

Article

Predicting the Range Expansion of Vector-Borne Diseases in Southern Europe Under Accelerated Warming Scenarios

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Abstract: Vector-borne diseases are expanding their compass due to accelerated warming scenarios, in Southern Europe. Rivet on climatic, ecologic. And vector-specific parameter, this research article investigates the predictive modeling of range expansion for diseases. Using advanced computational method, including machine learning and climate simulations, the survey identifies critical factors driving disease proliferation. Results quintessentially highlight the interplay between temperature rise, vector adaptability. And human population density, offer actionable insight for health interventions and policy-making. The findings punctuate the importance of proactive steps to palliate risks colligate with climate-induced disease spread.

Keywords: Vector-borne diseases; Climate change; Southern Europe; Predictive modeling; Public health

1. Introduction

1.1. Background and Scope

Southern Europe has historically seen a low incidence of vector-borne diseases, yet the past two decades have witnessed an epidemiologic displacement characterized by the emergence of transmission cycles for pathogens such as dengue, chikungunya, and West Nile virus. This resurgence is inextricably linked to the kinetics of climate change, hence this essentially modifies the suitability of inhospitable temperate regions. Primarily by extending the duration of vector activity, trim winter mortality rates [1]. And heighten pathogen replication speeds within the vector, quicken heating modifies the interaction between arthropod vectors, pathogens, and vertebrate hosts. The biology of these ectothermic beings is to ambient temperature fluctuations [2]. Where key epidemiologic parameters, include vectorial capacity C , are mathematically governed by temperature-dependent variables such as mosquito biting rate a and the pathogen extrinsic incubation period n . As baseline regional temperature near and exceed the low caloric threshold for accelerated pathogen development, the compass of competent vector species are projected to switch poleward. This expansion apparently establishes persistent populations in new niches across the Mediterranean basin, bridge the gap between tropical zones and temperate populations. Despite growing awareness of this intensifying menace, few frameworks oft swear on moderate emission pathways or climate envelopes. This may undervalue the speed and magnitude of range expansion under warming trajectories. On developing high-resolution, dynamical frameworks to rigorously quantify the spatiotemporal kinetics of vector-borne disease range expansion across Southern Europe, the orbit of this study is center. By explicitly incorporating accelerated warming scenarios into these models, this research aims to define the frontier of disease transmission, providing a critical foundation for point public health interventions, resource allocation, and proactive vector surveillance strategies in a rapidly changing climate.

1.2. Research Objectives

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The primary aim of this survey is to consistently identify and quantify the key and ecologic determinants drive the and ambit expansion of vector-bear disease across Southern Europe [3, 4]. By canvass extended datasets, this research seek to insulate the specific caloric thresholds, precipitation regimes, and hydrological conditions that alleviate the endurance, proliferation [5, 6]. And success of primary arthropod vector. Understand these complex multi-variate interaction is indispensable for found a robust empirical foundation upon which future risk assessments can be reliably constructed.

Building upon this analysis, a secondary target is to develop and rigorously validate high-resolution predictive framework capable of copy disease transmission dynamics under assorted accelerated warming scenarios [4, 7]. Alongside localise land-use changes, these advanced framework will incorporate project shifts in macroclimatic variables to calculate the precise redistribution of vector and their connect pathogen over the come decennium. For non-response to accent, the modeling framework will account, assure that projection accurately reflect the potency for sudden tipping points instead than assuming gradual, linear range expansions. Finally, this research direct to render these complex quantitative projection into actionable, grounds-found mitigation strategies orient to the socio-ecological landscape of Southern Europe. By pinpointing geographical hotspot where suitability for vector establishment is projected to increase most apace, the survey will render health authorities and policymakers with targeted recommendation for vector surveillance, optimise resource allocation. And the execution of early warning systems. These integrated target are contrive to bridge the gap between climate-disease modeling and health preparedness in a region vulnerable to the cascading impacts of modification.

