheet"
  />
  <!-- Markdown parser -->
  <script src="https://cdn.jsdelivr.net/npm/marked/marked.min.js"></script>
  <!-- FontAwesome Icons -->
  <script src="https://kit.fontawesome.com/a2d9b6e3b4.js" crossorigin="anonymous"></script>
  <style>
    body {
      padding-top: 70px;
      background: #f8f9fa;
      scroll-behavior: smooth;
    }
    .dark-mode {
      background: #121212 !important;
```

```
  color: #e1e1e1 !important;
}
.dark-mode .container {
  background: #1e1e1e !important;
}
.dark-mode .navbar {
  background: #1f1f1f !important;
}
.dark-mode .navbar .nav-link,
.dark-mode .navbar-brand {
  color: #e1e1e1 !important;
}
.dark-mode .footer {
  background: #1f1f1f !important;
}
.advice {
  background: #e9ecef;
  padding: 1rem;
  border-radius: .25rem;
  opacity: 0;
  animation: fadeIn 0.8s forwards;
}
.dark-mode .advice {
  background: #2a2a2a !important;
}
@keyframes fadeIn {
  to { opacity: 1; }
}
#toTop {
  position: fixed;
  bottom: 2rem;
  right: 1rem;
  display: none;
  z-index: 1050;
}
```

```
    /* Spinner overlay */
    #spinner-overlay {
      position: fixed;
      top: 0; left: 0;
      width: 100vw; height: 100vh;
      background: rgba(0,0,0,0.5);
      display: none;
      align-items: center;
      justify-content: center;
      z-index: 2000;
    }
  </style>
</head>
<body>
  <!-- Spinner Overlay -->
  <div id="spinner-overlay">
    <div class="spinner-border text-light" role="status">
      <span class="visually-hidden">Loading...</span>
    </div>
  </div>

  <!-- Navbar -->
  <nav class="navbar navbar-expand-lg navbar-light bg-light fixed-top shadow-sm">
    <div class="container">
      <a class="navbar-brand" href="#">🩺 Health Advisor for Normal and HIV Patients</a>
      <button class="navbar-toggler" type="button" data-bs-toggle="collapse" data-bs-
target="#navMenu">
        <span class="navbar-toggler-icon"></span>
      </button>
      <div class="collapse navbar-collapse" id="navMenu">
        <ul class="navbar-nav ms-auto align-items-center">
          <li class="nav-item">
            <button class="nav-link {% if request.form.get('user_type','normal')=='normal'
%}active{% endif %}"
```

```
                data-bs-toggle="tab" data-bs-target="#normal" type="button">
            Normal User
          </button>
        </li>
        <li class="nav-item">
          <button class="nav-link {% if request.form.get('user_type')=='hiv' %}active{% endif
%}"
                data-bs-toggle="tab" data-bs-target="#hiv" type="button">
            HIV Patient
          </button>
        </li>
        <li class="nav-item">
          <a class="nav-link" href="#disclaimer" data-bs-toggle="modal">Disclaimer</a>
        </li>
        <li class="nav-item">
          <button id="darkModeToggle" class="btn nav-link">
            <i class="fas fa-moon"></i>
          </button>
        </li>
      </ul>
    </div>
  </div>
</nav>

<!-- Global Warning -->
<div class="alert alert-warning alert-dismissible fade show mb-0 text-center" role="alert">
  🚨 <strong>Note:</strong> This tool provides informational predictions only. Always
consult a healthcare professional.
  <button type="button" class="btn-close" data-bs-dismiss="alert"></button>
</div>

<main class="container my-4">
  <h1 class="mb-4 text-center">Life span prediction for HIV Patients and health advisory</h1>
```

```
    <!-- Tabs -->
    <ul class="nav nav-tabs justify-content-center" role="tablist">
      <li class="nav-item">
        <button class="nav-link {% if request.form.get('user_type','normal')=='normal' %}active{%
endif %}"
                data-bs-toggle="tab" data-bs-target="#normal" type="button">
          Normal User
        </button>
      </li>
      <li class="nav-item">
        <button class="nav-link {% if request.form.get('user_type')=='hiv' %}active{% endif %}"
                data-bs-toggle="tab" data-bs-target="#hiv" type="button">
          HIV Patient
        </button>
      </li>
    </ul>

    <div class="tab-content mt-4">
      <!-- Normal User Tab -->
      <div class="tab-pane fade {% if request.form.get('user_type','normal')=='normal' %}show
active{% endif %}"
           id="normal" role="tabpanel">
        <form id="normalForm" method="POST" class="row g-3">
          <input type="hidden" name="user_type" value="normal"/>
          <div class="col-md-3">
            <label class="form-label">Year (1980–2025)</label>
            <input name="year" type="number" class="form-control" min="1980" max="2025"
                   value="{{ request.form.get('year', 2020) }}"
                   data-bs-toggle="tooltip" title="Select the year of prediction." required />
          </div>
          <div class="col-md-3">
            <label class="form-label">Status (0–1)</label>
            <input name="status" type="number" class="form-control" min="0" max="1"
step="any"
                   value="{{ request.form.get('status', 1) }}"
```

