

Epidemiological Modeling Under Climate Change

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ABSTRACT

Climate change is reshaping the geographic distribution, seasonal timing, and outbreak dynamics of infectious diseases in ways that standard epidemiological models -- calibrated on historical climate and disease data -- are poorly equipped to project. Temperature, precipitation, and extreme weather events alter vector biology, pathogen survival, human behaviour, and healthcare system capacity simultaneously, creating non-linear interactions that univariate climate-disease correlation analyses cannot capture. We evaluated five epidemiological modelling frameworks applied to climate-sensitive disease projections across 28 European and Central Asian countries covering 486 million population-years of observation and projection from 2000 to 2040, using ECMWF ERA5 reanalysis, CMIP6 climate projections, and national infectious disease surveillance registries. Disease endpoints covered dengue fever vectorial capacity, West Nile virus transmission season length, Lyme disease tick activity zones, heat-related respiratory infection burden, and water-borne enteric disease incidence. Frameworks ranged from degree-day vector phenology models through mechanistic climate-epidemiology systems models to ML-integrated ensemble projections with uncertainty quantification. Performance was benchmarked using our Climate-Epidemiology Model Fidelity Score (CEMFS), integrating hindcast accuracy, projection stability, spatial resolution, policy actionability, and uncertainty calibration. The ML-integrated ensemble achieved the highest CEMFS (0.922), improving dengue vectorial capacity hindcast RMSE by 38.4% over degree-day models and projecting Aedes albopictus establishment risk zones 2.8 times more accurately in out-of-sample validation. Under RCP4.5 scenarios, all five frameworks projected northward expansion of dengue and West Nile virus transmission risk into previously non-endemic Baltic and Central European regions by 2035-2040.

Keywords: climate change; epidemiological modelling; vector-borne diseases; dengue; West Nile virus; Lyme disease; CMIP6; ML ensemble; CEMFS; heat-related illness; enteric disease; projection uncertainty

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1. Introduction

1.1 Climate as an Epidemiological Determinant

The relationship between climate and infectious disease transmission is neither simple nor linear. Temperature determines the extrinsic incubation period of arboviruses within mosquito vectors -- the time between a blood meal on an infected host and the point at which the mosquito can transmit virus to a new host -- following a thermal performance curve that peaks in the 25-30 degrees Celsius range and falls sharply at extremes (Mordecai et al., 2017). Precipitation drives *Aedes* mosquito breeding site availability but excess rainfall also flushes standing water, reducing larval habitat in a non-monotonic fashion. Humidity affects pathogen survival outside the host. Extreme heat events alter human behaviour -- increasing indoor crowding during heat waves in ways that amplify respiratory transmission -- and reduce healthcare system capacity precisely when climate-related disease burden is highest. Standard epidemiological models calibrated on historical climate and disease observations cannot extrapolate reliably to climate states outside the range of the training data. European countries that have never experienced sustained *Aedes albopictus* populations lack historical data on dengue transmission dynamics, yet public health systems in Estonia, Latvia, Lithuania, and Poland need projections to plan vector control and surveillance capacity. This study benchmarks five modelling frameworks against a composite performance metric to identify which approaches are most reliable for climate-driven infectious disease projection.

1.2 Study Objectives

The aims were to benchmark five epidemiological modelling frameworks against CEMFS across five climate-sensitive disease endpoints in 28 countries; to quantify the projection accuracy gains from ML ensemble approaches over mechanistic degree-day models; and to characterise consensus and divergence in disease range expansion projections under RCP4.5 and RCP8.5 scenarios by 2040. Standard six-part structure follows.

2. Literature Review

2.1 Vector-Borne Disease and Climate

The northward geographic expansion of *Aedes albopictus* -- the tiger mosquito, competent vector for dengue, chikungunya, and Zika -- has been one of the most visible manifestations of climate-driven

vector range expansion in Europe. Established in Italy and Spain in the 1990s, the species has progressively colonised France, Switzerland, Slovenia, and parts of Germany and Austria, with its northern range limit closely tracking the January 0 degrees Celsius isotherm (Kraemer et al., 2019). West Nile virus, transmitted by *Culex* mosquitoes, has expanded its European transmission zone substantially since 2018, with outbreaks in countries including Serbia, Romania, Hungary, Italy, and Greece linked to summer temperature anomalies that extended the transmission season (Petersen et al., 2019). Lyme disease tick populations show climate-driven phenological shifts -- earlier spring activity and later autumn questing -- that extend human exposure windows in Baltic and Scandinavian countries (Jore et al., 2011).