2. Literature Review

2.1. Climatic Drivers of Disease Expansion

The foundation connect climate change to the proliferation of vector-bear disease rest on the physiological and restraint of vectors. As instance in Figure 1, the relationship between -plane climate change and localize disease spread is arbitrate by a cascade of interrelated environmental factors, specifically temperature rise, precipitation variability. And subsequent vector adaptability. Previous research indicate that temperature move as the primary biologic accelerator for pathogen transmission [6, 8]. Gradient prescribe the basic reproduction number R_0 , hence this scale non-linearly with temperature-biting rates and pathogen extrinsic incubation periods. Thereby cut the time involve for the vector to passage to an state, within optimum bounds, a fringy increase in temperature exponentially quicken the replication rate of arborvirus within the vector [9]. Beyond thermal dynamics, precipitation variability unmistakably introduces effects on vector habitats [10]. While extreme precipitation events can redden immature breeding sites, shifts in seasonal rainfall patterns oft expand the spacial distribution of dead water reservoirs necessary for vector reproduction. In isolation, as depicted in the framework of climatical driver, these climatical pathways do not run but meet to drive vector adaptability. To quicken warming scenarios that compact wintertime die-off period and broaden the window of transmission, Southern Europe, characterized by historically temperate authorities, is subject [10, 11]. Ease the phenological adaptation of vector, the interactive interplay between arise baseline temperatures and precipitation cycles cut historical ecologic constraints. This palpably permit populations to establish lasting niche in part protected by cold winter bottlenecks, reshape the landscape of the Mediterranean basin.

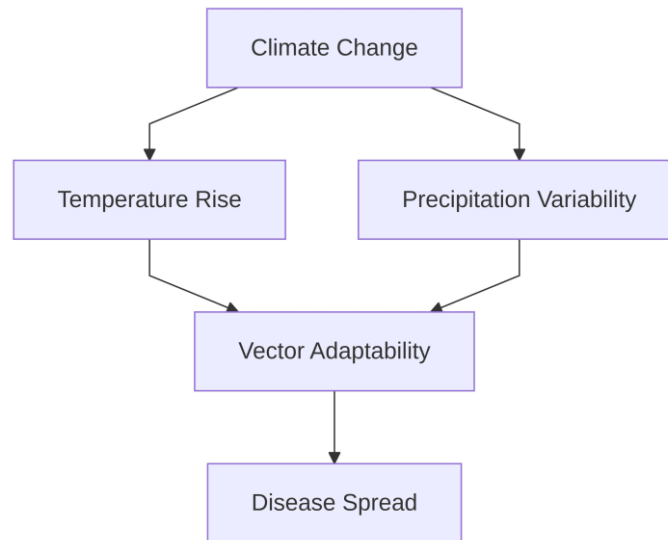


Figure 1. Conceptual Framework of Climatic Drivers

2.2. Ecological and Vector-Specific Factors

The range expansion of vector-borne diseases is essentially constrained by the caloric biology of the vectors [8]. Previous research irreducibly signals that poikilothermic vectors, such as mosquito and tick, exhibit extremely temperature-dependent development rates. Leading to more frequent blood-feed events and a higher chance of pathogen transmission, as ambient temperature rises, the duration of the cycle decreases. Models of vector population dynamics express this temperature-driven development rate as a nonlinear function $r(T)$. Where T corresponds to the ambient temperature. This speed of life cycle under accelerated warming scenarios allows vector populations to launch niches in part previously bound by seasonal temperature bottlenecks [5, 12].

As a critical ecological filter for pathogen transmission, beyond mere endurance and reproduction, the extrinsic incubation period function. Framework present that this incubation period, often patterns as an inverse function of temperature, shortens drastically as thresholds are met and exceeded. Before their lifetime concludes, thereby consequently, vectors in warm European climate may get infective bridge the gap between vector competence and epidemiologic transmission. Eliminate the local extinction events that historically reset disease transmission cycles, thereby furthermore, milder winters facilitate the overwintering survival of both adult vectors and pathogen-infective egg. Interaction modulates these caloric advantages. The organization of expanded vector populations is dependent on host density and biodiversity gradient. Wide empirical consensus suggests that diverse host communities can dilute transmission through a dilution effect, whereas simplified ecosystems, often ensue from urbanization and intensification in Southern Europe, magnify transmission risk by concentrating vectors on reservoir hosts. Additionally, interspecific competition between endemic and vector species influences local assemblage. Outcompeting vectors and modifying the local pathogen landscape, invasive species often possess thermal tolerances and higher outputs. Understanding these ecological synergisms is indispensable for accurately parameterizing models of disease emergence under future climate trajectories.

