One Health 22 (2026) 101331

Contents lists available at ScienceDirect

One Health

journal homepage: www.elsevier.com/locate/onehlt

# Predicting the spatio-temporal risk of human tick-borne encephalitis (TBE) in Europe by combining hazard and exposure drivers

Francesca Dagostin [a,*], Diana Erazo [b], Giovanni Marini [a], Daniele Da Re [a,c], Valentina Tagliapietra [a], Maria Avdicova [d], Tatjana Avšič-Županc [e], Timothée Dub [f], Nahuel Fiorito [g], Nataša Knap [e], Céline M. Gossner [h], Jana Kerlik [d], Henna Mäkelä [f], Mateusz Markowicz [i], Roya Olyazadeh [j], Lukas Richter [i], William Wint [j], Maria Grazia Zuccali [k], Milda Žygutienė [l], Simon Dellicour [b,m], Annapaola Rizzoli [a]

[a] Research and Innovation Centre, Fondazione Edmund Mach, San Michele all'Adige, TN, Italy
[b] Spatial Epidemiology Lab, Université Libre de Bruxelles, Bruxelles, Belgium
[c] Center for Agriculture Food Environment, University of Trento, Trento, Italy
[d] Regional Authority of Public Health in Banská Bystrica, Banská Bystrica, Slovakia
[e] Institute of Microbiology and Immunology, Faculty of Medicine, University of Ljubljana, Ljubljana, Slovenia
[f] Department of Health Security, Finnish Institute for Health and Welfare, Helsinki, Finland
[g] Unità Locale Socio Sanitaria Dolomiti, Belluno, Italy
[h] European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden
[i] Austrian Agency for Health and Food Safety, Vienna, Austria
[j] Environmental Research Group Oxford Ltd, c/o Dept Biology, Oxford, United Kingdom
[k] Azienda Provinciale Servizi Sanitari, Dipartimento di prevenzione, Trento, Italy
[l] National Public Health Center under the Ministry of Health, Vilnius, Lithuania
[m] Department of Hydrology and Hydraulic Engineering, Vrije Universiteit Brussel, Brussels, Belgium

ARTICLE INFO

*Keywords:*
Boosted regression trees
Ecological niche modelling
Europe
One health
Vector-borne disease
Tick-borne encephalitis

ABSTRACT

*Background:* Tick-borne encephalitis (TBE), caused by tick-borne encephalitis virus (TBEV), is a zoonotic disease that can lead to severe neurological symptoms. Given the increasing number of reported human TBE cases in Europe, we developed a spatio-temporal predictive model to infer the year-to-year probability of human TBE occurrence across Europe at the regional and municipal administrative levels.

*Methods:* We derived the distribution of human TBE cases at the regional level during 2017–2022 by using data provided by the European Centre for Disease Prevention and Control (ECDC), and at the municipal level by using data provided by Austria, Finland, Italy, Lithuania, and Slovakia. We modeled the probability of presence of human TBE cases at the regional and municipal levels for the period 2017–2025 with a boosted regression trees model, including covariates that affect both the natural hazard of virus circulation and human exposure to tick bites.

*Findings:* Areas with the highest probability of human TBE infections are located in central-eastern Europe, the Baltic states, and along the coastline of Nordic countries. Our results highlight a statistically significant rising trend in human TBE risk not only in north-western, but also in south-western European countries. Such areas are characterised by the presence of key tick host species, forested areas, intense human activity in forests, steep drops in late summer temperatures and high precipitation amounts during the driest months. The model showed good predictive performance, with a mean AUC of 0.84 (SD = 0.03), sensitivity of 0.83 (SD = 0.01), and specificity of 0.80 (SD = 0.01) at the regional level, and a mean AUC of 0.82 (SD = 0.03), sensitivity of 0.83 (SD = 0.01), and specificity of 0.69 (SD = 0.01) at the municipal level.

*Interpretation:* With ongoing climate and land use changes, the number of human TBE cases is likely to increase and spread into new areas. This highlights the importance of predictive models that can identify potential risk areas to support disease prevention and control efforts by public health authorities. The approach adopted, by

* **Corresponding author at:** Via E. Mach 1, 38010 San Michele all'Adige, TN, Italy.
*E-mail address:* francesca.dagostin@fmach.it (F. Dagostin).

https://doi.org/10.1016/j.onehlt.2026.101331
Received 9 September 2025; Received in revised form 9 January 2026; Accepted 11 January 2026
Available online 13 January 2026

fitting a One Health framework and leveraging lagged covaries, enables timely one-year-ahead predictions and enhances our current understanding of TBE risk under a global change scenario.

## 1. Introduction

Tick-borne encephalitis (TBE) is a severe viral infection of the central nervous system caused by the tick-borne encephalitis virus (TBEV) [1,2], which circulates in nature between hard ticks, mainly of the *Ixodes ricinus* complex, and various wildlife hosts [3]. The TBEV transmission system involves multiple interconnected components at the interface of animal, environmental, and human health. Various animal species can act as dead-end hosts or maintain and amplify the virus, with or without evident symptoms of the disease. Rodent species such as *Apodemus flavicollis*, *Apodemus sylvaticus* and *Clethrionomys glareolus* are considered among the main reservoir hosts for the maintenance and circulation of TBEV in Europe, while wild ungulates, considered not competent for virus transmission, play a major role in amplifying tick populations [4–6]. Ticks are both vectors and viral reservoirs, remaining infected throughout their life cycle [3]. TBEV circulation in the enzootic cycle also depends on specific environmental and climatic conditions associated to the presence of vectors and animal hosts and can therefore be influenced by climate change, ecosystem degradation and biodiversity loss [7]. Humans are considered "dead-end" hosts for the virus, primarily acquiring the infection through bites from infected ticks. However, TBEV transmission to humans can also occur through non-vectorial routes of infection, such as the consumption of unpasteurised milk and dairy products from infected ruminants [8], accounting for about 1% of all TBE cases reported annually in the EU/EEA. While mild cases may present flu-like symptoms, severe cases can lead to potentially life-threatening complications, and long-term neurological deficits in survivors [1,2]. The most widespread TBEV subtype circulating in the EU/EEA is the European subtype (TBEV-Eu), while the Siberian subtype (TBEV-Sib) occurs in some northeastern European countries [9].

Since 2012, TBE has been a notifiable disease in the EU/EEA, with mandatory reporting in nineteen countries, voluntary reporting in four (Belgium, France, Luxembourg, and the Netherlands) and 'not specified' in one country (Croatia). The increase in TBE cases across Europe (from 2412 in 2012 to 3514 in 2022), coupled with the emergence of new foci of infection in previously non-endemic countries [10–12], has risen the demand for predictive tools capable of identifying areas where human TBE infections are more likely to occur.