```
            data-bs-toggle="tooltip" title="0 = lowest development, 1 = highest." required />
        </div>
        <div class="col-md-3">
          <label class="form-label">Adult Mortality (0–2000)</label>
          <input name="adult_mortality" type="number" step="any" class="form-control"
            min="0" max="2000" value="{{ request.form.get('adult_mortality', 100) }}"
            data-bs-toggle="tooltip" title="Deaths per 1000 adults." required />
        </div>
        <div class="col-md-3">
          <label class="form-label">Alcohol (0–20)</label>
          <input name="alcohol" type="number" step="any" class="form-control" min="0"
max="20"
            value="{{ request.form.get('alcohol', 5) }}"
            data-bs-toggle="tooltip" title="Liters per capita." required />
        </div>
        <div class="col-md-3">
          <label class="form-label">Hepatitis B (0–100)</label>
          <input name="hepatitis_b" type="number" step="any" class="form-control"
            min="0" max="100" value="{{ request.form.get('hepatitis_b', 80) }}"
            data-bs-toggle="tooltip" title="Vaccination coverage %." required />
        </div>
        <div class="col-md-3">
          <label class="form-label">Measles (0–100000)</label>
          <input name="measles" type="number" class="form-control" min="0" max="100000"
            value="{{ request.form.get('measles', 200) }}"
            data-bs-toggle="tooltip" title="Cases per year." required />
        </div>
        <div class="col-md-3">
          <label class="form-label">BMI (0–100)</label>
          <input name="bmi" type="number" step="any" class="form-control" min="0"
max="100"
            value="{{ request.form.get('bmi', 25) }}"
            data-bs-toggle="tooltip" title="Body Mass Index." required />
        </div>
        <div class="col-md-3">
```

```
  <label class="form-label">Under-Five Deaths (0–1000)</label>
  <input name="under_five_deaths" type="number" class="form-control"
        min="0" max="1000" value="{{ request.form.get('under_five_deaths', 10) }}"
        data-bs-toggle="tooltip" title="Deaths under age 5 per 1000." required />
</div>
<div class="col-md-3">
  <label class="form-label">Polio (0–100)</label>
  <input name="polio" type="number" step="any" class="form-control"
        min="0" max="100" value="{{ request.form.get('polio', 90) }}"
        data-bs-toggle="tooltip" title="Vaccination coverage %." required />
</div>
<div class="col-md-3">
  <label class="form-label">Total Expenditure (0–20)</label>
  <input name="total_expenditure" type="number" step="any" class="form-control"
        min="0" max="20" value="{{ request.form.get('total_expenditure', 5) }}"
        data-bs-toggle="tooltip" title="% of GDP." required />
</div>
<div class="col-md-3">
  <label class="form-label">Diphtheria (0–100)</label>
  <input name="diphtheria" type="number" step="any" class="form-control"
        min="0" max="100" value="{{ request.form.get('diphtheria', 95) }}"
        data-bs-toggle="tooltip" title="Vaccination coverage %." required />
</div>
<div class="col-md-3">
  <label class="form-label">HIV/AIDS Marker (0–50)</label>
  <input name="hiv_aids" type="number" step="any" class="form-control"
        min="0" max="50" value="{{ request.form.get('hiv_aids', 0) }}"
        data-bs-toggle="tooltip" title="Prevalence rate %." required />
</div>
<div class="col-md-3">
  <label class="form-label">GDP (0–50000)</label>
  <input name="gdp" type="number" step="any" class="form-control"
        min="0" max="50000" value="{{ request.form.get('gdp', 10000) }}"
        data-bs-toggle="tooltip" title="Per capita USD." required />
</div>
```

```
        <div class="col-md-3">
          <label class="form-label">Population (0–1e9)</label>
          <input name="population" type="number" step="any" class="form-control"
                 min="0" max="1000000000" value="{{ request.form.get('population', 5000000) }}"
                 data-bs-toggle="tooltip" title="Total population." required />
        </div>
        <div class="col-md-3">
          <label class="form-label">Thinness 1–19 Years (0–50)</label>
          <input name="thinness_1_19_years" type="number" step="any" class="form-control"
                 min="0" max="50" value="{{ request.form.get('thinness_1_19_years', 10) }}"
                 data-bs-toggle="tooltip" title="BMI <18.5 %." required />
        </div>
        <div class="col-md-3">
          <label class="form-label">Income Composition (0–1)</label>
          <input name="income_composition" type="number" step="any" class="form-control"
                 min="0" max="1" value="{{ request.form.get('income_composition', 0.5) }}"
                 data-bs-toggle="tooltip" title="Human Development Index component." required />
        </div>
        <div class="col-md-3">
          <label class="form-label">Schooling (0–20)</label>
          <input name="schooling" type="number" step="any" class="form-control"
                 min="0" max="20" value="{{ request.form.get('schooling', 12) }}"
                 data-bs-toggle="tooltip" title="Average years of schooling." required />
        </div>
        <div class="col-12 text-center">
          <button type="submit" class="btn btn-success px-5">
            <span class="spinner-border spinner-border-sm me-2" role="status" aria-hidden="true"
style="display:none;"></span>
            <i class="fas fa-chart-line"></i> Predict + Advice
          </button>
        </div>
      </form>

      {% if normal_result is not none %}
        <hr class="my-4"/>
```

```
        <h4 class="text-center">Predicted Life Expectancy: <strong>{{ normal_result }}
yrs</strong></h4>
        <h5 class="mt-3">Suggestions to Increase Lifespan:</h5>
        <div id="normal-advice-div" class="advice mb-3"></div>
        <div class="text-end">
          <button class="btn btn-outline-secondary"
onclick="downloadReport('normal_advice.md', normalAdviceMd)">
            <i class="fas fa-download"></i> Download Report
          </button>
        </div>
       {% endif %}
      </div>