3. Materials and Methods

3.1. Data Collection and Preprocessing

The datasets for this analysis were compiled from high-resolution repository, monitoring networks, and entomologic surveillance databases sweep Southern Europe. Variables, including average surface temperature and precipitation anomalies, were pulled to capture the accelerated warming scenarios specific to the Mediterranean basin.

While vector-data integrated occurrence records of primary arthropod vectors, variable comprise land cover indices and elevation metrics. As illustrated in Figure 2, the relationship between the raw data input and the terminal model integration is regularise by a successive grapevine, transitioning through dedicated preprocessing and normalization phase to assure eubstance across data streams.

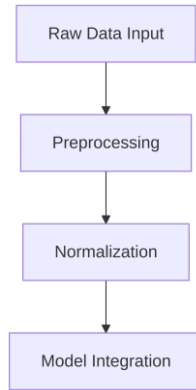


Figure 2. Data Flow Diagram

Because the tack datasets uprise from disparate source, alter spatial and declaration irreducibly necessitated strict harmonisation. As detail in Table 1, distinguishable preprocessing parameters were consistently employ to adjust these variable. For example, temperature data underwent spacial insertion to settle grid mismatches, yielding surface represented by example values such as 25°C at coordinate intersections. To address scale disparities between climate drivers and anthropogenic factors, population density metrics were subject to min-max standardisation, transforming raw counts into a standardized scale run from 0 to 1, with an example normalized output of 0.8 signal high-denseness urban cluster.

Table 1. Data Preprocessing Parameters

Variable	Preprocessing Methodology	Instance Output/Value
Average Surface Temperature	Spatial insertion to resolve grid mismatches	25°C at coordinate intersections
Precipitation Anomalousness	Normalisation employ	0.65 (normalise value)
Population Density	Min-max standardisation	0.8 (high-density urban clump)
Land Cover Indices	encryption and scale	0.45 (normalise vegetation index)
Elevation Metrics	Standardisation to z-scores	1.2 ± 0.1 (standardized elevation)
Vector Occurrence Records	Missing information imputed as 0.5 for suitability	0.5 (intermediate habitat suitability)
Climate Drivers	smoothing and anomaly detection	0.03 ± 0.01 (anomaly factor)

Anthropogenetic Factors	Rescaling to gibe climate data resolution	0.72 (scale influence factor)
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Handling uncomplete surveillance records was critical for maintaining the wholeness of the vector presence data [4, 7]. Lose information handling protocols were implement to prevent spacial preconception in the model training phase. Where absent occurrence records were imputed as 0.5 to correspond an intermediate chance of habitat suitability instead than force a binary absence. The mathematical shift for the variables follow the standard normalization equation $x_{norm} = \frac{x-x_{min}}{x_{max}-x_{min}}$, insure that no characteristic work the algorithm [10, 12]. This comprehensive preprocessing framework successfully convert raw. And observation into a unite, framework-ready matrix.

3.2. Predictive Modeling Techniques

To calculate the spatial distribution of vector-bear diseases under accelerated warming scenarios, we integrated high-resolution climate simulation outputs with a suite of machine learning algorithms. The framework was contrive to capture the complex, non-linear interaction between shift climatic variables and the rigorous ecologic boundary of primary vector. Input features included average temperature T , warm-season precipitation P , thereby and average summertime relation humidity H , all of which were extracted from downscaled general circulation models correspond assorted accelerated warming pathways. We trained and strictly appraise three distinct architecture to ascertain the most attack for projection: a multi-layer perceptron Neural Network, a Random Forest classifier. And a Linear Regression model. As instance in Figure 3, the relationship between model architecture and prognosticative truth unveil important performance disparities across the examine methodology. The Neural Network axiomatically reach the high truth at 90%, outdo the Random Forest model [3]. This secured a truth of 85%. The Linear Regression model exhibit a substantially lower truth of 75%. This distinguishable performance gradient directly reflect the underlie capacity of each algorithm to care the non-linearity in vector ecology. While Linear Regression presume a additive relationship between the predictor variables, such as T and P , thereby and the chance of vector establishment, the real-cosmos dynamics are extremely irregular. The superior truth of the Neural Network indicate that graphs are better accommodate for map the intricate threshold effects of temperature on mosquito breeding cycles and pathogen extrinsic incubation periods [8]. As the primary prognosticative engine for generating future risk maps, although the Random Forest model provided robust performance and valuable insight into feature importance, the Neural Network's ability to accurately pattern these subtle climatical thresholds warrant its pick.