In this context, mapping potential risk areas with the greatest possible spatial accuracy can support targeted public health interventions and improve our current understanding of the complex factors that promote the occurrence of human TBE cases. Machine learning techniques, which can handle complex non-linear relationships, have become increasingly valuable in predicting the ecological niche of diseases like dengue [13] and West Nile fever [14,15]. However, for tick-borne diseases, studies have predominantly focused on predicting the distribution of tick vectors [16,17] or ecological suitability for TBEV in tick or animal host populations [18], rather than the probability of occurrence of human infections. In the case of human TBE modelling, recent publications focus only on limited areas or specific countries, such as Finland [19], Germany [20], or Sweden [21].

Therefore, the development of a predictive model to estimate human TBE risk at the finest possible administrative scale based on a key set of environmental, animal, climatic and anthropogenic factors fitting a One Health framework, represents a step forward towards comprehensive TBE risk estimation in Europe. In response, this study presents a novel spatio-temporal modelling framework that provides annual predictions of the probability of presence of human TBE infections. In our model, we adopted a One Health approach by considering a set of predictors related to anthropogenic factors, climate, habitat, and animal hosts reflecting both the natural hazard of TBEV circulation and human exposure to tick bites, which is a dimension generally lacking in previous studies. We first trained the model on human TBE presence/absence data reported at the regional administrative level and later applied it to predictors averaged at the municipal level, obtaining two different outputs, one covering European regions and one covering European municipalities.

Our specific objectives are thus to (i) generate annual predictions for the probability of occurrence of human TBE cases at regional and municipal administrative levels which will be updated annually before the tick questing season, based on a key set of hazard and exposure drivers (ii) translate these results into maps that display the spatial probability of human TBE cases occurrence, and (iii) assess spatio-temporal trends in predicted TBE risk. This is, to our knowledge, the first predictive One Health framework to enable the European-wide estimation of human TBE risk areas one year in advance, leveraging lagged covariates related to both the hazard and exposure dimensions. These predictions could help public health authorities with surveillance and prevention planning, improving our understanding of human TBE risk across Europe.

## 2. Methods

### 2.1. Collection of epidemiological data

Data of reported human TBE cases were kindly provided by the European Centre for Disease Prevention and Control (ECDC). The dataset included, where available, the most likely place of infection at "nomenclature of territorial units for statistics" (NUTS) level 3 (small regions for specific diagnosis [22]). In our study, we used human TBE confirmed and probable cases reported to ECDC between 2017 and 2022. The choice to base our model on notified human TBE cases reflects the availability of systematically collected centralized data for several European countries across multiple years. To improve spatial accuracy, we excluded patients infected abroad or with unknown place of exposure, and to reduce potential bias in pseudo-absence sampling, we only included countries that provided the location of infection at NUTS-3 level for at least 75% of notified cases. In these countries, the absence of reported cases is more likely to reflect the actual absence of human TBE cases rather than limitations due to underdiagnosis or under-reporting. Based on these criteria, 13 countries with good reporting quality were included: Czechia, Denmark, Germany, Greece, Finland, France, Hungary, Italy, Lithuania, Poland, Romania, Slovakia, and Sweden. Additional datasets were obtained from Austria (AGES) and Slovenia (University of Ljubljana). We also included Ireland and Spain, where compulsory notification exists but no autochthonous cases were reported during the study period, to represent areas without recorded human TBE cases.

Within these countries, "presence" locations were defined as NUTS-3 units with at least one confirmed case per year, while "pseudo-absence" locations were defined as units with no reported cases. This assumption is supported by the fact that severe human TBE cases are generally reported consistently across European countries (personal observation from Dr. Céline Gossner, Head of Section Food-, Water-, Vector-borne and Zoonotic Diseases at ECDC, and co-author of this paper). Spatial units from countries with insufficient reporting were labelled as "unknown" and excluded from model training. To further improve our dataset, we obtained through ECDC's Emerging and Vector-borne Diseases Network the distribution of human TBE cases in Austrian districts between 2017 and 2022 (provided by AGES), and data collected between 2017 and 2022 in the municipalities of Finland (provided by the Finnish Institute of Health and Welfare, THL), Slovakia (provided by the Public Health Authority of the Slovak Republic), Lithuania (provided by

the National Public Health Centre under the Ministry of Health) and northern Italy (provided by the local public health agencies, APSS and ULSS1 Belluno). Based on these sources, we compiled two dichotomous datasets of presence and pseudo-absence locations of human TBE cases between 2017 and 2022, at regional (NUTS-3) and municipal levels, following the approach adopted in [7,14].

It is important to note that "pseudo-absence" here pertains solely to the lack of reported human TBE cases, not to the absence of TBEV circulation within ticks and hosts. Thus, regions categorized as "pseudo-absence" may indeed harbor TBEV within their tick and wildlife populations; however, no human cases have yet been detected, possibly due to lower human exposure to tick bites in these areas.

### 2.2. Hazard and exposure covariates

We used a set of covariates that reflect both hazard and exposure dimensions, as risk assessment relies on the interaction between these two components (Fig. 1). Specifically, hazard refers to any potential source of harm, and risk is the probability of harm occurring based on physical exposure to the hazard. Concerning tick-borne diseases, hazard can be defined as the presence or density of infected vectors in the environment, which depends on the interplay of complex ecological and environmental conditions that allow TBEV circulation among ticks and competent hosts [23]. Exposure, on the other hand, relates to human interactions with the environment that increase the likelihood of encountering infected ticks and depends on factors such as human outdoor activities and socio-economic variables [21].

We selected key hazard factors as suggested in [24]. These predictors included: (i) the proportion of administrative areas covered by forests (derived from the 2018 Corine Land Cover (CLC) data inventory with a resolution of 0.25 × 0.25 km [25]); (ii) the total precipitation of the driest quarter one year prior (calculated applying the formula stated in the World Climate (WorldClim) Database to the ECMWF ERA5-Land dataset at 30 arc *sec* resolution [26]); (iii) the autumnal cooling rate one year prior (computed by applying a linear regression to the average daily temperature against the Julian day in the period 1st August – 31st October, as described in [27], based on MODIS LST data with a resolution of 5.6 km [28]); (iv) the 1-km habitat suitability of critical TBEV reservoir and tick-amplification hosts (*A. flavicollis, M. glareolus, D. dama, C. elaphus, C. capreolus, A. alces, O. virginianus, L. europaeus, L. timidus*, *V. vulpes*) that was previously derived as described in [29]. To account for human exposure to tick bites, we also included: (v) the density of forest roads (computed based on OpenStreetMap data [30]) as proxy of accessibility to forested areas, assuming that roads increase access and that forests with roads are more likely to be entered by visitors [21] and (vi) human population density (derived from the WorldPop dataset [31]).

All explanatory variables were computed by averaging them for each administrative area included in the dataset, at the regional and municipal administrative levels. Time-dependent predictors, the autumnal cooling rate and the precipitation of the driest quarter, were computed for each year of analysis with a 1-year lag (see Supplementary material, Figs. S1-S6, for the mapped values of predictors).

