**Systematic Review Article**

**A Scoping Review on Mathematical Modelling Techniques Used in Non-Communicable Disease (NCD) Research**

**ABSTRACT**

**Aims:** To synthesise how mathematical and computational models, including deterministic, stochastic, Markov, agent-based and related approaches, have been applied to non-communicable disease (NCD) research, and to identify current strengths, gaps and future priorities.

**Study design:** Scoping review conducted in accordance with PRISMA-ScR guidelines.

**Place and Duration of Study:** Electronic searches of PubMed, Web of Science, Scopus and Google Scholar were performed remotely for articles published between 2004 and 2024.

**Methodology:** Titles and abstracts were screened against predefined inclusion criteria; full texts were assessed independently by two reviewers, with disagreements resolved by consensus. Eligible studies were charted and synthesised narratively with attention to modelling class, disease domain, data sources and analytic purpose.

**Results:** Deterministic ordinary- and partial-differential-equation systems dominated mechanistic work, illuminating cellular and organ-level processes in myocardial infarction, tumour growth and glycaemic regulation. Stochastic and agent-based models captured intrinsic noise and population heterogeneity, clarifying clonal evolution in cancer, β-cell attrition in diabetes and ventilation defects in chronic lung disease. Markov and microsimulation frameworks traced long-term disease trajectories and underpinned most health-economic evaluations, typically wrapped in Monte Carlo procedures for probabilistic sensitivity analysis. Machine-learning algorithms and regression techniques unlocked high-dimensional clinical and omics data, supplying parameter estimates, risk scores and fast emulators that augment mechanistic cores. Key limitations included fragmented datasets, multiscale numerical challenges and limited treatment of health equity.

**Conclusion:** Integrated modelling provides a powerful route to deeper biological insight, more accurate burden projections and rigorous appraisal of interventions across NCDs. Realising its full potential will require harmonised longitudinal data, hybrid multiscale architectures, statistically principled calibration and real-time model updating to inform the next generation of NCD research and policy.

*Keywords: Non-communicable diseases; Mathematical modelling; Agent-based simulation; Health-economic evaluation; Multiscale systems; Machine Learning*

1. **Introduction**

Non-communicable diseases (NCDs) are chronic non-contagious diseases associated with multiple risk factors, including improper nutrition, sedentary lifestyle, tobacco and alcohol use, that pose a global health burden accountable for about 71 per cent of deaths in low- and middle-income countries (Piovani et al., 2022; Krause et al., 2024; Wang & Wang, 2020). Currently, the major NCDs identified are cardiovascular diseases (17.9 million deaths; heart attacks, stroke), cancer (9.0 million; lung, ovarian, endometrial, breast, colorectal), diabetes (1.6 million), neurological and chronic respiratory diseases (3.9 million; chronic obstructive pulmonary disease, asthma) (Krause et al., 2024; Habib & Saha, 2010). These NCDs are linked to several factors, including genetic, physiological, behavioral, and environmental exposure (Budreviciute et al., 2020). NCDs have been projected to cause more deaths than infectious diseases, which might be a result of their increasing impact, largely borne by households rather than governments or insurance schemes (Kankeu et al., 2013; Coates et al., 2020). Evidence suggests that NCDs cause a rise in financial burden on households, with the poorer population being unable to afford treatment, leading to high morbidity and mortality worldwide (Coates et al., 2020; Adrianna et al., 2020; Gouda et al., 2019).

Given the widespread incidence and rising prevalence of NCDs, novel strategies for prevention, control, and management are the current research targets. It is worth noting that understanding the current projections and trajectories in NCD research requires mathematical models. Mathematical modeling serves as a critical epidemiological tool for understanding chronic disease dynamics, guiding healthcare policies, enhancing diagnosis and management, and informing evidence-based decision-making for optimizing health services (Kibachio et al., 2020). It also serves as a useful tool for improving the knowledge of disease mechanisms through adopting data-driven sources such as genomics and proteomics to improve drug development, optimize clinical trial design and provide personalized treatment strategies. Computational models in biomedical science, integrating physiological principles and data-driven simulations, have emerged as a powerful tool for elucidating complex biological processes, their interaction and behavior, offering distinct advantages in fundamental research and drug development (Ponnarengan et al., 2024; G. Li et al., 2024). Current trends in mathematical models suggest their ability to predict unrecognised disease states to improve healthcare demands through enabling medical resource allocation and effective clinical decision making (Y. Liu et al., 2023). It can give insight into disease severity and mechanism at the cellular and molecular level, providing a detailed overview of how the disease affects the body's systems. This review focuses on advances in computational and data-driven methodologies, as the field holds immense promise for addressing the pressing challenges of global health. We will explore innovative modeling techniques, including deterministic, stochastic, Markov, and agent-based approaches used in health research. We will also explore computational models used in different NCDs research, including cardiovascular diseases, cancer, diabetes, neurological and chronic respiratory diseases, examining how recent advances are helping address them.

1. **Methodology**

This scoping review was planned and conducted in full accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses Extension for Scoping Reviews (PRISMA-ScR) standards.

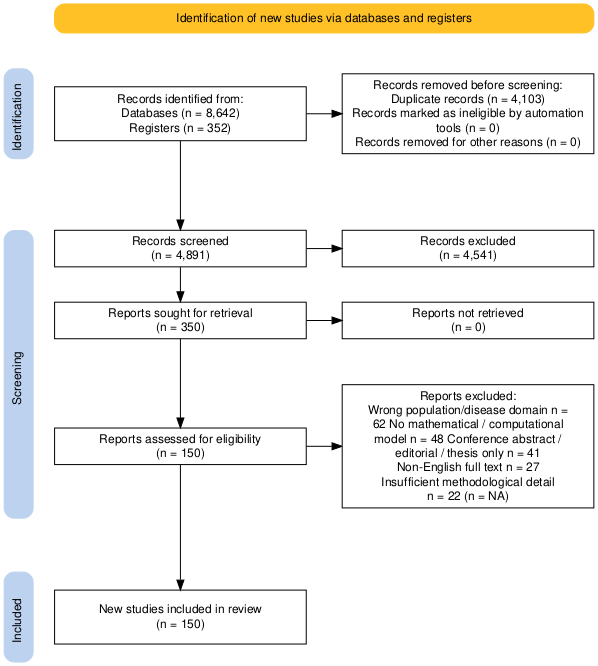
**2.1 Eligibility framework.**

Eligible records had to investigate one or more non-communicable diseases, specifically cardiovascular disorders, cancers, diabetes, neurological conditions, chronic respiratory disease, chronic kidney disease or obesity, by applying an explicit mathematical or computational modelling technique such as deterministic ordinary or partial differential equations, stochastic formulations, Markov or microsimulation frameworks, agent-based approaches, Monte-Carlo sampling strategies or machine-learning surrogates. Studies whose sole purpose was descriptive epidemiology, commentaries, editorials, conference abstracts without full texts, dissertations and non-English papers were excluded because they do not provide reproducible modelling detail. To capture contemporary practice while maintaining a manageable corpus, the temporal window was confined to 2004 through 2024.