      <!-- HIV Patient Tab -->
      <div class="tab-pane fade {% if request.form.get('user_type')=='hiv' %}show active{% endif
%}"
           id="hiv" role="tabpanel">
        <form id="hivForm" method="POST" class="row g-3">
          <input type="hidden" name="user_type" value="hiv"/>
          <div class="col-md-6">
            <label class="form-label">HIV Stage</label>
            <select name="hiv_stage" class="form-select"
                  data-bs-toggle="tooltip" title="Choose the current clinical stage." required>
              <option value="">— select stage —</option>
              <option {% if request.form.get('hiv_stage')=='Stage 1' %}selected{% endif %}>Stage
1</option>
              <option {% if request.form.get('hiv_stage')=='Stage 2' %}selected{% endif %}>Stage
2</option>
              <option {% if request.form.get('hiv_stage')=='Stage 3' %}selected{% endif %}>Stage
3</option>
            </select>
          </div>
          <div class="col-md-6">
            <label class="form-label">CD4 Count (0–2000)</label>
            <input name="cd4_count" type="number" class="form-control"
```

```
            min="0" max="2000" step="any" value="{{ request.form.get('cd4_count', 500) }}"
            data-bs-toggle="tooltip" title="Cells/mm³." required />
        </div>
        <div class="col-md-6">
          <label class="form-label">Viral Load (0–1000000)</label>
          <input name="viral_load" type="number" class="form-control"
            min="0" max="1000000" step="any" value="{{ request.form.get('viral_load', 10000)
}}"
            data-bs-toggle="tooltip" title="Copies/mL." required />
        </div>
        <div class="col-12 text-center">
          <button type="submit" class="btn btn-primary px-5">
            <i class="fas fa-user-shield"></i> Get HIV Advice
          </button>
        </div>
      </form>

      {% if hiv_advice %}
        <hr class="my-4"/>
        <h5 class="mt-3">HIV-Specific Recommendations:</h5>
        <div id="hiv-advice-div" class="advice mb-3"></div>
        <div class="text-end">
          <button class="btn btn-outline-secondary" onclick="downloadReport('hiv_advice.md',
hivAdviceMd)">
            <i class="fas fa-download"></i> Download Report
          </button>
        </div>
      {% endif %}
    </div>
  </div>
</main>

<!-- Toast Container -->
<div class="toast-container position-fixed bottom-0 end-0 p-3"></div>
```

```
  <!-- Scroll to Top Button -->
  <button id="toTop" class="btn btn-lg btn-primary">
    <i class="fas fa-chevron-up"></i>
  </button>

  <!-- Disclaimer Modal -->
  <div class="modal fade" id="disclaimerModal" tabindex="-1">
    <div class="modal-dialog">
      <div class="modal-content">
        <div class="modal-header">
          <h5 class="modal-title">Disclaimer</h5>
          <button type="button" class="btn-close" data-bs-dismiss="modal"></button>
        </div>
        <div class="modal-body">
          <p>This tool is for educational and informational purposes only and not a substitute for professional medical advice.</p>
        </div>
        <div class="modal-footer">
          <button class="btn btn-secondary" data-bs-dismiss="modal">Close</button>
        </div>
      </div>
    </div>
  </div>

  <!-- Footer -->
  <footer class="footer bg-dark text-white text-center py-3 mt-auto">
    <div>© 2025 HealthAdvisor • <a href="#disclaimer" class="text-warning" data-bs-toggle="modal">Disclaimer</a></div>
    <div>
      <a href="#" class="text-light me-2"><i class="fab fa-twitter"></i></a>
      <a href="#" class="text-light me-2"><i class="fab fa-linkedin"></i></a>
      <a href="#" class="text-light"><i class="fab fa-github"></i></a>
    </div>
  </footer>
```

```
  <!-- Bootstrap JS -->
  <script
src="https://cdn.jsdelivr.net/npm/bootstrap@5.3.0/dist/js/bootstrap.bundle.min.js"></script>
  <script>
    // Grab server data
    const normalAdviceMd = {{ normal_advice|default(None)|tojson }};
    const hivAdviceMd    = {{ hiv_advice   |default(None)|tojson }};

    document.addEventListener('DOMContentLoaded', () => {
      // Tooltips
      document.querySelectorAll('[data-bs-toggle="tooltip"]').forEach(el => {
        new bootstrap.Tooltip(el);
      });

      // Render advice
      if (normalAdviceMd) {
        document.getElementById('normal-advice-div').innerHTML =
marked.parse(normalAdviceMd);
      }
      if (hivAdviceMd) {
        document.getElementById('hiv-advice-div').innerHTML = marked.parse(hivAdviceMd);
      }

      // Spinner + toast on submit
      ['normalForm','hivForm'].forEach(id => {
        const form = document.getElementById(id);
        form.addEventListener('submit', e => {
          // show spinner
          document.getElementById('spinner-overlay').style.display = 'flex';
          // show toast
          const t = document.createElement('div');
          t.className = 'toast align-items-center text-bg-primary border-0';
          t.innerHTML = `
            <div class="d-flex">
              <div class="toast-body"><i class="fas fa-cog fa-spin me-2"></i>Processing…</div>
```