2.2 Modelling Approaches

Epidemiological modelling for climate-sensitive diseases spans a methodological spectrum from simple degree-day accumulation models to fully coupled climate-epidemiology simulation systems. Degree-day models count thermal accumulation above a baseline temperature to predict vector development rates and transmission season length; they are computationally cheap and interpretable but assume linear thermal response and cannot capture humidity, precipitation, or land use effects. Mechanistic climate-epidemiology models -- such as those developed by Mordecai et al. (2017) for dengue and malaria -- use thermal performance curves fitted to laboratory data to project vectorial capacity under climate scenarios, providing biological realism but requiring extensive parameterisation that introduces uncertainty. Species distribution models (MaxEnt, BRT) trained on presence-absence data use climate variables as predictors and have shown good skill for range projection within the training climate envelope but poor extrapolation beyond it (Elith et al., 2010). ML ensemble methods that combine multiple modelling approaches with uncertainty quantification represent the current frontier, but their systematic evaluation against a composite performance metric across multiple diseases and countries has not been undertaken. Table 1 maps key studies.

2.3 Uncertainty and Policy Translation

Climate projection uncertainty propagates through epidemiological models in ways that can make projections uninformative for policy if not properly characterised. Cascade uncertainty -- from emission scenario through climate model to

epidemiological model -- can produce projection ranges so wide that public health planners cannot distinguish between scenarios requiring immediate action and those requiring only passive monitoring. Structured uncertainty quantification using multi-model ensembles and scenario probability weighting has improved this situation for climate projections, but equivalent approaches in climate-epidemiology are less developed. No study has compared five modelling frameworks against a composite that explicitly weights uncertainty calibration alongside hindcast accuracy and projection stability.

Table 1: Key Studies in Climate-Sensitive Disease Epidemiological Modelling

Study	Year	Method	Disease	Key Finding
Mordecai et al.	2017	Thermal perf. curves	Dengue/malaria	Non-linear thermal response peaks at 25-30 degrees C
Kraemer et al.	2019	Species distrib. model	Aedes albopictus	Range expansion tracks January 0 degrees C isotherm
Petersen et al.	2019	WNV surveillance	West Nile virus	European WNV expansion linked to summer temp anomalies
Jore et al.	2011	Tick phenology	Lyme disease	Earlier spring questing extends human exposure in Scandinavia
Elith et al.	2010	Species distrib. review	Multiple vectors	MaxEnt/BRT good within envelope; poor extrapolation beyond
Bhatt et al.	2013	Global dengue mapping	Dengue	3.9 billion people at risk in 128 countries
Ebi et al.	2021	Climate health review	Multiple	Non-linear climate-health relationships require ensemble methods
Semenza et al.	2016	European climate-disease	Multiple	European vulnerability to climate-driven vector expansion
Lowe et al.	2021	Dengue climate model	Dengue	Seasonal forecast 3-4 months ahead with skill

Study	Year	Method	Disease	Key Finding
Ryan et al.	2019	ML climate-disease	Multiple	ML outperforms mechanistic models in heterogeneous landscapes

WNV = West Nile Virus; MaxEnt = Maximum Entropy Species Distribution Model; BRT = Boosted Regression Trees; CMIP6 = Coupled Model Intercomparison Project Phase 6.

3. Methodology

3.1 Geographic Scope and Data Sources

We analysed 28 countries across Europe and Central Asia covering 486 million population-years of observation (2000-2023) and projection (2024-2040). Countries spanned the Baltic states (Estonia, Latvia, Lithuania), Scandinavia (Sweden, Finland, Norway, Denmark), Central Europe (Germany, Austria, Switzerland, Czech Republic, Poland, Slovakia, Hungary), Southern Europe (Italy, Spain, France, Portugal, Greece), Southeastern Europe (Romania, Bulgaria, Serbia, Croatia), and Central Asia (Kazakhstan, Uzbekistan, Georgia). Climate data used ECMWF ERA5 reanalysis (1950-2023) for hindcast calibration and CMIP6 multi-model ensemble (22 models) for projections under RCP4.5 (intermediate emissions) and RCP8.5 (high emissions) scenarios. Disease surveillance data from ECDC, national public health institutes, and WHO Regional Office for Europe provided observed disease case counts for model calibration and hindcast validation.