**2.2 Information Sources and Search**

Four bibliographic databases, PubMed/MEDLINE, Web of Science Core Collection, Scopus and Google Scholar, were queried, because together they cover medicine, public health, engineering and computer science. In addition, the first three hundred Google Scholar hits (rank-ordered by relevance) were screened, and backward as well as forward citation chaining of all finally included articles was carried out within Scopus.

The search strategy combined controlled vocabulary and free text that captured the disease area, the modelling concept and the methodological descriptors. For example, the PubMed string linked synonyms for non-communicable disease with terms such as model, simulation, ordinary differential, stochastic, Markov, agent-based or machine learning, and with disease-specific keywords like cardiovascular, neoplasm, diabetes or COPD. The strategy was peer-reviewed and then adapted to the syntax of each database. The PRISMA-SCR flow chart is illustrated in figure 1.



**Fig. 1.** PRISMA-ScR Flow Diagram of Study Selection for the Scoping Review

**2.3 Selection Process.**

Results were exported to EndNote 20 for automatic and manual de-duplication, then screened. Two reviewers independently examined titles and abstracts against the eligibility criteria. Any record judged potentially relevant by at least one reviewer was retrieved in full and reassessed, again in duplicate. Disagreements were discussed; if consensus could not be reached a third reviewer arbitrated. A PRISMA flow diagram will illustrate the number of records identified, screened, excluded and included, together with specific reasons for full-text exclusion.

**2.4 Critical Appraisal**

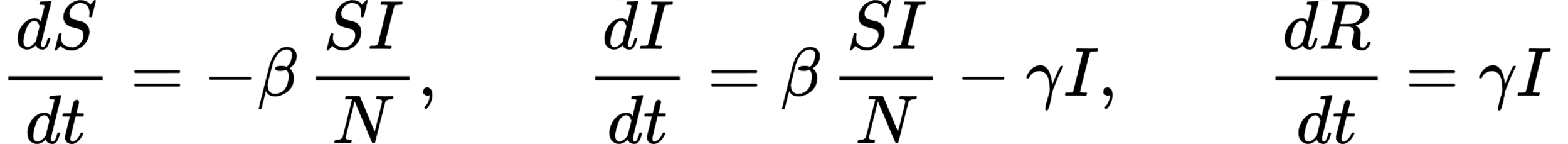
Because a scoping review aims to map rather than to judge the evidence base, no formal risk-of-bias scoring was performed.

**3.0 Discussion**

**3.1 Classification of Mathematical Modelling Techniques**

*Deterministic Model*

A deterministic model is a mathematical framework in which outcomes are fully determined by initial conditions and parameters, producing the same results for the same inputs without randomness (Vlazaki et al., 2019; Waters et al., 2021). These models rely on fixed equations that assume uniform behavior across the system and are primarily used to simulate and predict system dynamics under defined conditions (Olabode et al., 2021). They support stability analysis, outcome forecasting, and evaluation of interventions or policy decisions, particularly when uncertainty is minimal (Kadri et al., 2025). Deterministic models are often formulated using ordinary or partial differential equations or algebraic equations (Yin et al., 2019). A classic example is the SIR model:

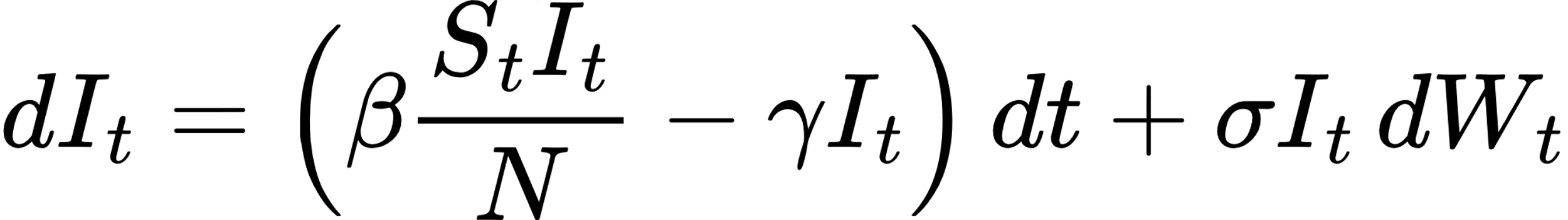


This describes infectious disease transmission in a closed population without random effects (Olabode et al., 2021; Ellner & Guckenheimer, 2021). These models are especially suited for reproducible systems like epidemic forecasting (M. Roberts et al., 2015) and are widely applied in epidemiology, drug development (Irurzun-Arana et al., 2020), and systems biology (Chandran et al., 2008). In public health, they help simulate interventions for diseases like COVID-19 (Kadri et al., 2025), and they also guide decision-making in fields such as pharmacokinetics, ecology, engineering, and economics (Zou et al., 2020).

*Stochastic Model*

Stochastic models yield the same results for identical inputs, and stochastic approaches allow for variability in outcomes, making them particularly valuable in modeling systems with unpredictable dynamics or small population sizes (Allen, 2017; Sunila et al., 2024). This model is important in cancer research and disease prediction, where uncertainty and limited data are common, as it better captures cellular heterogeneity and variability in gene expression (Sunila et al., 2024; Sabino et al., 2018). Additionally, Sun et al. demonstrate that stochastic methods are indispensable for modeling molecular interactions and low-copy-number events, where random fluctuations play a significant role in cellular processes (Sun et al., 2008). Therefore, the main function of the stochastic model is to offer a robust framework for addressing complex biological systems, providing more accurate predictions, enhancing treatment strategies, and informing public health policies (Ming et al., 2016). In the stochastic SIR framework, the susceptible and infected populations S(t) and I(t) are treated as continuous random variables on [0,N], evolving according to the probabilities of infection and recovery (Allen, 2017).

The equation

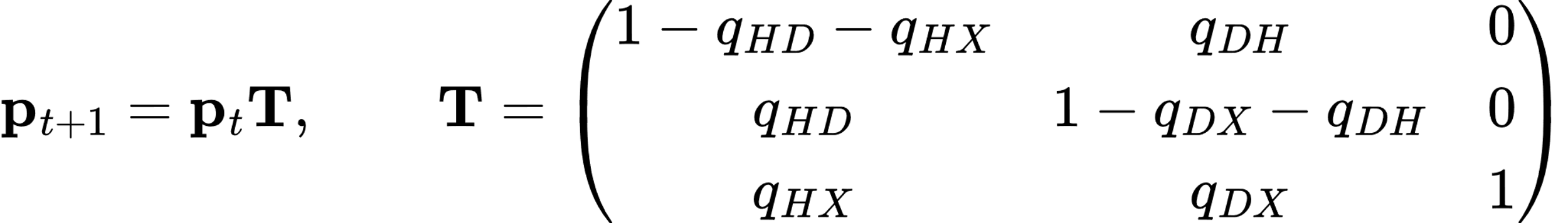


is the stochastic counterpart of the SIR model. The expression extends the classic SIR framework by keeping its familiar infection-minus-recovery drift and adding a Brownian-motion noise term whose strength scales with the current number infectious. This stochastic twist allows chance events to suppress or amplify outbreaks, something the purely deterministic model cannot capture, while still collapsing back to the standard SIR behaviour when the noise parameter is set to zero (M. Roberts et al., 2015).