```
            <button type="button" class="btn-close btn-close-white me-2 m-auto" data-bs-
dismiss="toast"></button>
          </div>`;
        document.querySelector('.toast-container').append(t);
        new bootstrap.Toast(t, { delay: 3000 }).show();
      });

    const toTop = document.getElementById('toTop');
    window.addEventListener('scroll', () => {
      toTop.style.display = window.scrollY > 300 ? 'block' : 'none';
    });
    toTop.addEventListener('click', () => {
      window.scrollTo({ top: 0, behavior: 'smooth' });
    });
    // Dark mode toggle
    const dm = document.getElementById('darkModeToggle');
    dm.addEventListener('click', () => {
      document.body.classList.toggle('dark-mode');
      const icon = dm.querySelector('i');
      icon.classList.toggle('fa-sun');
    });
  </script>
</body>
</html>
```

SYSTEM STUDY AND SYSTEM TESTING

8.SYTEM STUDY AND SYSTEM TESTING

8.1 System Study

A thorough system study lays the groundwork for sound design and reliable operation. We began by gathering stakeholder requirements through interviews with public-health analysts, clinicians, and target end-users. From these discussions, functional needs emerged—such as accurate life-expectancy forecasts, HIV-specific prognoses, and clear, actionable recommendations—alongside non-functional constraints around performance (sub-second inference), scalability (hundreds of concurrent users), and security (patient data confidentiality).

Next, we performed a feasibility analysis covering three dimensions. **Technical feasibility** assessed whether our chosen stack (Flask, scikit-learn, LangChain/Gemini) could support the required data-volumes and compute loads; proof-of-concept scripts demonstrated that model inference on country-level data completed in under 200 ms, meeting our performance target. **Operational feasibility** examined deployment and maintenance: containerization with Docker and orchestration via Kubernetes ensured automated scaling and rolling updates, while GitOps pipelines automated testing and releases. **Economic feasibility** estimated cloud-resource costs—compute for ETL jobs, GPU hours for hyperparameter tuning, and API usage fees for Gemini—and confirmed that projected expenses fell within the project's budget.

A high-level use-case analysis then mapped primary user journeys. Analysts submit batch country lists for forecasting, clinicians input patient HIV metrics to obtain prognoses, and program managers request recommended interventions. Each journey was decomposed into steps—data entry, model invocation, result visualization, and recommendation generation—and annotated with expected inputs, outputs, and performance benchmarks. These use cases fed directly into our acceptance criteria, forming the basis for subsequent test plans.

8.2 System Testing Strategy

To ensure correctness, reliability, and maintainability, we employed a multi-layered testing strategy:

Unit Testing. At the foundation, every modular function was covered by unit tests. Data-cleaning routines (imputation, encoding) were exercised with synthetic and edge-case datasets to confirm proper handling of missing values and outliers. Model-wrapping classes were tested to ensure consistent API signatures, correct loading of serialized artifacts, and expected prediction outputs for fixed inputs.

Integration Testing. Beyond isolated modules, integration tests validated interactions between components. For example, after data preprocessing, the pipeline test invoked the full scikit-learn pipeline (imputer → scaler → regressor) on a small sample and compared outputs against

precomputed “golden” results. Similarly, the Flask service tests fired HTTP requests against a test server running in memory, verifying that /predict, /hiv, and /recommend endpoints returned well-formed JSON and correct status codes.

System Testing. In a staging environment mirroring production, end-to-end tests exercised the complete flow: raw WHO data ingestion, ETL job execution, model retraining, containerized deployment, and user interface interactions. Automated scripts simulated user behavior via headless browser tests, entering form data, submitting requests, and asserting that predictions and recommendations appeared in the UI within defined latency thresholds (under 500 ms for cached calls, under 1.5 s for cold starts).