To assess potential multicollinearity among predictors, we conducted a preliminary correlation analysis. This analysis confirmed that the variables used in the model were not strongly correlated ($r < |0.5|$) (see Supplementary material, Fig. S7).

### 2.3. Boosted regression trees modelling framework

We modeled the probability of presence of human TBE cases using a boosted regression tree (BRT) machine-learning technique. BRT offer several advantages, including the capacity to handle complex interactions and correlations between predictors without overfitting, and to accommodate missing data [32]. We implemented the BRT algorithm with the "gbm" R package [33] using spatial cross-validation to limit model overfitting. Specifically, we applied a leave-location-out (LLO) resampling method within the 'mlr3' R framework [34] in which a test set is selected and all observations that correspond to the same location across multiple time points are omitted from the training sample. To consider spatial autocorrelation, spatial fold selection was defined based on the block generation method described by Valavi and colleagues and implemented in the R package "blockCV" [35]. As BRT builds the trees on random subsamples of the training dataset, we ran 50 independent

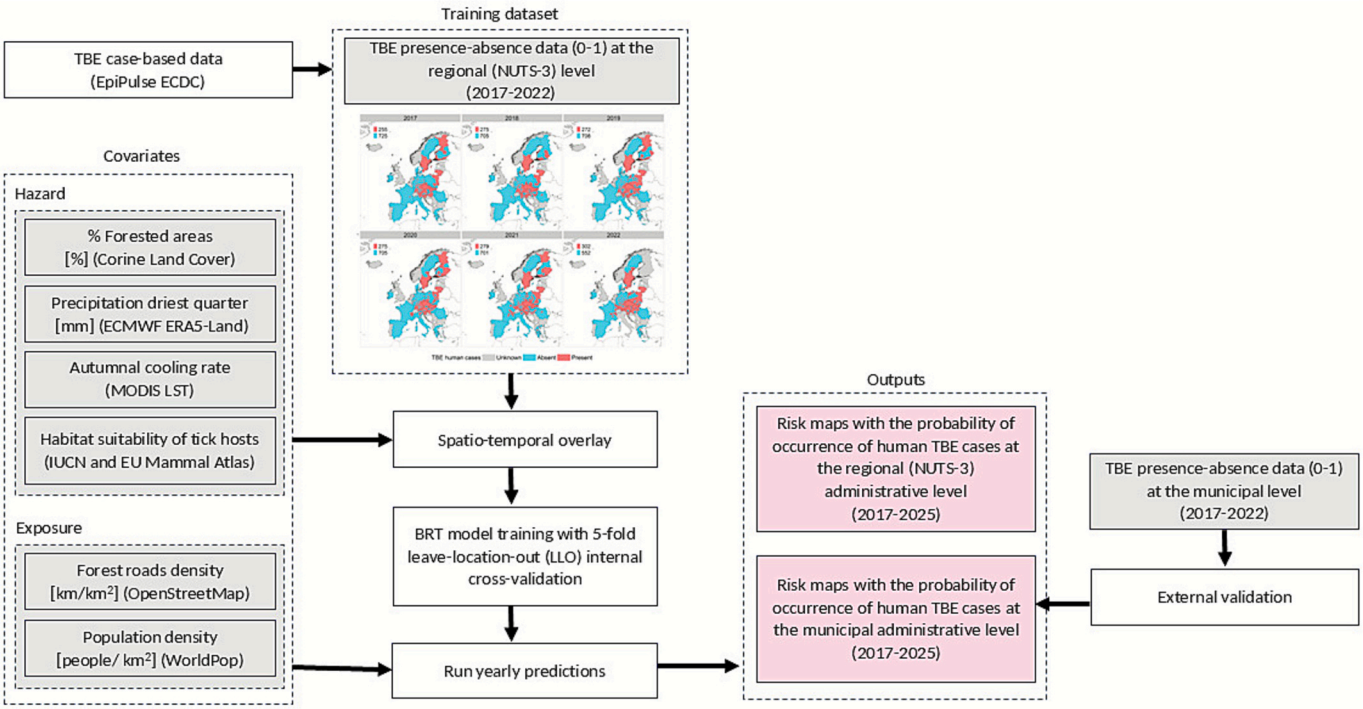


**Fig. 1.** Schematic representation of the modelling framework.

model replicates and averaged the results.

We trained the BRT model on human TBE presence-absence data reported between 2017 and 2022 at the NUTS-3 spatial level ("regional model"). The trained model was then applied to all NUTS-3 spatial units across Europe, including regions without available TBE observations. In these areas, the predicted probability of human TBE presence is inferred from the relationships between TBE occurrence and the covariates learned during model training, by applying the fitted model to the covariate values specific to each spatial unit [32]. Since the modelling framework relied on the standardized spatial units of the NUTS geocoding standard, we could not generate predictions for countries outside its coverage. We assessed the model predictive performance by estimating the area under the receiver operating characteristic curve (AUC), the sensitivity and specificity, and the prevalence-pseudoabsence-calibrated Sørensen's index ($SI_{ppc}$) [36], as the use of the AUC metric alone has been criticised in previous works because of its dependence on sample prevalence (i.e., the ratio between the number of presences and number of absences) [37]. As the computation of $SI_{ppc}$ needs binary presence-absence data, whereas our model instead returns predicted probability values, we performed an optimisation procedure by applying a threshold to the model's predictions to transform them into a presence-absence dataset. The threshold values were varied in the range [0,1] with a 0.01 step increment, and the threshold that maximised the $SI_{ppc}$ was eventually selected to compute the index (see [38] for the application of a similar approach). Performance metrics were calculated across the 50 replicates.

Finally, we applied the model, as described in the above paragraph, to predictors averaged at the municipal administrative level to obtain a higher resolution output [39], an approach that aligns with common downscaling practices, whereby models are trained at broader scales and then used to obtain predictions for finer spatial units [39,40]. To evaluate the model's generalizability and ensure reliable performance on independent data not used during model training, the accuracy of municipal predictions was externally assessed based on an independent presence/pseudo-absence dataset compiled at the municipal level for the period 2017–2022 (see Supplementary material, Fig. S8). We also computed the standard deviation (SD) of the predicted probability of human TBE presence across 50 model replicates at regional (Fig. S9) and municipal (Fig. S10) level, to show the absolute variability in predictions at each location.

The modelling framework enables the prediction of human TBE occurrence on an annual basis, using temporal covariates recorded one year prior, allowing results be updated yearly before the start of the tick questing season. For example, the prediction for 2026 could be made by February 2025, based on the covariates recorded in 2025. A schematic representation of the modelling framework is shown in Fig. 1.

Finally, linear regressions were performed to identify areas with either an increasing or decreasing statistically significant trend in the predicted probability of human TBE presence over the specified years and across the two administrative scales. Specifically, for each area, we fitted a generalised linear model (GLMs) to model predictions across the years (2017–2025), with the year as the predictor variable (formula: prediction ~ year). All analyses were performed using R Statistical Software v.4.1.2 [41].