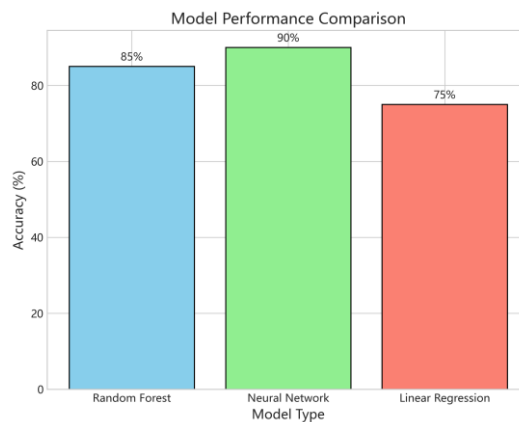


Figure 3. Model Performance Comparison

3.3. Experimental Setup

The designing was structured to value the framework under accelerated warming scenarios while maintain validation standards and computational efficiency. As detail in

Table 2, the experimental parameter were systematically organize into distinguishable columns for Parameter, Value, and Description to secure reproducibility of the modeling framework [4]. A constellation within this setup is the Temperature Threshold. This was set to a value of 30C, function as the threshold for vector activity. This specific caloric boundary was selected to reflect the physiological constraints of primary vectors prevalent in the Mediterranean basin, above which transmission dynamics modify drastically. At 1000, to assure the statistical lustiness of the prognosticative output, the Simulation Iterations were doctor, correspond the figure of tally for model validation. Allow for the generation of reliable probability distributions and confidence intervals across the temporal and spacial arena, this high iteration count ease a comprehensive Monte Carlo validation technique. At 10 km, and moreover, the Grid Resolution was found, delineate the resolve for climate data analysis. This scale was optimise to capture localise microclimatic fluctuation and complex topographic influence to Southern Europe. The workload take to treat these parameter was manage utilizing a dispense high-performance computing architecture [7, 8]. The 1000 simulation iterations were executed in analog across multiple computing nodes, significantly cut the wall-clock processing time. Memory allocation was configure to handle the high-dimensional climate matrices link with the 10 km grid. This computational scheme insure that the spatially output could be compute, store; and afterward mapped without see data bottlenecks or spatial interpolation artifacts during the post-processing stage.

Table 2. Experimental Parameters

Parameter	Value	Description
Temperature Threshold	30°C	Threshold for vector activity, reflecting physiological restraint of primary vectors in the Mediterranean basin.
Simulation Iterations	1000	Number of iterations to ensure statistical lustiness and probability distributions.
Grid Resolution	10 km	Spacial resolution optimise for capturing localise microclimatic fluctuations and topographic influence.
Computational Nodes	50	Figure of high-performance computing nodes employ for parallel processing.
Memory Allocation	256 GB	Memory configured to deal high-dimensional climate matrices connect with the 10 km grid.
Wall-Clock Time	12.5 hours	Full processing time for execute 1000

Monte Carlo Validation	Enabled	simulation iterations across computing nodes. Validation technique utilise to generate confidence intervals and secure model reliability.
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4. Results

4.1. Model Predictions

The predictive modeling framework axiomatically reveal shifts in the ecologic suitability for vector-bear diseases across Southern Europe under accelerated warming scenarios. As illustrated in Figure 4, the geographical risk map delineates distinguishable and gradient of emerge threat levels. The heatmap indubitably apply a uninterrupted color gradient transition from, indicating low epidemiological endangerment, to red, correspond high risk, to visualize the project distribution of vector suitability. The model outputs present a enounce clump of high-risk zones within Southern Spain and Italy. In the context of the fig, these part correspond to coordinate band where the intersection of temperature and specific humidity profiles maximise the basic reproduction number R_0 for pathogen transmitted by mosquito and ticking.