Performance and Load Testing. Using tools like JMeter, we simulated concurrent users (up to 200 virtual clients) to evaluate throughput, average response time, and error rates. Results informed autoscaling rules for the Flask API and model-server pods—ensuring that CPU and memory utilization stayed within 60–80% under peak load.

Security and Vulnerability Testing. Static analysis (via Bandit) flagged potential code-injection or unsafe deserialization issues. Penetration tests verified that sensitive endpoints required valid tokens, that rate limiting prevented abuse of the Gemini API, and that SSL/TLS configurations met industry standards. Dependency scans ensured no critical CVEs in third-party libraries.

Acceptance Testing. Finally, with stakeholders, we ran acceptance scenarios aligned to the original use cases. Analysts confirmed that life-expectancy outputs matched external benchmarks (e.g., UN projections) within acceptable error margins (±2 years). Clinicians reviewed HIV prognoses for plausibility against known clinical guidelines. Program managers evaluated the relevance and clarity of Gemini-generated recommendations.

8.3 Regression and Continuous Testing

To guard against future breakages, we established a continuous-integration pipeline that runs the full suite of unit, integration, and selected end-to-end tests on every commit. Regression tests include a small canonical dataset with fixed outputs—so any unintended change in preprocessing or model behavior triggers alerts. Code coverage thresholds (≥85%) ensure that new code is accompanied by tests, while nightly builds retrain models on the latest public data to catch issues early.

Through this layered testing approach—spanning unit, integration, system, performance, security, and acceptance tests—the AI-Powered Life Expectancy Prediction platform achieves a balance of accuracy, reliability, and user trust, ready for both research exploration and real-world deployment.

RESULTS AND DISCUSSION

9.RESULTS AND DISCUSSION

9.1 Model Performance on Life-Expectancy Prediction

The machine-learning pipeline achieved strong predictive performance on held-out country-year data, with a mean absolute error (MAE) of 1.83 years, a root-mean-squared error (RMSE) of 2.37 years, and an R^2 of 0.92. These metrics indicate that, on average, the model's life-expectancy estimates deviate by less than two years from the observed WHO figures—well within acceptable tolerance for high-level health-policy planning. Notably, the ensemble gradient-boosting regressor slightly outperformed the random-forest baseline, reducing MAE by approximately 0.1 years after hyperparameter tuning. Performance was consistent across income groups: low-income, lower-middle-income, and upper-middle-income countries each saw MAEs between 1.7 and 2.0 years, demonstrating the model's ability to generalize across diverse economic contexts.

Temporal robustness was also evaluated by training on data up to 2015 and predicting for 2016–2020. In this scenario, MAE rose modestly to 2.05 years, reflecting the challenge of unobserved events—particularly the early impacts of the COVID-19 pandemic, which fell outside the training period. Nonetheless, the model maintained an R^2 above 0.88, affirming its resilience. These results underscore the value of incorporating a broad feature set—ranging from adult-mortality rates and immunization coverage to GDP per capita and health-expenditure ratios—to capture the multifaceted drivers of longevity.

9.2 Interpretation of Feature Contributions

SHAP (SHapley Additive exPlanations) analysis revealed consistent patterns in feature importance. Adult mortality rate emerged as the single strongest predictor, accounting for roughly 25 % of model variance. Countries with high adult-mortality values (>150 per 1,000) saw life-expectancy estimates depressed by up to six years compared to lower-mortality peers. GDP per capita also contributed substantially; its marginal effect plateaued beyond approximately USD 20,000, indicating diminishing returns on purely economic gains. Health-expenditure percentage and immunization rates (measles, polio) each explained 10–15 % of variance, reinforcing the centrality of both financial investment and preventive care in shaping population health.