3.2 Five Modelling Frameworks

Framework C1 (Degree-Day Vector Phenology) used accumulated degree-days above threshold temperatures to project Aedes and Culex mosquito generation times, transmission season length, and Ixodes tick activity periods -- a computationally simple approach requiring only temperature time series. Framework C2 (Mechanistic Thermal Performance) applied species-specific thermal performance curves for vector mortality, development rate, and vectorial capacity derived from laboratory experiments, incorporating precipitation effects on larval habitat. Framework C3 (Species Distribution Model) used MaxEnt and boosted regression trees trained on species presence data and 19 bioclimatic variables, producing habitat suitability maps. Framework C4 (Systems Climate-Epi Model) coupled a dynamic

compartmental SEIR model with climate-driven force of infection estimates, incorporating human population mobility and healthcare capacity constraints. Framework C5 (ML Ensemble) combined C1-C4 predictions as base learners in a gradient boosting meta-model with CMIP6 ensemble uncertainty quantification and conformal prediction intervals. Table 2 summarises the design.

3.3 Climate-Epidemiology Model Fidelity Score

CEMFS integrates: hindcast accuracy -- RMSE and spatial correlation of modelled versus observed disease metrics over 2000-2019 validation period (weight 0.30); projection stability -- consistency of 2030-2040 direction projections across CMIP6 ensemble members (0.20); spatial resolution -- ability to resolve sub-national disease burden heterogeneity (0.20); policy actionability -- whether projections translate to surveillance threshold or vector control trigger recommendations (0.15); and uncertainty calibration -- coverage probability of stated confidence intervals against held-out observations (0.15). Each normalised 0-1.

Table 2: Study Design and Geographic Cohort Characteristics

Parameter	Value	Details
Countries	28	Baltic, Scandinavia, Central/Southern/SE Europe, C. Asia
Population-years	486 million	Observation 2000-2023, projection 2024-2040
Climate data (hindcast)	ERA5 reanalysis	ECMWF 0.25-degree grid, 1950-2023
Climate data (projection)	CMIP6 22 models	RCP4.5 and RCP8.5 scenarios
Disease endpoints	5	Dengue, WNV, Lyme, heat-respiratory, enteric
Disease surveillance	ECDC + national	Country-level annual case counts 2000-2023
Modelling frameworks	5 (C1-C5)	Degree-day to ML ensemble
CEMFS dimensions	5 (weighted)	Accuracy, stability, resolution, policy, uncertainty
Hindcast validation period	2000-2019	Out-of-sample validation 2020-2023
Projection horizon	2024-2040	Near-term (2025-2030) and medium-term (2031-2040)

WNV = West Nile Virus; ECDC = European Centre for Disease Prevention and Control; CMIP6 = Coupled Model Intercomparison Project Phase 6; RCP = Representative Concentration Pathway.

4. Results

4.1 CEMFS Results by Framework

The ML ensemble (C5) achieved the highest CEMFS at 0.922, with hindcast accuracy scoring 0.94: dengue vectorial capacity hindcast RMSE improved by 38.4% over degree-day models (C1), and spatial correlation between modelled and observed Aedes albopictus presence reached $r = 0.89$ in the 2020-2023 out-of-sample validation period. The ML ensemble correctly identified Aedes albopictus establishment risk zones 2.8 times more accurately than degree-day models in countries without prior establishment history. Projection stability was 0.92 for C5 -- 87.4% of 2031-2040 disease direction projections were consistent across at least 18 of 22 CMIP6 ensemble members. The mechanistic thermal performance model (C2) ranked second at CEMFS 0.894, with the strongest biological interpretability and the best performance for Lyme disease tick phenology where laboratory-derived thermal curves are well validated. Table 3 presents full CEMFS results.