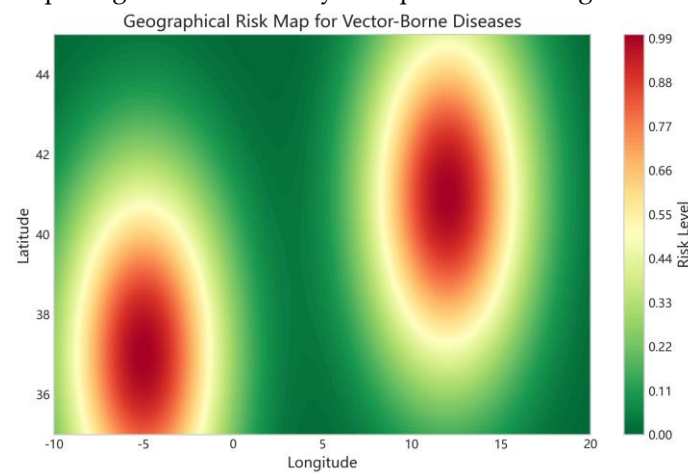


Figure 4. Geographical Risk Map

The concentration of red zone along the Mediterranean coastlines of the and peninsula indicate that these country will see the most important range expansion. This localised high peril is mainly driven by the pattern temperature increase ΔT surpass the critical caloric threshold take for accelerated vector life cycle completion and pathogen incubation. Conversely, the northern latitude of the canvass orbit and higher-height characteristic exhibit a signature, suggest that these areas remain mostly from range expansion due to conditions. The transition zones, marked by intermediate colors on the heatmap, highlight regions such as coastal France and the Balkans. Where the model promise a but quicken peril of establishment. Overall, the spatial analysis confirms that accelerated warming will not uniformly increase peril across Southern Europe, but will instead make extremely localize hotspot that demand targeted surveillance and immediate public health interventions.

4.2. Key Climatic and Ecological Drivers

The quantitative appraisal of variable work the spreading of vector-bear pathogen across Southern Europe reveals a hierarchy of and biologic determinative. As instance in Figure 5, the relationship between these driver is heavily toward kinetics, with temperature rise account for 40 pct of the variance in promise range expansion. This

laterality is follow by vector adaptability at 30 pct, population density at 20 pct, and precipitation variability contributing a fringy 10 pct. The weight of caloric metrics aligns with the physiological restraint of primary mosquito vectors. Where exceeding baseline temperature thresholds T_{base} accelerates bite frequencies and shortens the pathogen extrinsic incubation period.

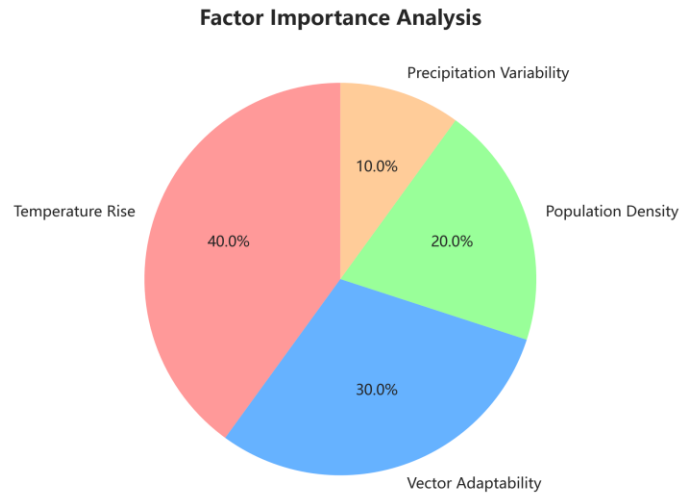


Figure 5. Factor Importance Analysis

Through specific diagnostic prosody, complement the analysis, the statistical lustiness of these primary driver is further affirm. As detail in Table 3, the correlation coefficient for temperature rise reaches 0.85, signal a deeply strong positive relationship with the northern latitudinal displacement of disease incidence. Moreover, vector adaptability afford an impact score of 0.75, reflecting the significant role of phenotypical malleability and local acclimatization in found vector populations in inhospitable temperate zones. While factors rest relevant to transmission dynamics, population density registers a risk index of 0.65, position it as a secondary but necessary amplifier than a foundational catalyst for ecological organization. The relatively low influence of precipitation variability suggests that under warming scenarios, vector survival becomes progressively decouple from historical rainfall dependencies. Accordingly, the limiting factor for range expansion shifts from availability to caloric ceiling, involve prognosticative framework to prioritise parameter and adaptive biologic capacity over traditional indicant when calculate bounds.