## 3. Results

Over the period spanning 2017 to 2022, 15 European countries reported at least one confirmed, autochthonous human case with a known place of infection at the regional level. Overall, this dataset comprised a total of 1658 "presences" in NUTS-3 regions over the period of analysis, spanning 15 European countries (Austria, Czech Republic, Denmark, Germany, Greece, Finland, France, Hungary, Italy, Lithuania, Poland, Romania, Slovakia, Slovenia, and Sweden). The number of NUTS-3 positive regions (i.e., that notified at least one human TBE case), increased from 255 regions in 2017 to 302 regions in 2022. Within the same timeframe, no human TBE cases were reported from 4096 other regions within the 15 countries mentioned above, plus Spain and Ireland (Fig. 2).

### 3.1. Fitted functions and relative importance of variables

BRT fitted functions can be visualised using partial dependence plots (Fig. 3), showing the effect of a predictor on the response after accounting for the average effects of all other variables. The contribution of each environmental factor is given by its relative influence (RI) in the BRT model and is computed as the number of times the variable is selected for splitting a tree, weighted by the squared improvement to the model resulting from each split averaged over all trees [32]. Variables which showed a positive trend are the habitat suitability of vertebrate hosts (RI = 39.28); the density of roads and pathways in forested areas (RI = 22.46); the total precipitation of the driest quarter (RI = 19.76); the proportion of forested areas (RI = 13.11); and population density (RI = 2.16). The autumnal cooling rate (RI = 3.22, which is negative by definition and measures the rate of decrease in late summer temperatures, showed a negative trend, meaning that human TBE risk is higher when such temperature decrease is steeper.

### 3.2. Predicted probability of human TBE presence at the regional and municipal level across Europe

The predicted probability of human TBE presence at the regional level is shown in Fig. 4. Fig. 5 provides higher-resolution maps showing predicted probabilities at the municipal level, obtained by applying the model trained at the regional level to predictors averaged at the municipal scale. These maps complement those in Fig. 4 by offering finer spatial detail. The mean AUC was 0.84 (standard deviation (SD) = 0.03) for the regional model, derived from internal cross-validation, and 0.82 (SD = 0.03) for the model at the municipal scale, derived from external validation. The predictive performance at the regional scale showed good sensitivity (0.83, SD = 0.01) and specificity (0.80, SD = 0.01), while specificity decreased when downscaling the results at the municipal scale (0.69, SD = 0.01). Similarly, the Sorensen's Index showed a variation from 0.71 (SD = 0.01) (regional model) to 0.55 (SD = 0.01) (municipal model) (see Supporting Information, Table S1, for detailed performance metrics).

We also computed the standard deviation (SD) of the predicted probability of occurrence of human TBE cases across 50 model replicates at regional (Fig. S9) and municipal (Fig. S10) level, capturing the absolute variability in predictions at each location. Overall, the SD values were low across most regions, with a maximum value of 0.07 at regional level and 0.08 at municipal, indicating good stability and consistency of the model predictions.

### 3.3. Short-term variability of predicted human TBE presence in Europe

To examine potential trends in model predictions from 2017 to 2025, we conducted GLM analyses for each specific administrative unit, considering model predictions as the response variable and the year as the predictor variable, and mapped statistically significant coefficients both at the regional (Fig. 6a) and municipal (Fig. 6b) levels. The results suggest a statistically significant increase in the relative human TBE risk across central-western European countries (e.g. Switzerland and Germany), with the emergence of new suitable areas extending in a north-westerly and potentially south-westerly direction (e.g. Belgium and the United Kingdom). As only a few autochthonous cases have been reported in these latter countries to date, while the GLM trends suggest an increasing risk, such results should be interpreted considering the predicted baseline probability in these countries. Areas with larger significant increases in the predicted probability of human TBE presence are concentrated in western Germany, southern Belgium and eastern France (dark red areas). In contrast, areas of slight decrease in predicted TBE