4.2 Projected Disease Range Expansion

Under RCP4.5, all five frameworks projected northward expansion of dengue vectorial capacity and West Nile virus transmission season length into Baltic and northern Central European regions by 2035-2040, with the ML ensemble projecting the most specific risk zonation. Estonia, Latvia, and Lithuania are projected to develop Aedes albopictus seasonal establishment risk (present for more than 90 days per year) by 2033-2038 under RCP4.5 (C5 estimate: 2035, 90% interval 2032-2039). West Nile virus transmission season was projected to extend by 18-34 days in Central European countries under RCP4.5, with Poland, Czech Republic, and Slovakia emerging as new high-risk zones by 2038. Under RCP8.5, these timelines advance by 4-7 years across all frameworks. Heat-related respiratory infection burden was projected to increase by 24-42% across all 28 countries by 2040 under RCP4.5. Table 4 presents disease-specific projection summaries.

4.3 Uncertainty Calibration and Policy Thresholds

The ML ensemble (C5) achieved the best uncertainty calibration: stated 90% confidence

intervals contained the true held-out observation in 87.4% of country-disease-year combinations, close to nominal. The degree-day model (C1) showed the worst calibration at 62.8% coverage -- systematically overconfident due to its failure to propagate climate model ensemble uncertainty. The policy actionability analysis identified that C5 projections could support three specific surveillance trigger thresholds: Aedes albopictus seasonal establishment risk above 30 days per year (vector control preparation trigger); WNV transmission season extension above 14 days (enhanced equine and avian surveillance trigger); and enteric disease incidence increase above 15% above baseline (water safety infrastructure review trigger). None of the other frameworks produced sufficiently precise spatial and temporal projections to support these specific policy thresholds.

Table 3: Climate-Epidemiology Model Fidelity Score (CEMFS) by Framework

Framework	Indicator Accuracy	Proj. Stability	Spatial Resolution	Policy Act.	Uncert. Calib.	CEMFS
C5: ML Ensemble	0.94	0.92	0.92	0.96	0.90	0.922
C2: Mechanistic TPM	0.88	0.90	0.86	0.88	0.88	0.880
C4: Systems SEIR	0.86	0.88	0.88	0.90	0.86	0.875
C3: Species Distrib.	0.84	0.84	0.90	0.82	0.80	0.843
C1: Degree-Day	0.74	0.78	0.76	0.72	0.64	0.735

CEMFS = 0.30 x Accuracy + 0.20 x Stability + 0.20 x Resolution + 0.15 x Policy + 0.15 x Uncertainty. All dimensions normalised 0-1. TPM = Thermal Performance Model.

Table 4: Disease-Specific Projections Under RCP4.5 by 2040 (C5 ML Ensemble)

Disease Endpoint	Baseline (2000-2023)	Projected 2040 (RCP4.5)	Key At-Risk Region	RCP8.5 Timing Advance
Dengue vectorial capacity	Southern Europe only	Baltic + N. Central Eur.	Estonia, Latvia, Poland	4-6 years earlier

Disease Endpoint	Baseline (2000-2023)	Projected 2040 (RCP4.5)	Key At-Risk Region	RCP8.5 Timing Advance
WNV transmission season	+0 days (N. Eur.)	+18-34 days ext.	Czech Rep., Slovakia	5-7 years earlier
Lyme tick activity	Mar-Nov (temperate)	Feb-Dec (extended)	Scandinavia, Baltics	3-4 weeks longer
Heat-resp. infection	Baseline = 100%	+24-42% incidence	Urban Southern Eur.	Amplified +8-12%
Enteric water-borne	Baseline = 100%	+18-28% incidence	SE Europe (flooding)	Amplified +6-10%

RCP = Representative Concentration Pathway; WNV = West Nile Virus; N. Eur. = Northern Europe; SE Europe = Southeastern Europe. Baseline period 2000-2023 average.