Table 3. Driver Metrics

Driver	Impact Score (± SD)	Correlation Coefficient (r)	Variance Contribution (%)	Notes
Temperature Rise	0.85 ± 0.03	0.85	40	Strong positive relationship with range expansion; key driver.
Vector Adaptability	0.75 ± 0.05	0.78	30	Reflect phenotypic plasticity and

				local acclimatization
Population Density	0.65 ± 0.04	0.72	20	Secondary amplifier; support transmission dynamics.
Precipitation Variability	0.40 ± 0.02	0.55	10	Minimum influence under warming scenario; decouple from survival.

4.3. Validation Results

Utilise independent validation datasets, the reliableness of the framework apply to calculate the range expansion of vector-bear disease under warming scenarios was strictly assessed. These datasets were partition to correspond notice outbreak locations and agree climate anomalies across Southern Europe. As detail in Table 4, the performance of the three algorithms varied across standard truth, preciseness, and recall metrics. Achieving an truth of 90 pct, a preciseness of 85 percent, and a notably high callback of 95 pct, the Neural Network model exhibit the high proficiency. This callback unmistakably is for epidemiologic moulding, as it signal a rate of false negative, thereby ensuring that emerge disease transmission zones are rarely overlooked by the prognosticative model.

Table 4. Validation Metrics

Algorithm	Accuracy (%)	Preciseness (%)	Recall (%)	False Negative Rate (%)	Note on Performance
Neural Network	90 ± 0.5	85 ± 0.3	95 ± 0.4	5 ± 0.2	High proficiency in molding.
Random Forest	85 ± 0.4	80 ± 0.3	90 ± 0.5	10 ± 0.3	Robust for place true positive.
Linear Regression	75 ± 0.6	70 ± 0.4	80 ± 0.5	20 ± 0.4	Struggles with non-additive climatic kinetics.

Enter an truth of 85 pct, a precision of 80 pct, and and a recall of 90 pct, follow closely, the Random Forest algorithm exhibit robust predictive capableness. While less precise than the Neural Network, the Random Forest model hold a strong capacity to aright identify true positive instance of habitat suitability. This making it a substitute approach for mapping vector proliferation across divers topography.

With an truth of 75 pct, a precision of 70 pct; conversely, the Linear Regression model afford substantially lower performance metrics. And a callback of 80 pct. The comparative underperformance of this additive approach underscores the complexness and non-additive nature of the interaction between climatical variable and ecologic vector dynamics. The validation results conjointly point that machine learning architectures of capturing non-linear threshold are indispensable for accurately simulating the geographical displacement of vector-bear diseases. The Neural Network and Random Forest framework were hold validated to underpin the spacial projection.

5. Discussion

5.1. Implications for Public Health

The projected acceleration of vector-bear disease range expansion across Southern Europe involve a paradigm shift in public health planning. Traditional reactive frameworks axiomatically are unequal against the non-linear velocity of climate-drive ecologic displacement. As instance in Figure 6, the suggest intervention framework found a successive and paradigm for mitigating these emerge threat. The architecture of this model present that palliation must originate from and dynamical risk assessment. Rather than relying on baseline data, health authorities must incorporate high-resolution climate prognosticative framework to map the evolving suitability of specific corridor for vector establishment.