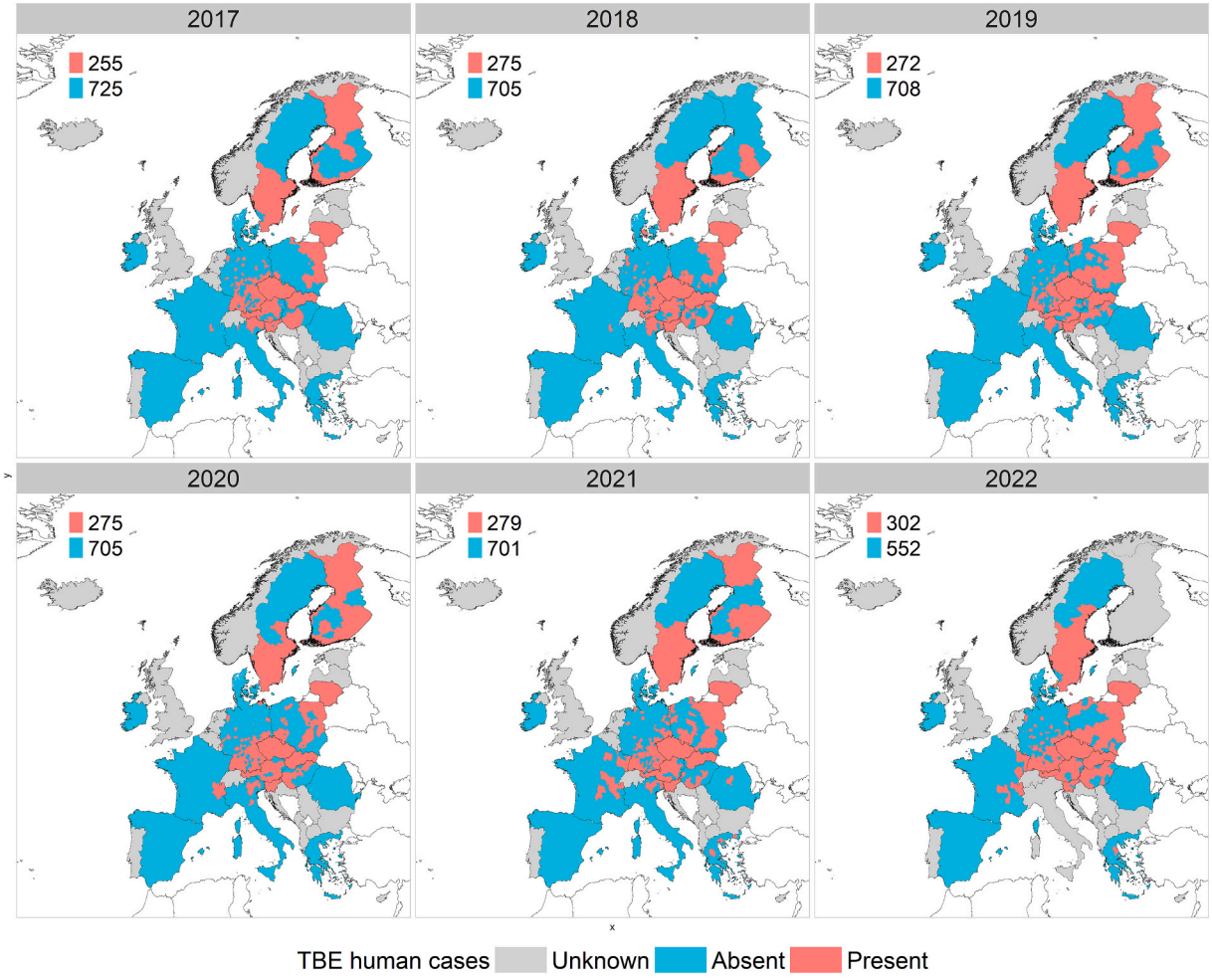


**Fig. 2.** Presence (in red) and pseudo-absence (in blue) of human TBE cases at the NUTS-3 (regional) administrative level (2017–2022). The total number of presences (red) and pseudo-absences (blue) for each year is displayed in the upper left corner of each panel. Areas where human TBE presence is unknown are masked in grey. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

risk can be seen in parts of Eastern Europe (light purple areas). This decrease only implies a reduction in the predicted probability, meaning that human TBE infections may still occur in these areas, but there has been a decreasing trend in recent years.

## 4. Discussion

The current spread and emergence of TBE cases across Europe has led to a greater demand for high-resolution predictive models to enhance our understanding of the ecological and anthropogenic factors that enhance TBE risk. Here, we present a machine learning modelling framework that enables the assessment of the probability of human TBE occurrence across European regions and municipalities, on a yearly basis. The model is based on a set of covariates that reflect both the hazard of virus circulation among vectors and reservoir hosts and the likelihood of human exposure to tick bites, fitting a One Health framework. TBEV circulates in small, localized hotspots [42], however, due to the lack of centralized and consistent monitoring, comprehensive data on TBEV prevalence in wildlife and vectors are not available continent-wide. Therefore, in this study, we specifically trained our model on a standardized dataset of confirmed human TBE cases reported to ECDC from countries with mandatory reporting. This choice provides a standardized, cross-border dataset that, while coarser in resolution, offers a robust basis for regional predictions across Europe. This decision underscores our focus on human TBE cases, addressing the public health impact of TBE in the human population. For the same reason, we used not only standardized environmental predictors related to the natural hazard of TBE virus circulation, such as climate, vegetation, and presence of vertebrate hosts, which influence tick abundance and TBEV prevalence in ticks, but also drivers related to human exposure to tick bites. Including the exposure dimension is particularly important when modelling the occurrence of human TBE cases, as the presence of TBEV in the environment does not necessarily lead to human infections, especially in areas with low exposure to infected ticks.

At this stage, our approach does not differentiate between tick-borne and food-borne human TBE infections, due to the unavailability of information on the specific mode of TBEV transmission, and the model indicates potential areas for TBEV transmission to humans regardless of the infection mode. Nonetheless, food-borne TBE infections are considered relatively rare as the proportion of food-borne cases in Europe is minimal compared to the number of infections acquired through tick bites [8] and for this reason we do not expect that their inclusion substantially affects the outcome of our model. In the future, TBE surveillance could be enhanced by the systematic collection and incorporation of data on food-borne TBE infections and data on TBEV seroprevalence in cattle, sheep and goats, which are known to be useful sentinels and potential sources of TBEV. Furthermore, the model could be enhanced by the availability of vaccination coverage across Europe, which would enable to predict changes in the true incidence of TBE in the human population, rather than just the probability of its presence.

Interestingly, model predictions suggest a shift of human TBE probability of occurrence towards northern, western, and possibly also

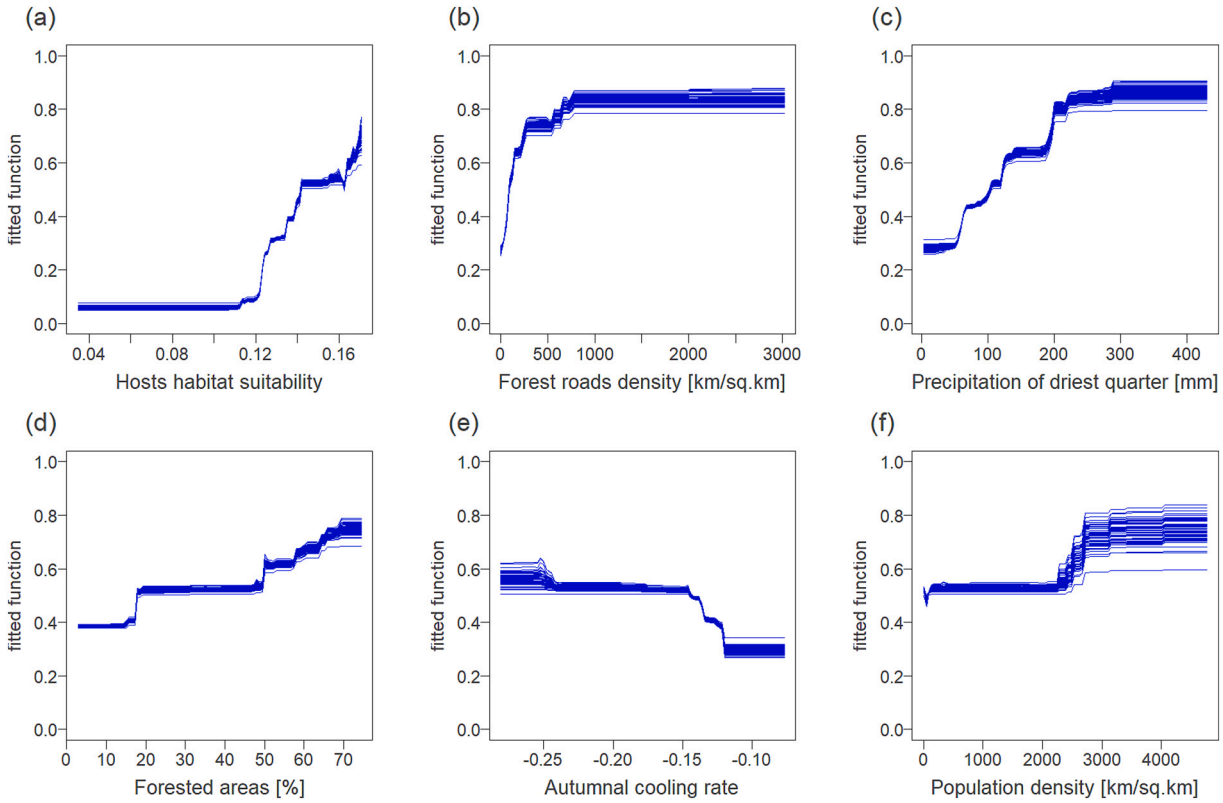


**Fig. 3.** Fitted functions of each variable across the 50 replicates of the BRT model. (a) Habitat suitability of vertebrate hosts (RI = 39.28, SD = 0,2); (b) Forest roads density (RI = 22.47, SD = 0,2); (c) Precipitation of the driest quarter (RI = 19.76, SD = 0,1); (d) Percentage of forested areas (RI = 13.11, SD = 0,1); (e) Autumnal cooling rate (RI = 3.22, SD = 0,4); (f) Population density (RI = 2.16, SD = 0,5).