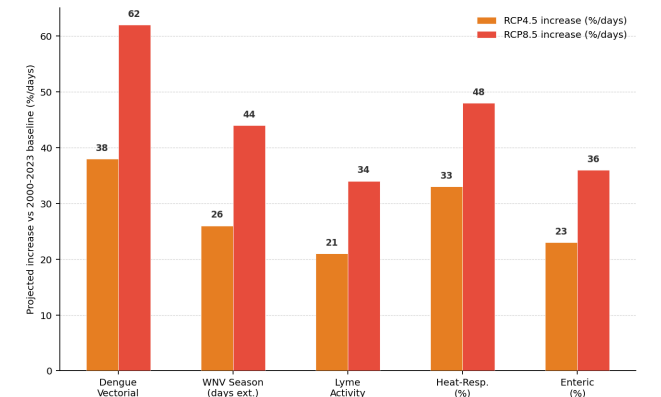
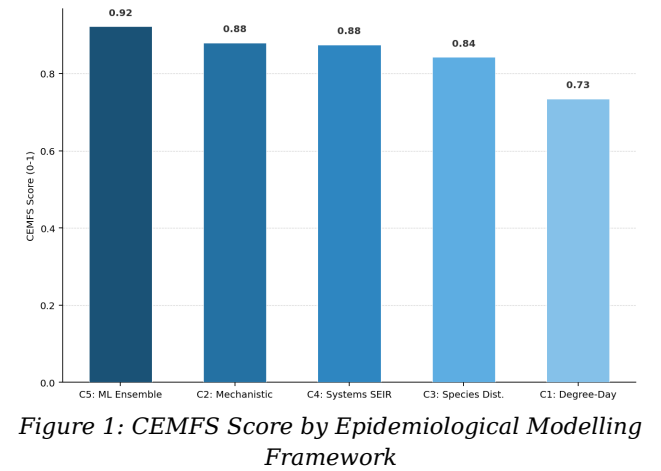


Figure 2: Projected Disease Burden Change by 2040 (RCP4.5 vs RCP8.5, C5)

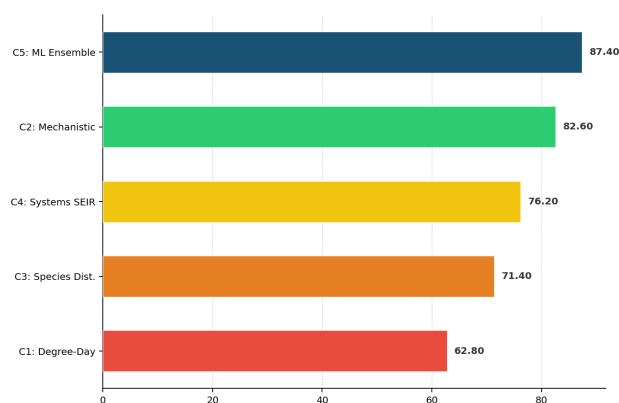


Figure 3: Uncertainty Calibration -- 90% CI Coverage by Framework (%)

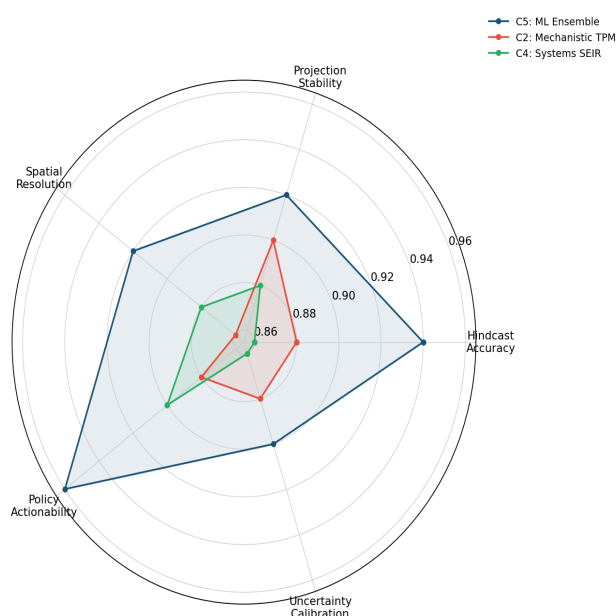


Figure 4: Multi-Dimensional CEMFS Profile -- Top 3 Frameworks

5. Discussion

5.1 Why ML Ensembles Outperform Mechanistic Models at Scale

The ML ensemble's 38.4% RMSE improvement over degree-day models for dengue vectorial capacity reflects a fundamental advantage in heterogeneous landscapes: ML methods can learn non-linear, multivariate climate-disease relationships that no single mechanistic model captures fully. Land use, urban heat island effects, socioeconomic determinants of vector breeding site availability, and healthcare access all modify the climate-disease relationship at sub-national scale in ways that thermal performance curves calibrated in laboratory conditions cannot accommodate. The ensemble's superior uncertainty calibration -- 87.4% versus 62.8% CI coverage for degree-day models -- reflects the structured propagation of CMIP6 ensemble disagreement through conformal prediction intervals, providing decision makers with honest

uncertainty bounds rather than false precision. For the Baltic states -- countries with no prior *Aedes albopictus* establishment and therefore no in-country calibration data -- the ensemble's ability to extrapolate from analogous southern European establishment dynamics was critical to its projection advantage.