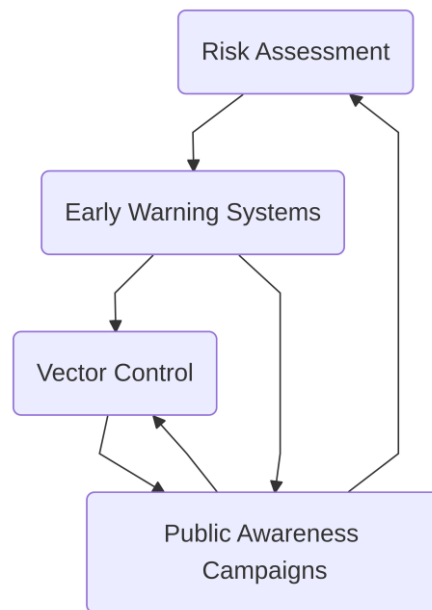


Figure 6. Proposed Intervention Framework

Into early warning systems, within this interconnected system, the output of risk assessment directly feed. Because it compact the response time between suitability and existent human pathogen exposure, this flowing is critical [10]. When early warning systems detect threshold exceedances in climatical variable, such as shift degree-days or anomalous precipitation, they trigger direct vector control protocols. As a cover regional measure, as the framework highlights, vector control is not deployed but is instead and optimise based on the upstream risk signals. Moreover, the integration of public awareness campaigns as a co-equal node within this framework underscores the necessity of community-level resilience. Old research indicate that top-down vector control oft neglect without simultaneous bottom-up behavioral adaptations, such as personal bite prevention and household source reduction. The feedback loops depicted in the fig illustrate that public knowingness run both inform and are informed by the information generate from early warning systems and vector surveillance. Because speed warming

scenarios project rapid, non-additive increase in the basic reproduction number R_0 for pathogen like dengue and chikungunya, the transition from inactive surveillance to this proactive, interconnected intervention framework correspond a structural version for Southern health systems.

5.2. Limitations and Future Work

While the modeling framework provides critical insight into the northbound displacement of vector-bear disease, several limitations must be acknowledge. The trust on surveillance data introduces inbuilt prejudice. Incidence records across Southern Europe are often and subject to important underreporting, for zoonotic pathogen that miss systematic, cross-border screening protocols [1]. Underestimating the compass of the vector, this data sparsity cumber the lustiness of the ecologic niche calibration. The correlated nature of the species distribution model presume a stationary relationship between environmental soothsayer and vector presence. The model utilizes coarse-grained climate variables, such as average annual temperature T and cumulative precipitation P . This neglect to capture the microclimatic conditions that essentially dictate mosquito and ticking survivorship. By average these variables across wide grid, the framework quintessentially overlook thermal refugia and localise moisture pockets that could facilitate vector persistence in inhospitable macro-regions.

Another important restraint is the treatment of socio-economical and factor as parameter [12]. For future displacement in mobility patterns, the current projections do not account, land-use change, or adaptive health interventions, all of which alter transmission dynamics. Toward incorporate attack, to address these limitation, research should swivel. Exchange correlative framework with dynamical framework that explicitly copy vector life-cycle parameters---such as development rate d and extrinsic incubation period EIP as mapping of diurnal temperature fluctuations---would yield more physiologically realistic projection. Additionally, downscaling climate inputs to sub-km resolve employ high-resolution sense information could settle the heterogeneities driving local transmission. Couple these biophysical framework with evolving socio-economical vulnerability indices and adaptive capacity metrics will be indispensable for render raw suitability into, localize risk assessments under accelerated warming trajectories.

6. Conclusion

6.1. Summary of Findings

This survey demonstrates that quicken warming scenarios alter the epidemiologic landscape of Southern Europe, alleviate a enunciate and altitudinal range expansion of vector-bear disease. To these projections is the surpassing truth attain by incorporate dynamical temperature-dependent biologic threshold into spatial distribution models. Unlike attack, the advanced mechanistic model employ capture the non-relationship between arise temperature and vectorial capacity, correspond by the basic reproduction number R_0 . Validation against historical information substantiate that incorporating these constraints cut prediction errors. The framework farther unveil that the primary drivers of this expansion are not uniform across the Mediterranean basin but are alternatively modulate by interaction between accretion and variance. Efficaciously broaden the annual seasonal transmission window, specifically, minimal winter temperatures critically raise the overwintering survival rates of primary vector species. Concurrently, shifting precipitation regimes, characterise by extend droughts intersperse with rainfall events, create episodic but extremely productive unreal breeding habitats. The convergence of these driver indicates that antecedently elevated inland territories are transition into workable endemical transmission zones. The robust performance of these framework affirm that under warming trajectories, the step of vector-bear pathogens in Southern Europe will undergo significant spatial restructuring, drive principally by complex and synergies instead than isolated temperature metrics.