southwestern countries, with a significant positive trend in areas where TBEV is already recognised as endemic, such as Germany and Switzerland, and also in countries where so far only a few autochthonous cases have been detected, such as Belgium [43], France [44], and the UK [45]. Unfortunately, data from emerging TBE cases in countries such as the UK, Belgium, and the Netherlands, were either unavailable in the ECDC dataset or not recorded at the NUTS-3 level. To improve predictive accuracy for these areas, future studies should incorporate data from emerging regions as they become available. Model predictions were notably high in eastern European countries such as Latvia, Estonia, Lithuania, and Poland, which border countries outside the study area, including Ukraine and Belarus. Although these neighboring countries lie beyond the formal boundaries of our study region, their proximity makes potential virus circulation epidemiologically relevant. TBE is known to be endemic in both Ukraine and Belarus: unofficial reports estimate around 50 human cases annually in Ukraine, while in Belarus, TBE incidence has risen in recent years, reaching 4.1 cases per 100,000 people in 2023 [46]. These patterns suggest that the elevated predicted probabilities near the eastern borders may also be influenced by ongoing virus circulation in adjacent areas.

Our results are consistent with the recent longitudinal and latitudinal shifts already observed [10,11], which imply retraction from some areas as well as expansion into others, that were observed in cases reported to ECDC [10] but also suggest a possible new pathway of TBE emergence towards southwestern areas. We speculate these patterns could be driven by changes in climatic and ecological factors, such as the expansion of ticks range of activity, coupled with host movements, including wildlife and domestic animal reservoirs, changes in land use patterns and rise in human exposure driven by human behaviour such as the increased use of green areas also in relation to a warmer climate [47]. From a One Health perspective, these dynamics highlight the importance of adopting an integrated approach when modelling TBE risk, accounting for environmental factors, animal reservoirs, and human exposure to tick bites. Warming temperatures are also helping ticks push the physiological limits of their latitudinal ranges and altitudinal limits [48]. Layers representing the distribution of the vectors, *Ixodes ricinus* and *Ixodes persulcatus* were initially considered as predictors but had no significant impact on the model's performance and were therefore excluded from further analyses. This can be explained by the fact that the mere presence of the vector is not sufficient for the circulation of the virus in the enzootic cycle. The presence of ticks alone is, in fact, usually not sufficient for TBEV to actively circulate within a foci; rather, enhanced viral transmission requires the co-occurrence of competent hosts (reservoirs), amplifier hosts (usually ungulates) and favourable environmental conditions (e.g., temperature and humidity levels that support tick survival and activity [42], see Supplementary material “Additional discussion on the influence of variables on model predictions”). Temporally explicit models of host distribution would be ideal to reflect seasonal and interannual fluctuations in host population density and, in small-scale studies, this is usually achieved by relying on locally recorded densities derived from game hunting records [4,49]. However, high-resolution host data are still not available on a continental scale, which is why this information is generally not considered in European-wide studies. For this reason, we used a variable describing the habitat suitability of vertebrate host species [29] which had already been shown to be a good predictor of TBE incidence across Europe [24].

To explore local patterns of human TBE risk areas across Europe, we downscaled our results to the municipal administrative level. The enhanced resolution of the municipal predictions shown in Fig. 5 highlights geographical heterogeneity in the occurrence of human TBE over the years of analysis. While the model demonstrated good predictive performance, we could only validate the municipal predictions using recorded human TBE cases from five European countries: Austria, Finland, Italy, Lithuania and Slovakia.