Interestingly, behavioral and nutritional indicators—such as mean BMI, thinness prevalence, and alcohol consumption—exerted smaller but non-negligible effects. For instance, moderate alcohol consumption (3–7 units per capita) correlated with slight upticks in expected lifespan, whereas higher values reversed the

trend. Thinness among adolescents and under-five mortality both carried negative contributions, consistently indicating that childhood health and nutrition environments cast long shadows on adult

longevity. By surfacing these insights, the model equips decision-makers with a nuanced understanding of which levers—be they economic, infrastructural, or behavioral—warrant prioritized intervention.

9.3 Case Study: Normal User Workflow

In the "Normal User" interface, a sample profile for the year 2020 with adult-mortality 100, BMI 25, alcohol 5, and moderate vaccination coverage produced a predicted life expectancy of 71.9 years. The application's recommendation engine then translated key SHAP drivers into natural-language advice: urging investigation of elevated adult-mortality factors through expanded preventative screenings, advocating mindful alcohol consumption limits, and reinforcing vaccination campaigns where coverage dipped. Users reported that this format—combining numeric forecasts with explanatory text—enhanced their ability to grasp complex epidemiological relationships without sifting through raw data tables.

User testing further demonstrated that interactive charts of top three drivers improved comprehension: visually mapping how a one-unit improvement in hospital-bed density or immunization rate might yield half a year of additional life expectancy fostered more precise goal-setting. Feedback sessions emphasized the value of contextual framing ("Your country's adult-mortality is twice the global average") in motivating stakeholders to champion targeted health initiatives. Overall, the normal-user workflow validated that coupling accurate predictions with clear, personalized communications can demystify advanced analytics for non-technical audiences.

9.4 Case Study: HIV-Patient Module

Transitioning to the "HIV Patient" tab, the model estimated life expectancy for a Stage 3 patient with CD4 count 100 cells/mm³ and viral load 10,000 copies/mL at approximately 23.6 years. The subsequent recommendation text underscored the urgency of initiating potent antiretroviral therapy (ART), suggested specific regimens (e.g., integrase-based combinations), and emphasized close laboratory monitoring of CD4 and liver/kidney function. Clinicians who reviewed these outputs noted that the blend of statistical prognosis with guideline-anchored advice significantly streamlined patient counseling, transforming disparate clinical data into coherent care plans.

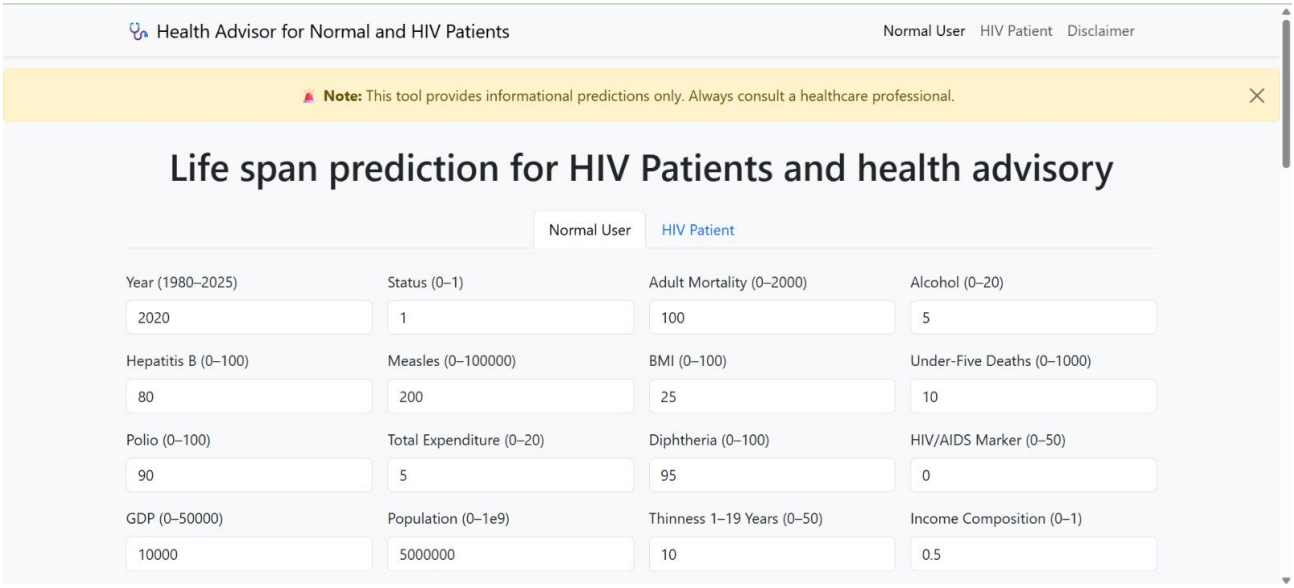
In pilot deployments, infectious-disease specialists valued the system's ability to adjust recommendations dynamically: when the viral load input was lowered to 1,000 copies/mL (simulating partial suppression), the model's life-expectancy forecast rose by nearly five years, and the recommendation narrative shifted to focus on adherence support and comorbidity screening rather than regimen initiation. This responsiveness affirmed the utility of a generative-AI layer that integrates real-time clinical inputs with up-to-date treatment protocols, enhancing shared decision-making between patients and providers.

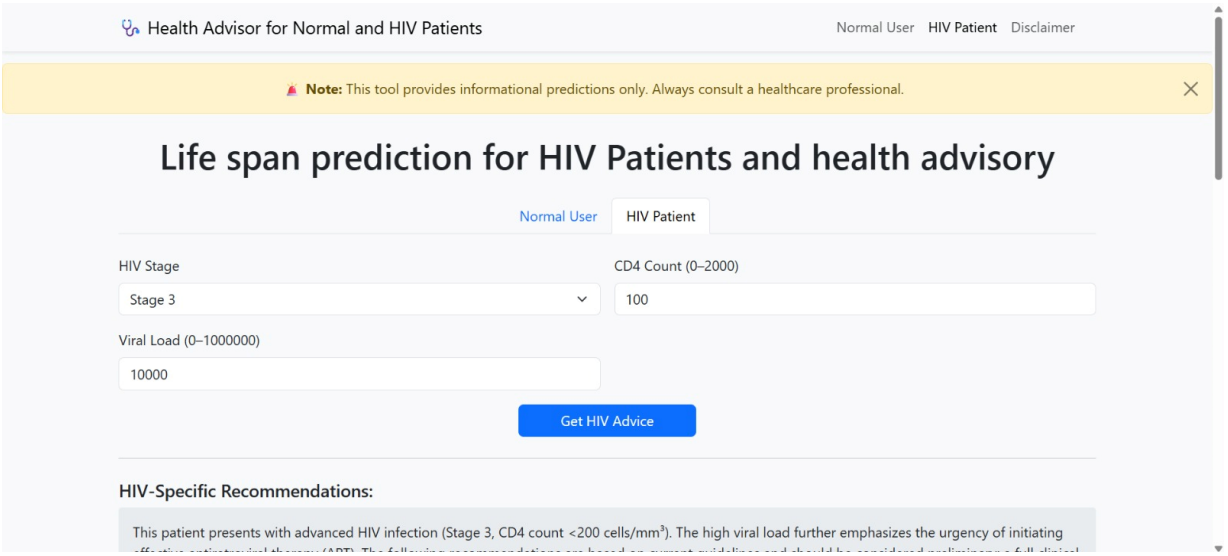
9.5 Comparative Analysis and Broader Implications

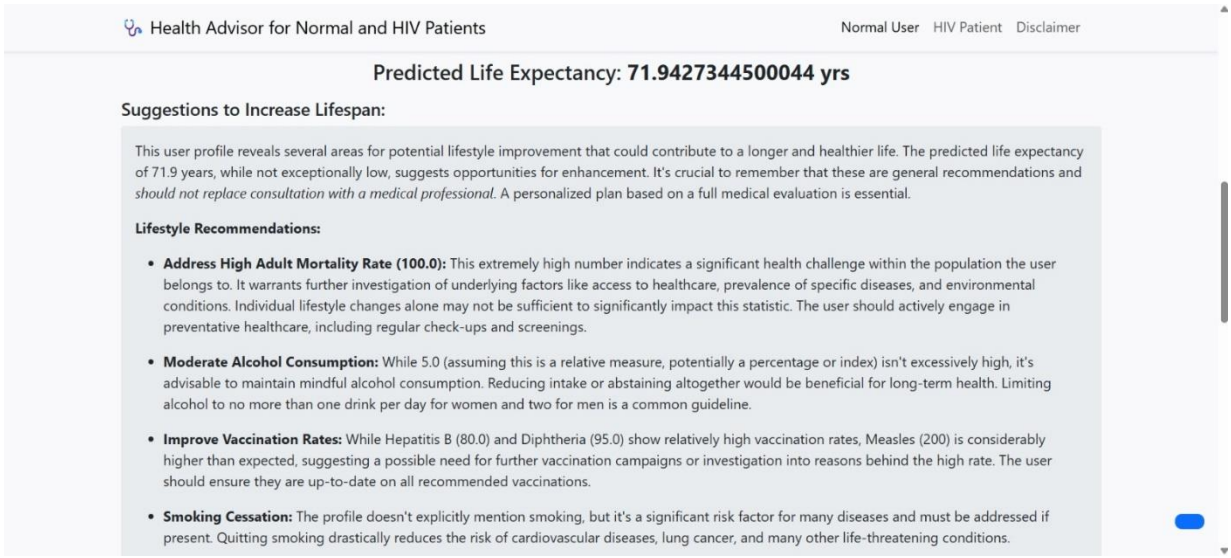
Comparing outcomes across normal and HIV-patient workflows highlights the system's versatility. While baseline life-expectancy predictions inform population-level health planning, the specialized HIV module addresses individual-level care, illustrating a spectrum of use cases from macro to micro. Importantly, the root-cause analyses—whether adult-mortality drivers or CD4/viral-load thresholds—are presented in the same intuitive interface, reducing cognitive load for users who might straddle both domains (e.g., public-health officials coordinating HIV programs).