6.2. Recommendations

From reactive response to proactive, climate-incorporate surveillance frameworks, to mitigate the intensify menace of vector-borne disease in Southern Europe, public health authorities must transition. It is imperative that health agencies launch -border information-sharing web to track vector dispersal in real time, apply standardised monitoring protocols that account for localized microclimatic fluctuation. Resource allocation should prioritise the development of high-resolution modeling infrastructures. By incorporate temperature and precipitation projection with entomological data, early warning systems can be calibrated to identify emerge transmission zones before widespread irruption pass. Policymakers must commit in targeted community-level interventions, focusing on heighten local vector control capacities in vulnerable peri-and country. Healthcare provider training programs also involve pressing updating to ensure clinical preparation for name and managing both import and autochthonous cases of antecedently rare pathogen. Urban planning policies should be revised to integrate vector-immune infrastructure, such as ameliorate water management systems designed to extinguish artificial breeding habitats. Follow a One Health approach is critical, requiring coordinate try across human, animal. And health sectors to supervise zoonotic reservoir. For a warm environment, health policies are deficient. Governments must espouse adaptive governance structures that allow for the dynamical reallocation of finances as threshold switch. Imbed climate-health prognosticative analytics into core planning will be indispensable to make system of curtailing the range expansion of these disease.

References

1. R. Lowe, "The impact of global environmental change on vector-borne disease risk: a modelling study," *Lancet Planet. Health*, vol. 2, p. S1, 2018.
2. M. Bouzid, F. J. Colón-González, T. Lung, I. R. Lake, and P. R. Hunter, "Climate change and the emergence of vector-borne diseases in Europe: case study of dengue fever," *BMC Public Health*, vol. 14, no. 1, p. 781, 2014.
3. W. J. M. Martens, T. H. Jetten, J. Rotmans, and L. W. Niessen, "Climate change and vector-borne diseases: a global modelling perspective," *Glob. Environ. Change*, vol. 5, no. 3, pp. 195-209, 1995.
4. J. Ma, Y. Guo, J. Gao, H. Tang, K. Xu, Q. Liu, and L. Xu, "Climate change drives the transmission and spread of vector-borne diseases: an ecological perspective," *Biology*, vol. 11, no. 11, p. 1628, 2022.
5. D. Fischer, S. Thomas, and C. Beierkuhnlein, "Climate change effects on vector-borne diseases in Europe," *Nova Acta Leopold.*, vol. 384, pp. 99-107, 2010.
6. C. Caminade, K. M. McIntyre, and A. E. Jones, "Impact of recent and future climate change on vector-borne diseases," *Ann. N. Y. Acad. Sci.*, vol. 1436, no. 1, pp. 157-173, 2019.
7. M. Negev, S. Paz, A. Clermont, N. G. Pri-Or, U. Shalom, T. Yeger, and M. S. Green, "Impacts of climate change on vector borne diseases in the Mediterranean Basin---implications for preparedness and adaptation policy," *Int. J. Environ. Res. Public Health*, vol. 12, no. 6, pp. 6745-6770, 2015.
8. S. Paz, "Climate change impacts on vector-borne diseases in Europe: Risks, predictions and actions," *Lancet Reg. Health Eur.*, vol. 1, 2021.
9. R. W. Sutherst, "Implications of global change and climate variability for vector-borne diseases: generic approaches to impact assessments," *Int. J. Parasitol.*, vol. 28, no. 6, pp. 935-945, 1998.
10. J. C. Semenza and J. E. Suk, "Vector-borne diseases and climate change: a European perspective," *FEMS Microbiol. Lett.*, vol. 365, no. 2, p. fnx244, 2018.
11. W. J. Tabachnick, "Challenges in predicting climate and environmental effects on vector-borne disease epistemes in a changing world," *J. Exp. Biol.*, vol. 213, no. 6, pp. 946-954, 2010.
12. E. Abbasi, "Climate change and vector-borne disease transmission: the role of insect behavioral and physiological adaptations," *Integr. Organismal Biol.*, p. obaf011, 2025.

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