*Markov Model*

Markov models describes systems which undergo transitions between states over time, based on probability (Komorowski & Raffa, 2016). These models are useful when the system's future state depends solely on its current state, rather than on the sequence of events that preceded it (Kim & Deka, 2021). This approach is commonly applied in biological and healthcare-related fields due to its ability to model processes that evolve over time with clearly defined states and transition probabilities (Carta & Conversano, 2020; Rao & Diamond, 2017). In infertility treatments, Markov models have been applied to assess the impact of different treatment strategies by considering multiple clinical states that a patient might transition through during the treatment process, such as pregnancy or treatment failure (Rao & Diamond, 2017). This allows for the calculation of probabilities of different outcomes over time, helping to guide medical decisions (Rao & Diamond, 2017). Similarly, in the realm of biological sequence analysis, hidden markov models (HMMs) are widely used to model biological sequences like DNA or protein structures, where the system's states are not directly observable (Yoon, 2009). These models rely on the assumption of constant transition probabilities over time and are particularly powerful for long-term projections and policy-making (Carta & Conversano, 2020; King et al., 2021). They also provide a framework for simulating the impact of interventions across different population groups, allowing healthcare providers and researchers to optimize strategies and anticipate outcomes.

A Markov model can be represented as:

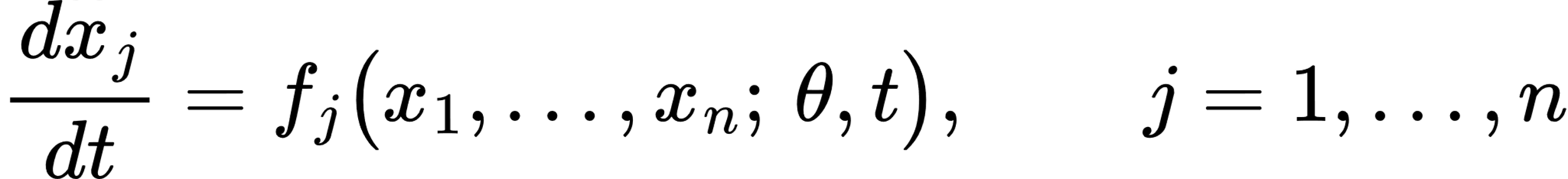


Viewed through the Markov-chain lens, the model describes a time-homogeneous, first-order process with three mutually exclusive states: Healthy (H), Diseased (D), and an absorbing exit state (X). At each discrete step the row-vector of state probabilities is premultiplied by a fixed transition matrix, so the distribution at time t+1 depends only on the distribution at time t, never on how the population arrived there. The entries labelled qHD, qHX, qDH, and qDX play the classic role of one-step transition probabilities: qHD moves an individual from H to D, qHX from H directly to X, and so on. Because every column in the matrix sums to one, total probability is conserved; because the column for X contains a single unity, that state is absorbing, once reached, it cannot be left. Iterating the matrix–vector multiplication therefore traces the evolution of the cohort’s health distribution exactly as a standard discrete-time Markov chain would (Ross, 2014).

*Ordinary Differential Equations (ODEs)*

This model serves as a foundational mathematical tool for modeling dynamic systems in the biomedical sciences, allowing researchers to describe how variables change continuously over time based on specific rates (Dattner et al., 2024). ODEs are particularly effective in capturing the time evolution of biological processes such as disease progression, drug absorption, or cellular responses, where system dynamics are governed by deterministic rules (Truong et al., 2022). ODEs offer a compact, analytical structure that helps identify cause-effect relationships and predict future states of the system from current and initial conditions (Dai et al., 2024). A key advantage of using ODEs is in their ability to be parametrized from experimental data, enabling efficient simulation, sensitivity analysis, and model selection using statistical testing approaches (Dattner et al., 2024; Son & Kim, 2023). Statistical techniques such as data cloning and likelihood-based estimation are increasingly integrated to improve the accuracy of parameter estimation in ODE-based models, especially in complex systems like gene regulatory networks (Son & Kim, 2023). Despite the utility of ODEs, they assume continuous, deterministic, and homogeneous behavior, which can limit their applicability when modeling stochastic or discrete biological phenomena (Yasui, 2022).

Mathematically, an ODE can be represented as;