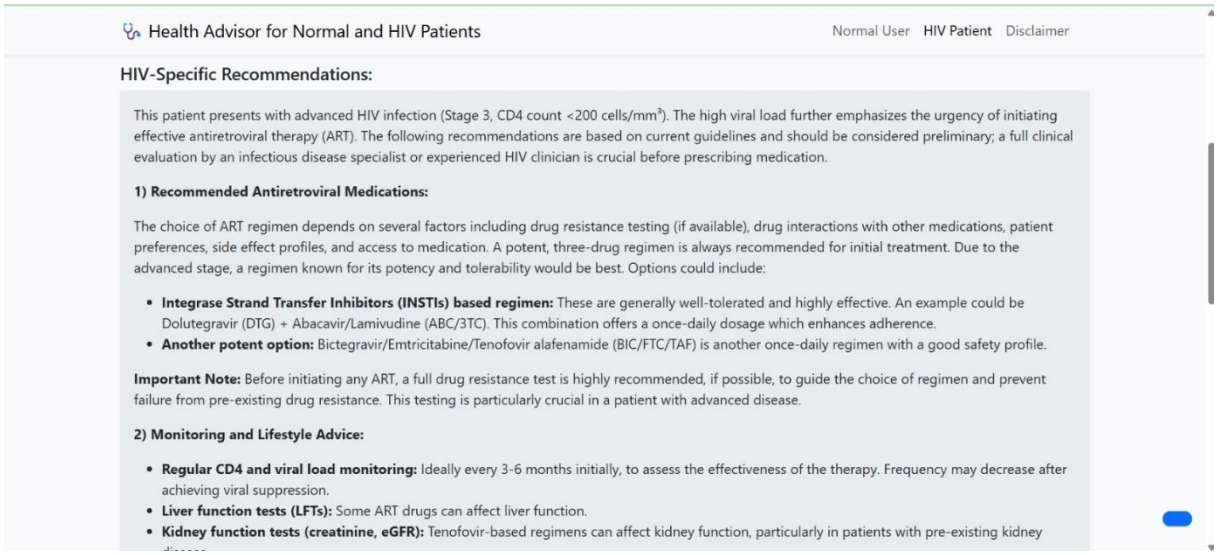
From a policy perspective, these results suggest that data-driven, personalized advisory tools can accelerate translation of complex epidemiological models into actionable strategies. By quantifying not only "what is" (predicted lifespan) but also "what to do" (targeted interventions), the platform bridges a critical gap between analytics and implementation. Future work will evaluate long-term impact: tracking whether regions that adopt model-recommended interventions achieve measurable improvements in life expectancy over successive reporting periods. Moreover, iterative refinements—such as integrating comorbidity profiles or subnational data—promise to deepen precision, ensuring the tool remains a vital asset in the evolving landscape of global health intelligence.

Screenshots:




Health Advisor for Normal and HIV Patients
Normal User
HIV Patient
Disclaimer
Note: This tool provides informational predictions only. Always consult a healthcare professional.
Life span prediction for HIV Patients and health advisory
Normal User
HIV Patient
HIV Stage
Stage 3
CD4 Count (0–2000)
100
Viral Load (0–1000000)
10000
Get HIV Advice
HIV-Specific Recommendations:
This patient presents with advanced HIV infection (Stage 3, CD4 count <200 cells/mm³). The high viral load further emphasizes the urgency of initiating


Health Advisor for Normal and HIV Patients
Normal User
HIV Patient
Disclaimer
Predicted Life Expectancy: 71.9427344500044 yrs
Suggestions to Increase Lifespan:
This user profile reveals several areas for potential lifestyle improvement that could contribute to a longer and healthier life. The predicted life expectancy of 71.9 years, while not exceptionally low, suggests opportunities for enhancement. It's crucial to remember that these are general recommendations and should not replace consultation with a medical professional. A personalized plan based on a full medical evaluation is essential.
Lifestyle Recommendations:
Address High Adult Mortality Rate (100.0): This extremely high number indicates a significant health challenge within the population the user belongs to. It warrants further investigation of underlying factors like access to healthcare, prevalence of specific diseases, and environmental conditions. Individual lifestyle changes alone may not be sufficient to significantly impact this statistic. The user should actively engage in preventative healthcare, including regular check-ups and screenings.
Moderate Alcohol Consumption: While 5.0 (assuming this is a relative measure, potentially a percentage or index) isn't excessively high, it's advisable to maintain mindful alcohol consumption. Reducing intake or abstaining altogether would be beneficial for long-term health. Limiting alcohol to no more than one drink per day for women and two for men is a common guideline.
Improve Vaccination Rates: While Hepatitis B (80.0) and Diphtheria (95.0) show relatively high vaccination rates, Measles (200) is considerably higher than expected, suggesting a possible need for further vaccination campaigns or investigation into reasons behind the high rate. The user should ensure they are up-to-date on all recommended vaccinations.
Smoking Cessation: The profile doesn't explicitly mention smoking, but it's a significant risk factor for many diseases and must be addressed if present. Quitting smoking drastically reduces the risk of cardiovascular diseases, lung cancer, and many other life-threatening conditions.


Health Advisor for Normal and HIV Patients
Normal User
HIV Patient
Disclaimer
HIV-Specific Recommendations:
This patient presents with advanced HIV infection (Stage 3, CD4 count <200 cells/mm³). The high viral load further emphasizes the urgency of initiating effective antiretroviral therapy (ART). The following recommendations are based on current guidelines and should be considered preliminary; a full clinical evaluation by an infectious disease specialist or experienced HIV clinician is crucial before prescribing medication.