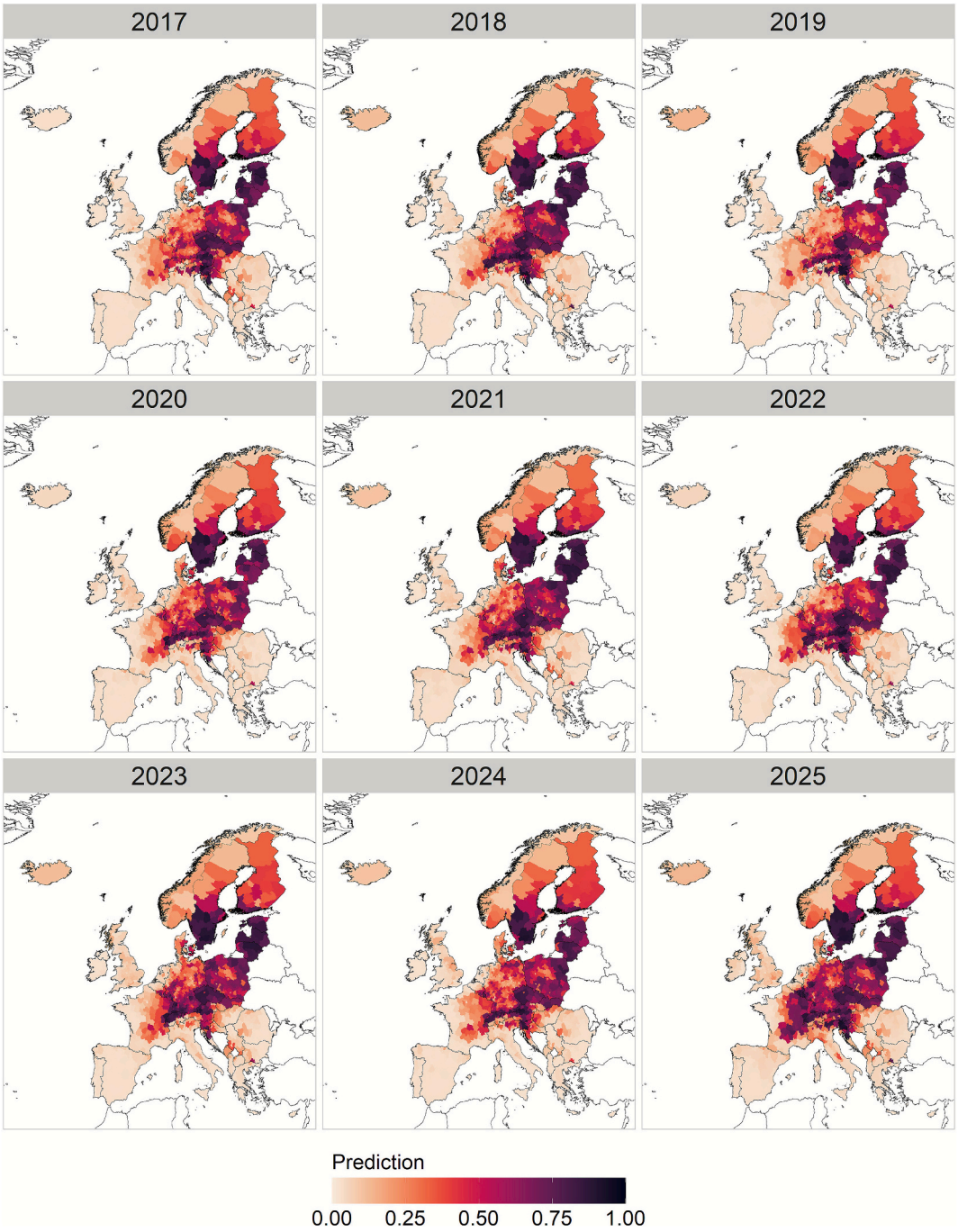


**Fig. 4.** The predicted probability of the occurrence of human TBE cases at the regional (NUTS-3) level, 2017–2025.

The limited availability of local human TBE case data was a limitation of this study. Other limitations, discussed in this section and briefly summarised here, mainly relate to data availability and resolution, including the lack of information on vaccination coverage, the inability to distinguish between food-borne and tick-borne infections, and the limited availability of harmonised data on the density or abundance of animal reservoirs, which were therefore represented through proxy variables. To facilitate future efforts to model human TBE occurrence at a high spatial resolution, it would therefore be beneficial to collect epidemiological data in a standardized and integrated manner across Europe, not only at the regional level, but also at the municipal level.

## 5. Conclusion

In this study, we present a validated framework for annually predicting areas at risk of human TBE infections before the start of the tick questing season. In the current context of global climatic and environmental change, predictive frameworks that identify potential new TBE risk areas across Europe are crucial to support public health actions aimed at reducing the burden of infection. At the same time, model outputs should always be interpreted considering local expertise and epidemiological knowledge. By integrating standardized and biologically consistent covariates that capture both the hazard of viral circulation in the environment among vectors and reservoir hosts, and human exposure to tick bites, our model provides a novel and practical tool for assessing potential areas at risk of human TBE infections fitting a One

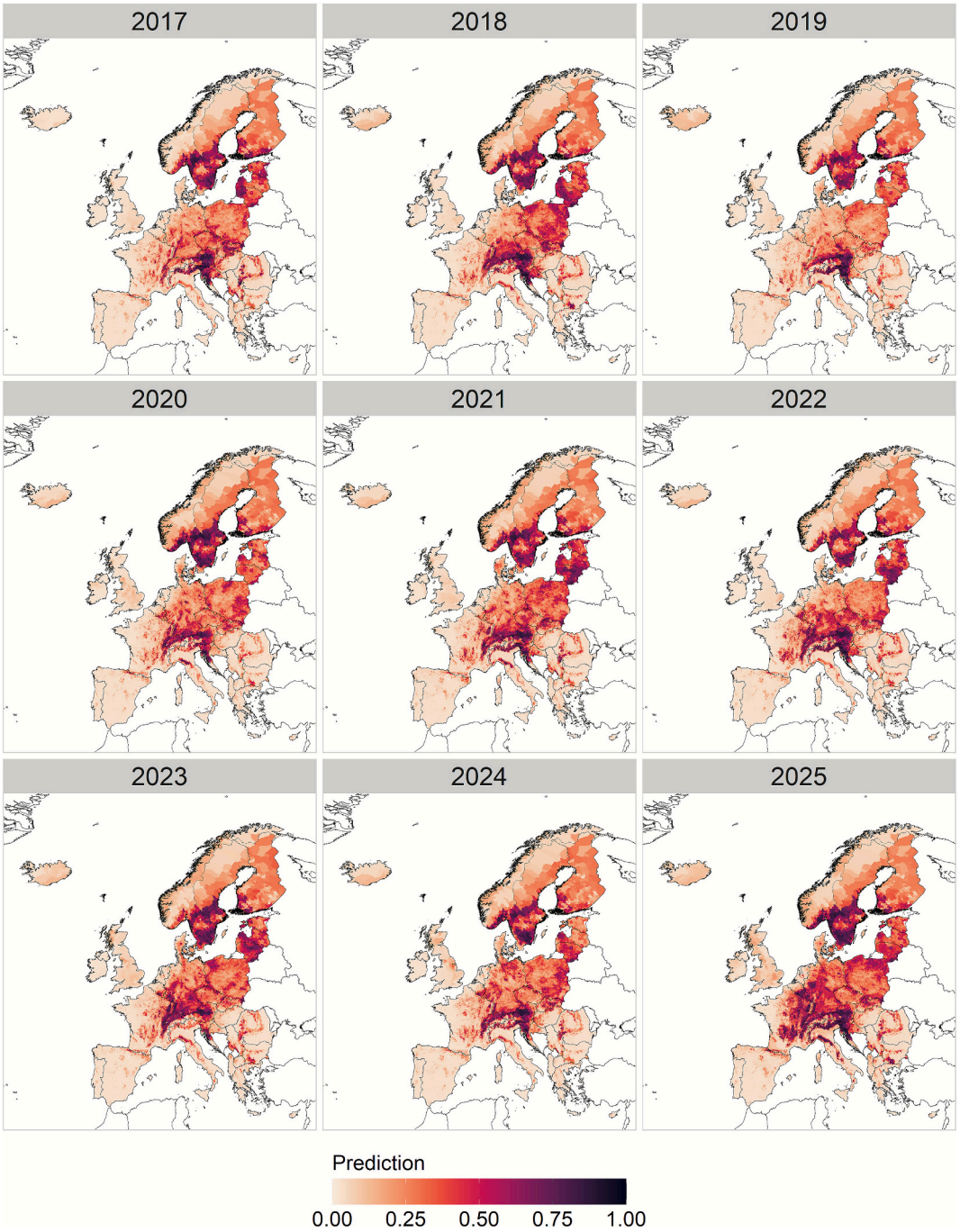


**Fig. 5.** The predicted probability of the occurrence of human TBE cases at the municipal level, 2017–2025.

Health approach, thereby enhancing the current understanding of TBE risk across Europe.

## Data sharing

The source code used for the analyses and the results presented in this manuscript is available on Zenodo at link doi:https://doi.org/10.5281/zenodo.15740470.

The epidemiological data that support the findings of this study were obtained through formal data-sharing agreements with the European Centre for Disease Prevention and Control (ECDC) and national public health institutes. Aggregated epidemiological data are openly available at https://www.ecdc.europa.eu/en/surveillance-atlas-infectious-diseases. Access to EU/EEA surveillance data for third parties can be requested to ECDC through the "Request form" available at https://www.ecdc.europa.eu/en/publications-data/access-eueea-surveillance-data-third-parties. Contact: data.access@ecdc.europa.eu. Access to municipal data can be requested to the following national institutes: Azienda Provinciale per i Servizi Sanitari Provincia Autonoma di Trento (APSS) (contact: apss@pec.apss.tn.it, urp@apss.tn.it); Unità Locale Socio Sanitaria Dolomiti (ULSS N.1 Dolomiti) (contact: urp@aulss1.veneto.it); Public Health Authority of the Slovak Republic (contact: ruvzbb@vzbb.sk); Austrian Agency for Health and Food Safety (AGES) (contact: management@ages.at); Finnish Institute for Health and Welfare (THL) (contact: international@thl.fi); National Public Health Center under the Ministry of Health (Lithuania) (contact: info@nvsc.lt); University of Ljubljana (contact: dekanat@mf.uni-lj.si).