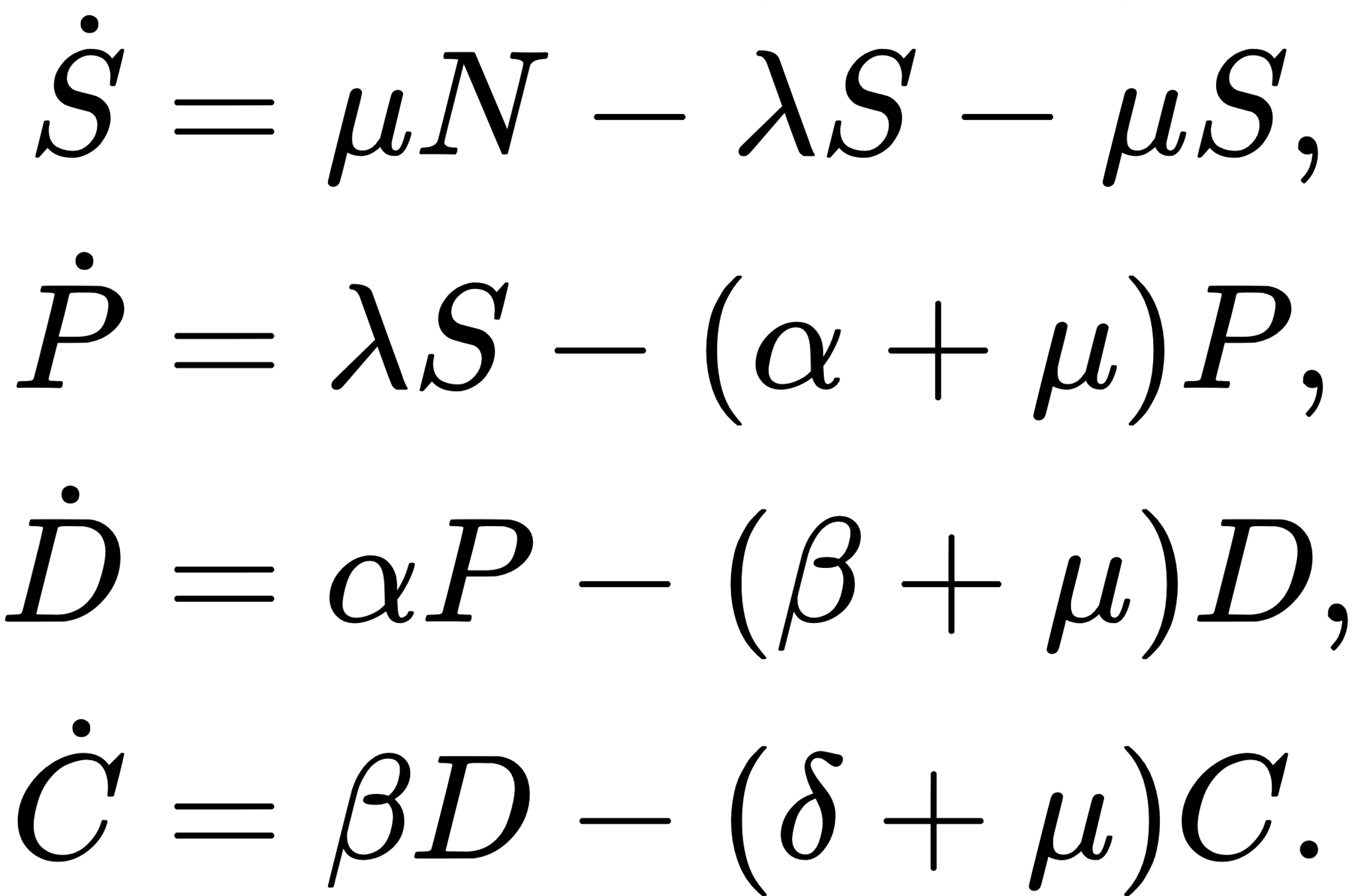


In this general ordinary-differential-equation (ODE) statement, the left-hand term expresses the instantaneous rate at which a particular state variable changes with respect to time, while the right-hand function stipulates that this rate is governed by the current values of every variable in the system, by a vector of fixed parameters that encode constants such as rate coefficients or binding affinities, and, if necessary, by time itself to accommodate external forcing; the subscripted index simply reminds the reader that an equation of this form is written for each of the n variables that together constitute the model’s state vector (Dattner et al., 2024)

*Compartmental models adapted for NCDs*

Compartmental models have been increasingly adapted to study NCDs, segmenting populations into distinct health states or compartments and simulating transitions between them over time using fixed equations and allowing researchers to capture disease progression, treatment effects, and demographic shifts (Iqbal et al., 2025; Smit et al., 2020). For instance, Smit et al., used a compartmental modeling approach to project the future burden of NCDs such as cardiovascular disease and diabetes among people living with HIV in Kenya, demonstrating how treatment programs for infectious diseases can shape NCD outcomes (Smit et al., 2020). Haacker et al., applied a similar modeling strategy in Botswana to assess the dual burden of HIV and NCDs, showing how the integration of NCD care into existing HIV programs could improve health outcomes and reduce costs (Haacker et al., 2019). These models allow quantification of future disease cases, deaths averted and are especially useful for policy planning, as they enable decision-makers to simulate different health intervention scenarios and anticipate long-term system demands (BMJ, 2018). However, this allows the model to remain a widely accepted choice in quantitative health impact assessments due to their balance of simplicity, transparency, and capacity to incorporate real-world epidemiological and demographic data (Mueller et al., 2023).

Below is a mathematical representation of compartmental models;



The four coupled differential equations form a deterministic compartmental model that tracks how a population moves through the diabetes cascade: the first line shows that the stock of individuals who are still metabolically healthy (S) grows through births (or immigration) at rate μN and shrinks through background mortality at rate μS and through progression to pre-diabetes at rate λS; the second line states that the pre-diabetic compartment (P) is fed by that same progression flow λS and loses members both to background death μP and to onset of overt diabetes at rate αP; the third equation does the same bookkeeping for diagnosed diabetes (D), whose inflow is αP and whose outflows are background mortality μD and transition to complications at rate βD; finally, the last equation governs the pool experiencing complications (C), which receives new cases at rate βD and experiences both background and excess mortality, the latter represented by the parameter δ; together, the system captures incidence, progression and disease-specific excess deaths within a single, transparent framework for policy analysis (Boutayeb et al., 2004).

*Monte Carlo Simulations*

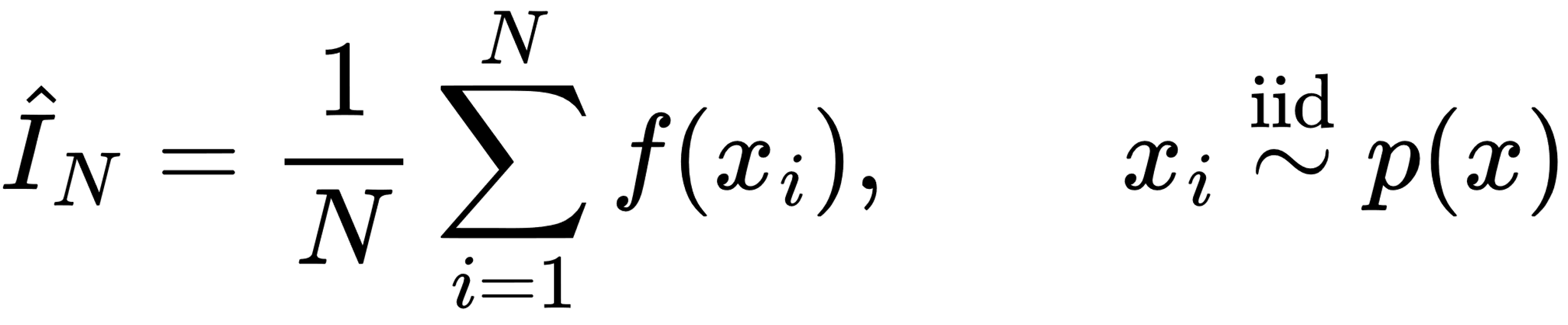
Monte Carlo simulation (MCS) is a computer-based technique that draws large numbers of random samples from the probability distributions assigned to uncertain inputs, then aggregates the resulting outputs to approximate the full output distribution (Kroese et al., 2014). By repeating the model thousands of times, investigators obtain means, confidence intervals, and tail risks that are otherwise analytically intractable, hence its routine use in health-technology-assessment modelling (Hatswell et al., 2018). A modern run of MCS follows three simple steps: (1) describe every uncertain input, such as a drug’s true success rate or a patient’s breathing motion, with a probability curve; (2) draw a random set of inputs and push them through the model; (3) repeat thousands of times until the outputs settles into a stable distribution (Kroese et al., 2014). Radiation oncologists treat MCS as the “gold standard” for tracking how individual protons or X-ray photons scatter and deposit energy inside the body, especially where tissues change density (Holmes et al., 2024). In a recent review of proton therapy, fast GPU-accelerated Monte Carlo codes trimmed calculation times to minutes yet still revealed subtle hot- and cold-spots that simpler algorithms miss, guiding safer dose prescriptions (Holmes et al., 2024).

Additionally, agencies that decide which treatments to fund wrap MCS around Markov or microsimulation models in a procedure called probabilistic sensitivity analysis; the technique shows how often, given all input uncertainty, an intervention beats its comparator on cost per quality-adjusted life-year (Lewkowicz et al., 2023). For example, a 10,000-iteration study of an app-based low-back-pain therapy found that the app was cost-effective in only ~55 % of simulated worlds, signalling caution to payers (Lewkowicz et al., 2023).

Furthermore, risk assessors feed field measurements of contaminants and human exposure habits into MCS to capture the full spread of possible doses. A 2024 investigation of Egypt’s Siwa Oasis groundwater combined Monte Carlo draws with source-apportionment models and showed that cadmium, chromium, and lead pose carcinogenic risks well above U.S. EPA levels, especially for children (Eid et al., 2024).

Across these settings, MCS converts hidden uncertainty into visible probability: instead of one answer, stakeholders get a risk curve or cost-effectiveness cloud that makes transparent both expected performance and worst-case tails (Kroese et al., 2014).

The expression below is the basic Monte-Carlo estimator.