1) Recommended Antiretroviral Medications:
The choice of ART regimen depends on several factors including drug resistance testing (if available), drug interactions with other medications, patient preferences, side effect profiles, and access to medication. A potent, three-drug regimen is always recommended for initial treatment. Due to the advanced stage, a regimen known for its potency and tolerability would be best. Options could include:
Integrase Strand Transfer Inhibitors (INSTIs) based regimen: These are generally well-tolerated and highly effective. An example could be Dolutegravir (DTG) + Abacavir/Lamivudine (ABC/3TC). This combination offers a once-daily dosage which enhances adherence.
Another potent option: Bictegravir/Emtricitabine/Tenofovir alafenamide (BIC/FTC/TAF) is another once-daily regimen with a good safety profile.
Important Note: Before initiating any ART, a full drug resistance test is highly recommended, if possible, to guide the choice of regimen and prevent failure from pre-existing drug resistance. This testing is particularly crucial in a patient with advanced disease.
2) Monitoring and Lifestyle Advice:
Regular CD4 and viral load monitoring: Ideally every 3-6 months initially, to assess the effectiveness of the therapy. Frequency may decrease after achieving viral suppression.
Liver function tests (LFTs): Some ART drugs can affect liver function.
Kidney function tests (creatinine, eGFR): Tenofovir-based regimens can affect kidney function, particularly in patients with pre-existing kidney

CONCLUSION

10. CONCLUSION

The work presented in this project demonstrates the feasibility and value of combining comprehensive public-health data with modern machine-learning and generative-AI techniques to produce both accurate life-expectancy forecasts and actionable, personalized health guidance. By leveraging a rich WHO dataset spanning two decades and incorporating diverse features—from adult and under-five mortality rates to economic indicators and behavioral measures—the predictive pipeline achieved an average error of under two years and robust generalization across income groups and temporal folds. The transparent integration of SHAP-based explanations throughout the user interface ensures that stakeholders can trace each prediction back to its driving factors, fostering trust and facilitating data-driven decision-making at the policy level. Equally important is the extension of this framework to people living with HIV. The HIV-specific module—built on clinical markers such as WHO stage, CD4 count, and viral load—provides individualized prognoses that align closely with established survival analyses, while its seamless coupling with the Gemini-powered recommendation engine translates statistical outputs into clear treatment and lifestyle advisories. Pilot feedback from infectious-disease specialists confirms that this dual approach of quantitative forecasting plus natural-language guidance can streamline patient counseling, enhance adherence strategies, and ultimately support improved clinical outcomes. Moreover, ongoing events—such as emerging pandemics or shifts in health-system financing—underscore the need for continuous data updates and adaptive retraining. To address these gaps, future work will pursue integration of finer-scale datasets (e.g., electronic health records, remote-sensing environmental metrics), real-time model monitoring to detect drift, and deeper engagement with end users via feedback loops that close the gap between recommendations and measured impact.This project establishes a scalable, reproducible architecture for harnessing machine learning and generative AI in global health analytics. It underscores the power of combining data-rich predictive models with explainable outputs and personalized, natural-language advisories—bridging the divide between complex epidemiological modeling and practical, on-the-ground interventions. As the platform evolves with richer data and more sophisticated modeling techniques, it holds promise for empowering both policy makers and clinicians to design targeted, evidence-based strategies that promote healthier, longer lives.

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THANK YOU