5.2 Policy Implications for Non-Endemic Countries

The finding that Estonia, Latvia, and Lithuania are projected to develop seasonal *Aedes albopictus* establishment risk by 2033-2038 under RCP4.5 -- within the planning horizon of current national health infrastructure investments -- has direct public health preparedness implications. Vector control capacity for *Aedes* mosquitoes requires entomological expertise, surveillance networks, insecticide procurement channels, and public communication infrastructure that cannot be assembled in response to an outbreak. Estonia's current vector control capacity is oriented toward *Culex* mosquitoes for WNV prevention and *Ixodes* ticks for Lyme disease; neither provides the *Aedes*-specific capabilities -- ovitrap surveillance, targeted larval source reduction in urban environments -- needed for dengue prevention. The 10-15 year projection window provided by the C5 framework gives a policy-actionable preparedness timeline that degree-day models, with their wider and poorly calibrated uncertainty intervals, could not deliver.

5.3 Limitations

Three limitations apply. First, the ML ensemble was trained on historical European and Central Asian disease-climate data; its extrapolation to climate states outside the historical range -- precisely the states relevant for 2035-2040 projections -- relies on the assumption that climate-disease relationships remain structurally similar at temperatures not yet observed in the training period. Second, disease surveillance data quality varied substantially across the 28 countries, with case reporting completeness estimated at 40-60% for dengue and 60-80% for Lyme disease in several Eastern European countries; models calibrated on incomplete surveillance underestimate true disease burden, affecting hindcast accuracy assessment. Third, the SEIR systems model (C4) required country-specific human mobility and healthcare capacity parameters that were not available for all 28 countries, requiring imputation that may have underestimated C4 performance in data-sparse settings.

6. Conclusion

6.1 Key Findings

Among five epidemiological modelling frameworks evaluated across 28 countries and five climate-sensitive disease endpoints, the ML ensemble (CEMFS 0.922) achieved a 38.4% dengue vectorial capacity RMSE improvement over degree-day models, 87.4% uncertainty interval calibration, and the most policy-actionable spatial projections. All five frameworks projected northward expansion of dengue and WNV transmission risk into Baltic and northern Central European regions by 2035-2040 under RCP4.5, with RCP8.5 advancing these timelines by 4-7 years. Estonia, Latvia, and Lithuania are projected to develop seasonal *Aedes albopictus* establishment risk within the 2033-2038 window under RCP4.5, providing a 10-15 year preparedness horizon for vector control capacity development.

6.2 Recommendations

Three recommendations follow. First, European public health agencies should adopt ML ensemble climate-epidemiology models as the standard for disease range expansion projection, replacing degree-day models that systematically understate projection uncertainty and lack spatial resolution for sub-national preparedness planning. Second, the Baltic states and northern Central European countries should initiate *Aedes albopictus* surveillance and vector control capacity development within the current policy cycle, using the 2033-2038 establishment risk window as the planning horizon -- waiting for establishment to occur before building capacity is a reactive strategy that the projection data do not support. Third, ECDC should invest in harmonising infectious disease surveillance reporting across member states, as the current variation in case ascertainment fractions introduces systematic bias into cross-national model calibration that degrades projection accuracy in precisely the countries most likely to face new disease risks. All model code, CMIP6 forcing data, and the CEMFS calculator are available from the corresponding author.

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Declarations

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Conflict of Interest

Both authors declare no competing interests and no financial relationships with climate modelling commercial entities or vector control industry stakeholders.

Data Availability Statement

ERA5 and CMIP6 climate data are publicly available from ECMWF and PCMDI respectively. Aggregated country-disease projection outputs and the CEMFS calculation tool are available from the corresponding author. ECDC surveillance data are publicly accessible at ecdc.europa.eu.

Ethical Approval

This study used publicly available aggregated disease surveillance and climate data and did not involve individual patient data. Ethical review by the Baltic AI Research University Research Ethics Board (BARU-REB-2023-218) confirmed exemption from individual consent requirements.

Appendix A

CEMFS Scoring Rubric and ML Ensemble Architecture

Full CEMFS dimension scoring criteria and technical specifications of the ML ensemble modelling framework (C5).