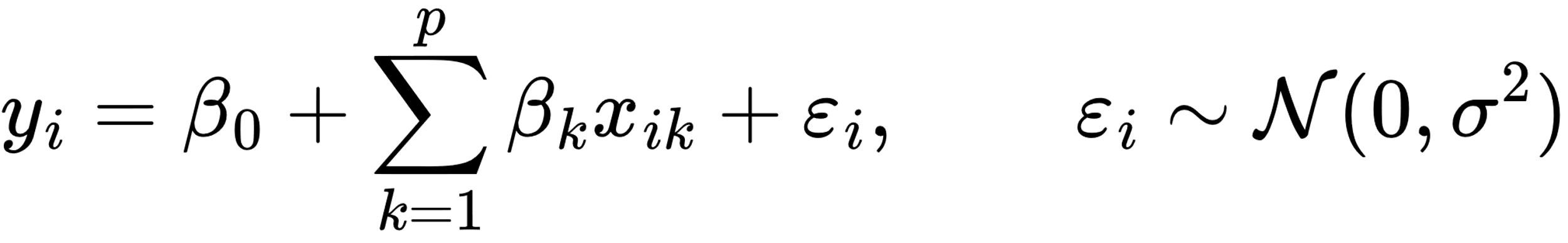


To approximate an integral or, equivalently, the expected value of a function f under a probability distribution p(x), one draws N independent samples x1,…,xN from that distribution and then averages the function values; the resulting quantity I^N converges to the true expectation as N grows, by the law of large numbers, and its sampling variance falls at the canonical 1/N rate (Kroese et al., 2014).

*Regression Models*

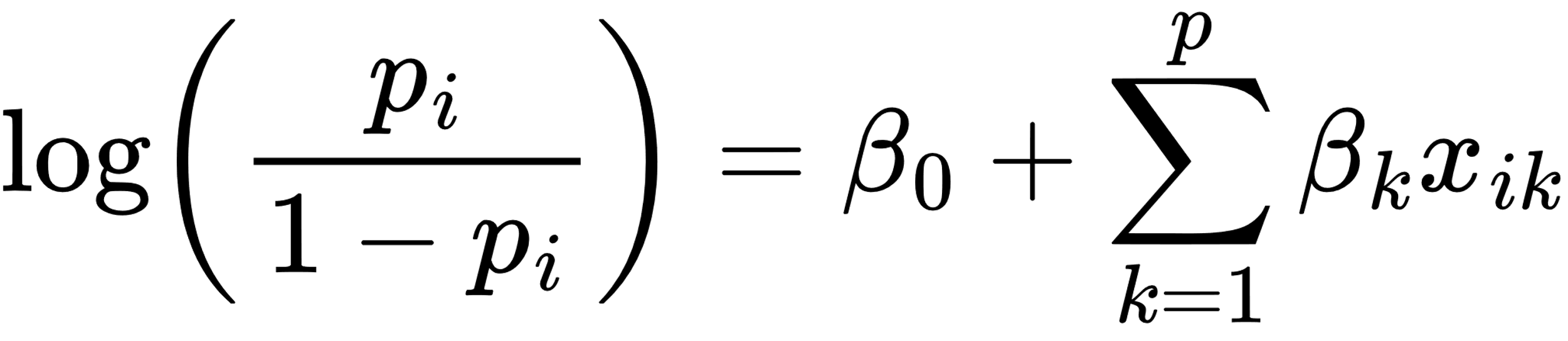
Regression models are statistical “rulers” that relate an outcome to one or more predictors while holding the other variables steady, letting researchers turn messy data into interpretable numbers (Roustaei, 2024; Zapf et al., 2024). They work by finding the line, curve, or set of coefficients that minimises the overall prediction error, producing slopes and intercepts whose units map directly onto clinical questions (Roustaei, 2024).

There are different models of regression. Linear regression handles continuous outcomes such as intra-ocular pressure or serum cholesterol and reports easily interpreted “per-unit” changes (Roustaei, 2024).



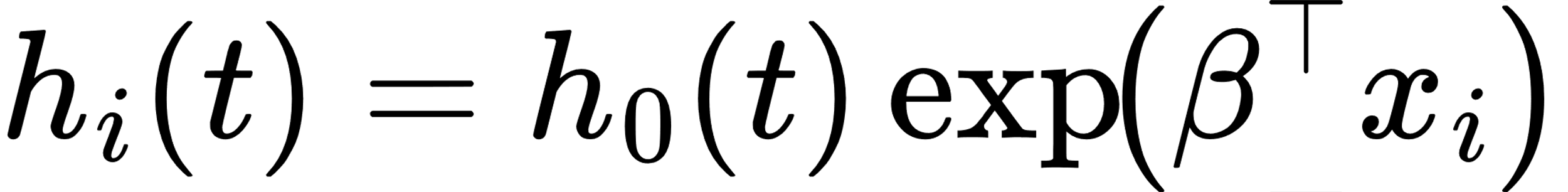
The equation of linear regression is the standard multiple-linear-regression model; for each observation ‘I’, the outcome ‘y’ is described as the sum of an intercept β0 plus a weighted combination of ‘p’ predictor values xik, where the weight (or slope) attached to the kth predictor is βk; the difference between the value predicted by this linear combination and the value actually observed is captured by the error term εi, which is assumed to be independently and identically distributed with mean zero and constant variance σ2 (Zapf et al., 2024).

Furthermore, logistic regression wraps the same idea in an S-shaped (sigmoid) link so that coefficients translate into odds ratios for yes/no events, an approach widely used in cancer risk prediction and treatment response studies (Kumar & Gota, 2023).



The expression for logistic regression is shown above. The log-odds change linearly with the covariates, and those changes are governed by the beta coefficients; exponentiating both sides converts the linear predictor into the familiar S-shaped probability curve (Kumar & Gota, 2023).

Cox proportional-hazards regression extends the framework to time-to-event data; a recent machine-learning variant, “stable Cox,” explicitly guards against distribution shifts between hospitals or cohorts (Fan et al., 2024).



The baseline hazard in the Cox regression above captures how the underlying risk changes over time when every covariate is zero, while the exponentiated linear predictor scales that baseline up or down according to the person’s characteristics (Fan et al., 2024).

When patients are clustered within wards or hospitals, multilevel (mixed-effects) regression adds random terms so that within-cluster and between-cluster information are disentangled, avoiding spuriously narrow confidence intervals (Austin et al., 2024).

Across all models, good practice starts with a prespecified, clinically plausible variable list, continues with assumption checks (e.g., linearity, proportional hazards, independence), and finishes with internal validation or penalisation to tame over-fitting (Efthimiou et al., 2024). Observational studies need extra care: causal diagrams help distinguish confounders from mediators or colliders before any coefficients are estimated (Zapf et al., 2024). Diagnostics such as residual plots, R-squared, or calibration curves show whether the model’s story matches the data it was given (Roustaei, 2024). For decision making, effect sizes from logistic models, hazard ratios from Cox models, or predicted risk curves can be paired with net-benefit analyses to reveal clinical utility (Efthimiou et al., 2024).

*Machine Learning and AI-Based Approaches*

Machine Learning (ML) is a subset of artificial intelligence that involves computational methods enabling systems to learn from data and improve performance over time without explicit programming (Rowe, 2019). ML encompasses various learning paradigms, including supervised, unsupervised, and reinforcement learning, each suited to different types of tasks and data structures (Habehh & Gohel, 2021). Artificial intelligence is the development of computer systems capable of performing tasks that typically require human intelligence, such as pattern recognition, learning from data, and decision-making. In healthcare, AI applications range from data interpretation and diagnostics to clinical decision-making and treatment planning. AI systems utilise complex algorithms to analyse large datasets, enhancing healthcare delivery's accuracy and efficiency (Mudey et al., 2024).

Most state-of-the-art systems rely on supervised deep-learning architectures that can equal or surpass human specialists on narrowly defined tasks such as retinal-disease grading or clinical‐note summarization (Dai et al., 2024; Van Veen et al., 2024). A recent Nature Medicine study pretrained on 717,308 fundus photographs showed that its convolutional network predicted each patient’s time to diabetic-retinopathy progression up to five years ahead, achieving concordance indices of 0.75–0.85 and supporting personalised screening intervals (Dai et al., 2024). Large-language models (LLMs) fine-tuned for health documentation have likewise outperformed expert readers in summarising radiology reports, progress notes, and doctor–patient dialogues, promising sizeable reductions in clerical workload (Van Veen et al., 2024).

ML and AI already uncover hidden signals, automate labour-intensive tasks, and generate patient-specific risk forecasts, but their safe uptake still hinges on high-quality data, prospective trials, transparent explanations, and guideline-compliant reporting (Morone et al., 2025; Rosenbacke et al., 2024).

**3.2 Overview of Mathematical Modelling in Health Research**

*Historical Background*

Mathematical modeling has been applied to biomedical problems for centuries. One of the first examples was Daniel Bernoulli’s 1766 analysis of smallpox mortality, a pioneering attempt to use equations to understand disease dynamics (Dembek et al., 2018). By the 19th century, quantitative models were already widespread in biology and medicine (Deichmann, 2019). For instance, Gregor Mendel’s laws of inheritance provided a mathematical framework for heredity (Deichmann, 2019). Throughout the 20th century, modeling expanded into many domains of biomedicine (Torres & Santos, 2015). Researchers developed theoretical models for epidemics and for physiological processes, laying a foundation for modern computational biology (Torres & Santos, 2015). In recent years, the explosion of biomedical data (such as genomic sequencing) and advances in computing have dramatically accelerated mathematical modeling approaches (Yang et al., 2024). This historical trajectory shows that modeling has evolved from simple formulas to sophisticated in silico simulations important in biomedical research today.

*The current mathematical model used in Health Research*

Contemporary biomedical researchers employ a wide variety of mathematical models, each suited to different questions (Y. Liu et al., 2023). Differential equation models are common; they use equations to represent biochemical kinetics or population changes over time, allowing simulation of processes like drug metabolism, tumor growth, or neuron firing (Truong et al., 2022). Statistical models are also widely used to analyze clinical and epidemiological data – for example, regression models can link risk factors to health outcomes or evaluate treatment effects from patient datasets (Henley et al., 2019). With the rise of big data, machine learning models have become prominent. Techniques such as neural networks and support vector machines learn patterns from large biomedical datasets, for instance, to detect diseases from imaging or predict drug targets (Taha, 2025). Network models also capture interactions in complex biological systems, networks can represent gene regulation, protein–protein interactions, or disease spread through populations (Torres & Santos, 2015). These various modeling approaches are often combined and tailored to address specific biomedical research problems, reflecting the interdisciplinary toolkit of modern mathematical biology.

*Purpose and Benefits of Modelling in Health Research*

Mathematical models are used in biomedical research because they enable scientists and clinicians to investigate complex problems in ways that experiments alone often cannot (Vera et al., 2021). Building a model forces researchers to synthesize data from multiple sources into a coherent framework, allowing an integrated analysis of otherwise complicated systems (Kretzschmar, 2020). In practice, this means models can help elucidate disease mechanisms by linking molecular findings (from in vitro or animal studies) with clinical outcomes in humans (Y. Liu et al., 2023). Models also serve as virtual laboratories. Since real-world experiments can be costly, slow, or unethical, a well-constructed model lets researchers test hypotheses and explore scenarios rapidly in silico (Jit & Cook, 2024). For example, a model of tumor growth can predict how a cancer might respond to a new drug before that drug is ever given to a patient (Diegmiller et al., 2022). The use of modeling thus speeds up discovery and can flag the most promising avenues for actual experiments (Vera et al., 2021). In the public health arena, mathematical modeling provides critical foresight (Mutubuki et al., 2024). Models are used to project disease trends and assess potential impacts of interventions. During the COVID-19 pandemic, for instance, models were widely used to estimate transmission dynamics and guide policy decisions on control measures (Guan et al., 2020). Mathematical modeling offers a powerful means to integrate knowledge, generate testable predictions, and inform decision-making in biomedical science (Pandey & Padamwar, 2019). By complementing human, animal, and cell-based studies, models help translate findings across scales and suggest optimal strategies for prevention and treatment (Vera et al., 2021).

*Comparison between NCD and Infectious Disease Modelling*

Modeling approaches can differ greatly between infectious diseases and non-communicable diseases (NCDs) due to the distinct nature of these conditions. Infectious disease models typically center on pathogen transmission dynamics (Baguelin et al., 2020). They often employ population-level compartmental frameworks (such as susceptible–infected–recovered models) or agent-based simulations to capture how infections spread and respond to interventions (Rui et al., 2024). This area of modeling has a long and well-established tradition in epidemiology (Yadav & Akhter, 2021). Communicable disease modeling has become an essential tool for public health decision-making, with a history of use in outbreak response and epidemic forecasting (Fischer et al., 2016). In contrast, non-communicable diseases are chronic conditions not spread person-to-person, and their modeling reflects different challenges (Wang & Wang, 2020). NCD models must account for multifactorial etiologies – for example, a chronic disease might involve genetic predisposition, environmental exposures, and lifestyle behaviors all at once (Budreviciute et al., 2020). As a result, NCD modeling often requires capturing individual risk factors and long-term disease progression within a population. Researchers frequently use individual-level simulation models (such as Markov models or microsimulations) for NCDs to represent population heterogeneity in risk profiles and outcomes​ (Briggs et al., 2016). These models can incorporate interactions between individuals and their environment over decades, something less critical in many infectious disease models (Emmert-Fees et al., 2021). Another contrast is that NCD interventions (such as diet changes, screening programs, or policy measures) are usually complex and multi-faceted (Budreviciute et al., 2020). Modeling their impact may demand frameworks that include social and behavioral factors, whereas infectious disease models more narrowly focus on infection and immunity (Domínguez-Miranda et al., 2025).

**3.3 Application of Mathematical Models in NCD**

*Mathematical Models for Cardiovascular Diseases*

Cardiovascular disease, including coronary heart disease, stroke and vascular disease a well-documented non-communicable disease, has been identified as a major cause of the increase in death rate worldwide (Flora & Nayak, 2019; Ghamri et al., 2019). It is pertinent to note that the majority of cardiovascular-related morbidity and mortality occur prematurely and can be prevented by improving healthcare management through improved diet planning, lifestyle adjustment and drug interventions (Wu et al., 2025). Data mining provides evidence of CVD detection, risk prediction models for more effective intervention outcomes using a statistical regression model (Jia et al., 2019; G et al., 2022) and the ARIMA model. Mathematical models have been reported to provide knowledge toward precise and reliable diagnosis, management, and treatment strategies implemented in heart and vessel-related problems (Tolkacheva et al., 2017). Ordinary or partial differential equations have been implemented as an effective computation system to predict, diagnose and provide novel drug combinations for the treatment of chronic diseases such as myocardial infarction (Moise & Friedman, 2022), stroke (G. Li et al., 2024; Herrgårdh et al., 2021). In the same vein, stochastic modeling approaches have been used in real-world patient data, providing insight into disease progression, especially chronic diseases, for more effective monitoring and timely intervention strategies (Brahma et al., 2024).

*Mathematical Models for Cancer*

The advances in understanding tumor heterogeneity and cancer evolution have enhanced insights into drug resistance, with models aiding personalized, resistance-overcoming therapies (Yin et al., 2019). Mathematical modelling remains a holistic approach in cancer that addresses several questions concerning tumor initiation, progression and metastases, intra-tumor heterogeneity, treatment responses and resistance (Altrock et al., 2015). It helps predict how and why cells function the way they do in response to stressors such as hypoxia, DNA damage, retinoblastoma protein degradation, and oncogene activation or in response to external factors such as nutrient or oxygen deprivation (Cesario & Marcus, 2011). Evidence has identified basic tools used in computational modeling of tumorigenesis by a multistep stochastic process, modeled with a Markov chain (on-and-off gene activities), which involves quantitatively modeled gene-specific mutation rates in key signaling pathways (like energy metabolism, cell cycle control, apoptosis resistance) (Alameddine et al., 2018). Cancer cells are presented with indefinite growth ability compared to normal cells. Deterministic mathematical models have been widely used by researchers to understand the growth of a tumor and to predict their growth pattern and random variation. These models track changes in tumor size employing ordinary differential equations (ODEs) (Lv et al., 2022). Seven form of deterministic model have been widely used, including an exponential model, predicting the volume of cancer growth with no reference to angiogenesis and nutrient reduction, logistic model predicting cancer cell proliferation a notable limitation of the exponential model, and Gompertz model which theorized exponential proliferation of tumor cell indicated by an S-shaped curve that model the size of tumor (Lv et al., 2022; Vaghi et al., 2020) and Bertalanffy’s model that predicts tumor growth dynamics of the metabolic process (Bekisz & Geris, 2020; J. A. Roberts & Al Themairi, 2017; Benzekry et al., 2014; Tabassum, 2019).

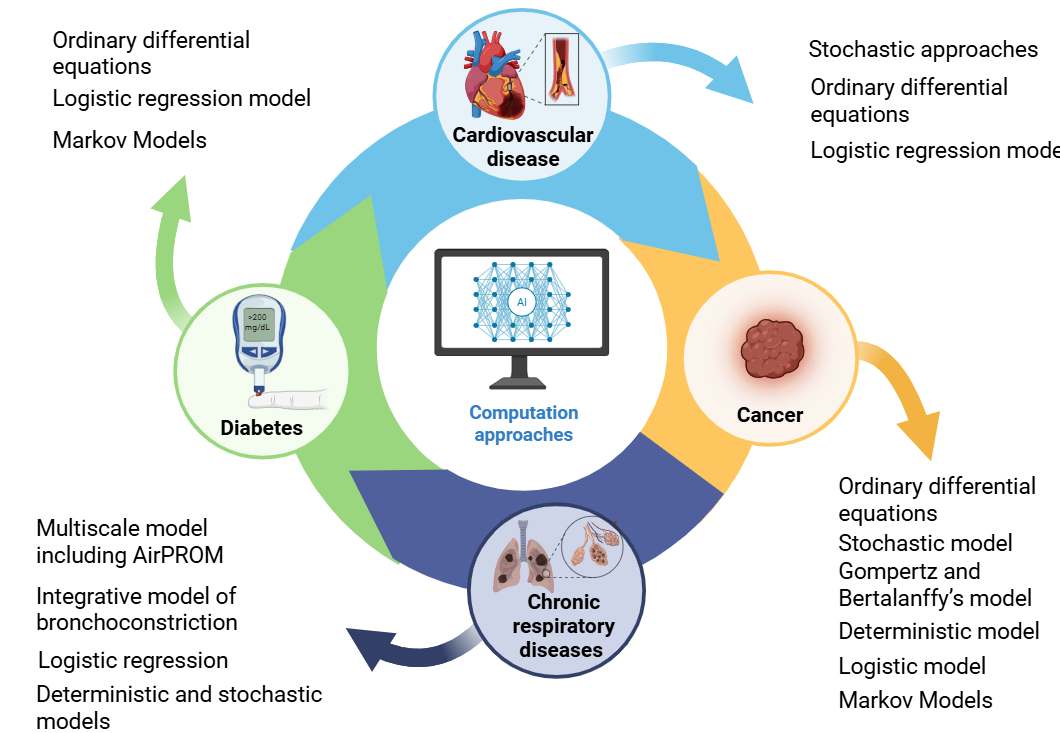
*Mathematical Models for Diabetes*

Diabetes is a well-known non-communicable disease that can affect anyone. It is characterized by a sustained increase in glucose level, impaired insulin production and utilization, posing significant public health issues globally (Hossain et al., 2024; M. AlShurbaji et al., 2023). Diabetes mellitus (DM) exists as type 1, presented by loss of β-pancreatic cell function, having no or little insulin produced, and type 2, characterized by failure of the β-pancreatic cell function associated with the body’s resistance to insulin (Niu et al., 2024; Diane et al., 2024). Studies have reported the use of mathematical models as an effective method to predict the prevalence of diabetes, the mechanistic pathway and ways of developing effective strategies to regulate the occurrence of DM and its complications (Al Ali et al., 2022; Mohammad AlShurbaji et al., 2023). Using ordinary differential equations (ODEs), the prevalence, complication and control of diabetes have been reported (Boutayeb et al., 2004; Akinsola & and Oluyo, 2019; Chervoneva et al., 2014). The ordinary differential equations were numerically represented in five ways via an explicit Euler, implicit Euler, Heun’s, Runge-Kutta 4th order, and Adams-Bashforth-Moulton 4th order methods reviewed by Alshurbaji et al. (M. AlShurbaji et al., 2023) that provided values indicating the probability of developing diabetic complications, mortality and natural mortality rate. Prior studies have suggested the stochastic approach, which predicts the dynamic behavior of diabetes mellitus (Z. Zhang et al., 2019), accounting for the glucose and insulin dynamic process (Y. Zhang et al., 2016), glycemic disturbance (Clausen et al., 2021), and pancreatic islet disruption (Portuesi et al., 2013). Machine learning and artificial intelligence techniques are models reported previously on detecting the type of DM, diagnosis and self-management (Chaki et al., 2022; García-Ordás et al., 2021; Pradhan et al., 2020). Using the logistic regression technique, evidence on the prediction of the probability that a patient has DM based on demographic information has also been documented, which ensures early diagnosis, prevention and treatment of the health condition (Zhu et al., 2019; Lai et al., 2019; Rajendra & Latifi, 2021). Given the nature of DM patient health conditions, mathematical model of physiological processes through the application of hidden Markov Models provides dynamic prognostic assessment to inform future care and treatment strategies (Perveen et al., 2019). Generally, by combining demographic data and physiologic parameters, these models can contribute to the early detection, personalized treatment plan and health care system preparedness in managing DM.

*Mathematical Models for Chronic Respiratory Diseases*

Chronic respiratory diseases (CRDs) are non-communicable diseases characterized by structural and functional abnormalities in the airways, alveoli, and lungs parenchyma (Labaki & Han, 2020; Li et al., 2025). CRDs represent the third leading cause of death and disability worldwide (Luan et al., 2023). Currently identified CRDs include asthma, chronic obstructive pulmonary disease, lung fibrosis, pulmonary sarcoidosis, and pneumoconioses (silicosis and asbestosis) are characterized by an impaired immune system, microbial pathogenesis (Labaki & Han, 2020; Nascimento et al., 2016; Gould et al., 2023). Mathematical models have emerged as a powerful tool in the understanding of CRDs, enabling effective prediction, monitoring and optimization of treatment intervention (Redlarski & Jaworski, 2013).

Multi-scale approaches have been incorporated to integrate molecular, cellular, and organ-system dynamics in disease progression and therapeutic intervention. According to previous (Burrowes et al., 2014; Burrowes et al., 2013) an AirPROM project (Airway disease Predicting Outcomes through patient-specific computational Modelling) designed to unravel the pathophysiological mechanisms in asthma and COPD patients and predict ventilation dysfunction using large data across multiple disciplines, including clinical, physiologic, and image data. Additionally, the Integrative model of bronchoconstriction has been employed to provide insight into the self-organizing behavior of airway constriction and the emergence of ventilation defects (Winkler et al., 2015). While recent advances in the application of machine learning, including logistic regression and neural networks, have been reported to be effective in predicting asthma exacerbation using patients' self-generated data (de Hond et al., 2022). Deterministic models and stochastic differential equation models have been used to provide knowledge on public health policy for optimal prevention and control strategies of air pollution-related respiratory diseases (He et al., 2023; He et al., 2024; Q. Liu, 2023).



**Fig.** **2**. Mathematical model application in NCD

**3.4 Challenges and Limitations**

Mathematical models help researchers and governments understand non-communicable diseases (NCDs) such as heart disease, cancer, diabetes, and chronic lung illness. They let us test ideas on a computer before we try them in the real world, and can save time, money and lives (Dubey & Malinzi, 2024). Even so, modelling NCDs is harder than modelling infections. We can often write clean equations for a virus that link contact rates with new cases. By contrast, conditions like high blood pressure grow out of slow and tangled mixes of genes, the epigenome, diet, stress, and social policy, and no short set of equations can capture all of that complexity (Devaux et al., 2020).

Furthermore, data gaps make the job tougher. In rich countries, electronic health records hold millions of patient files, yet they still miss migrants, uninsured people and those who rarely visit clinics. In poorer countries, health workers must rely on small surveys and paper registers, giving only scattered snapshots of disease (Guralnik, 2023; Hyder et al., 2023). Modellers fill the holes with statistical tricks such as imputation and borrowing numbers from other regions, but these carry hidden errors that can spread through the whole model (Li et al., 2024).

Time adds another layer of challenge. An obesity programme started today may not prevent heart attacks for fifty years, during which climate change, economic shifts and new medicines could rewrite the background risk. Health-economic studies often “discount” far-off benefits so that distant lives saved count less than near-term ones, but many scholars warn that this practice undervalues prevention (Standaert & Ethgen, 2023).

No model of chronic disease can ignore heterogeneity. The same body-mass index may be harmless for one person and dangerous for another, depending on age, sex or ancestry (Lim et al., 2024). Agent-based and microsimulation models can track individuals one by one and show how policies reach, or miss, different groups (Hennessy et al., 2016). But these detailed models need thousands of behavioural rules that are rarely backed by solid evidence, potentially turning calibration into a guessing game.

Because such simulations run slowly, many teams now train machine-learning surrogates that copy the behaviour of the big model in a fraction of a second. These make large sensitivity studies possible, yet they may hide the original causal logic behind a black box and may mislead users who are not careful (Angione et al., 2022).

Openness and trust matter as much as fancy code. Policymakers often see only the final charts, not the assumptions buried in the model files. A recent survey found that most health-economic models remain closed-source because the data come from commercial trials or because the developers hope to sell their tools (Pouwels et al., 2022). When ethical choices, such as how to value life-years in poorer groups, stay hidden, results can be accepted or rejected for political reasons rather than scientific ones. New reviews call for clearer reporting and for methods that put equity on the same footing as efficiency (Muir et al., 2024).

Finally, only careful follow-up can show whether a model works. For example, taxes on sugar-sweetened drinks, do cut sales in many cities, but untangling the model’s accuracy from changes in marketing or wider diet trends is not simple (Andreyeva et al., 2022). The shock of COVID-19 also proved that one unexpected event can destroy usual forecasts, yet many long-term NCD scenarios still glide smoothly to 2050 as if no more surprises wait ahead (Devaux et al., 2020).

Modelling NCDs walks a tightrope. The equations must stay simple enough to solve, detailed enough to reflect real life, and transparent enough to earn trust.

**3.5 Future Directions**

Looking across the evidence reviewed, the immediate path forward rests on strengthening the data foundations that underpin every model. Much of the current uncertainty in NCD projections comes from patchy electronic records, short-run surveys and the routine practice of importing parameters from high-income to low- and middle-income settings. Building secure, interoperable pipelines that knit together clinical, genomic, environmental and behavioural information, particularly in regions where such systems are still emerging, will allow models to reflect the true diversity of risk and response. With richer inputs in place, the next step is to marry mechanistic insight with data-driven flexibility: cellular- or organ-level ordinary differential-equation frameworks can be wrapped inside stochastic, agent-based or microsimulation shells, while fast machine-learning surrogates can accelerate scenario exploration without discarding biological meaning. Such hybrid architectures must be coupled with equity-centred reporting that breaks results out by sex, age, socio-economic position and ancestry so policy makers can see not only average benefits but also who gains most, and who may be left behind. None of this will matter, however, unless transparency, reproducibility and continuous feedback become routine. Open code repositories, prespecified protocols and collaborations that link modellers with front-line implementers and evaluators will turn once-off projections into living tools that adapt as new data arrive and as interventions move from paper to practice.

1. **Conclusion**

Non-communicable diseases are a leading cause of death worldwide, and the review shows that mathematical and computational modelling has already become indispensable for understanding, predicting and managing this complex burden. Deterministic and stochastic differential equations, Markov and compartmental formulations, Monte Carlo simulations, regression techniques, and machine-learning systems each illuminate different facets of cardiovascular disease, cancer, diabetes and chronic respiratory disorders. Together they transform fragmented observations into coherent pictures of disease dynamics, test policy options in silico, and suggest personalised pathways of care. Yet the same studies also reveal persistent limitations: incomplete or biased data streams, long latency between intervention and outcome, computational cost, hidden assumptions and a frequent neglect of distributional impacts. By investing in integrated, representative data, embracing hybrid multi-scale approaches, foregrounding equity and openness, and linking modelling more tightly to real-world evaluation, researchers and decision-makers can turn these powerful methods into practical engines for healthier, longer and more equitable lives.

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