All other data sources used (e.g., environmental layers used to

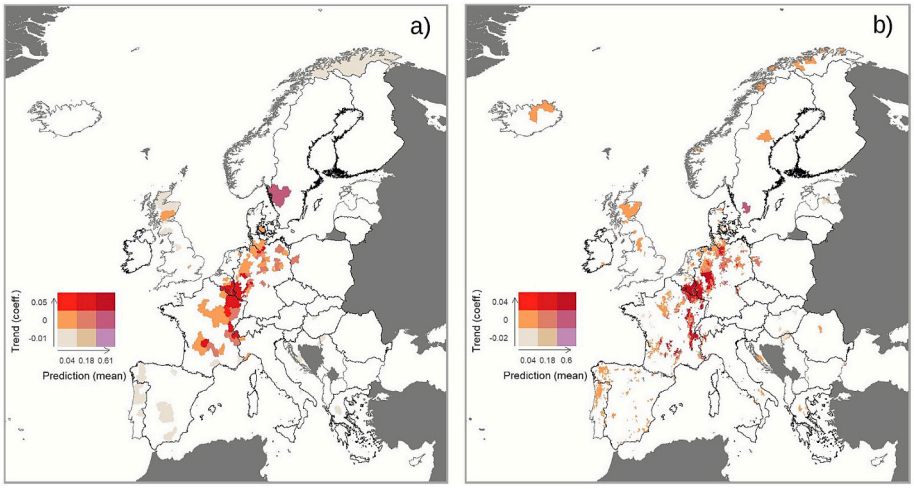


**Fig. 6.** Significant coefficients ($p < 0.05$) of linear regression models fitted separately for each area over the period 2017–2025 with year as predictor, at the regional (a) and municipal (b) levels. Only areas with statistically significant trends are shown in the maps. Colors represent a bivariate classification, encoding both the direction and magnitude of the temporal trend (regression coefficient), and the baseline mean predicted probability for each area. Countries included in the training dataset are outlined with a black border.

compute covariates) are publicly available and referenced in the manuscript and in the Supporting Information. Raw environmental data sources can also be downloaded from https://mood-platform.avia-gis.com. Base map data were obtained from Eurostat GISCO (https://ec.europa.eu/eurostat/web/gisco/geodata, copyrighted by EuroGeographics for the administrative boundaries) and geoBoundaries.

(https://www.geoboundaries.org/globalDownloads.html) under license CC BY 4.0.

## CRediT authorship contribution statement

**Francesca Dagostin:** Writing – original draft, Methodology, Formal analysis, Data curation, Conceptualization. **Diana Erazo:** Writing – review & editing, Methodology, Conceptualization. **Giovanni Marini:** Writing – review & editing, Methodology, Conceptualization. **Daniele Da Re:** Writing – review & editing, Methodology, Conceptualization. **Valentina Tagliapietra:** Writing – review & editing, Methodology, Conceptualization. **Maria Avdicova:** Writing – review & editing, Resources. **Tatjana Avšič-Županc:** Writing – review & editing, Resources. **Timothée Dub:** Writing – review & editing, Resources, Conceptualization. **Nahuel Fiorito:** Writing – review & editing, Resources. **Nataša Knap:** Writing – review & editing, Resources. **Céline M. Gossner:** Writing – review & editing, Resources. **Jana Kerlik:** Writing – review & editing, Resources. **Henna Mäkelä:** Writing – review & editing, Resources. **Mateusz Markowicz:** Writing – review & editing, Resources. **Roya Olyazadeh:** Writing – review & editing, Resources. **Lukas Richter:** Writing – review & editing, Resources. **William Wint:** Writing – review & editing, Resources. **Maria Grazia Zuccali:** Writing – review & editing, Resources. **Milda Žygutienė:** Writing – review & editing, Resources. **Simon Dellicour:** Writing – review & editing, Methodology. **Annapaola Rizzoli:** Writing – review & editing, Methodology, Conceptualization.

## Ethical statement

Ethical approval was not needed.

## Disclaimer

The views and opinions of the authors expressed herein do not necessarily state or reflect those of ECDC. The accuracy of the authors' statistical analysis and the findings they report are not the responsibility of ECDC. ECDC is not responsible for conclusions or opinions drawn from the data provided. ECDC is not responsible for the correctness of the data and for data management, data merging and data collation after provision of the data. ECDC shall not be held liable for improper or incorrect use of the data.

## Funding

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 874850 and is catalogued as MOOD 081. The contents of this publication are the sole responsibility of the authors and don't necessarily reflect the views of the European Commission.

## Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

## Acknowledgments

The authors warmly thank the members of the emerging and vector-borne disease network of ECDC for their support in the surveillance of tick-borne encephalitis in the EU/EEA and the provision of disease data, and national institutes who provided local epidemiological data, including Azienda Provinciale per i Servizi Sanitari Provincia Autonoma di Trento (APSS), Unità Locale Socio Sanitaria Dolomiti (ULSS N.1 Dolomiti), Public Health Authority of the Slovak Republic, Austrian Agency for Health and Food Safety (AGES), Finnish Institute for Health and Welfare (THL), National Public Health Center under the Ministry of Health and University of Ljubljana.

## Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.onehlt.2026.101331.

## Data availability

The source code used for the analyses and the results presented in this manuscript is available on Zenodo at link https://doi.org/10.5281/

zenodo.15740470.

## References


[1] T.S. Gritsun, V.A. Lashkevich, E.A. Gould, Tick-borne encephalitis, Antivir. Res. 57 (2003) 129–146, https://doi.org/10.1016/s0166-3542(02)00206-1.

[2] L. Lindquist, O. Vapalahti, Tick-borne encephalitis, Lancet 371 (2008) 1861–1871, https://doi.org/10.1016/S0140-6736(08)60800-4.

[3] M. Labuda, O. Kozuch, E. Zuffová, E. Elecková, R.S. Hails, P.A. Nuttall, Tick-borne encephalitis virus transmission between ticks cofeeding on specific immune natural rodent hosts, Virology 235 (1997) 138–143, https://doi.org/10.1006/viro.1997.8622.

[4] A. Rizzoli, H.C. Hauffe, V. Tagliapietra, M. Neteler, R. Rosà, Forest structure and roe deer abundance predict tick-borne encephalitis risk in Italy, PLoS One 4 (2009) e4336, https://doi.org/10.1371/journal.pone.0004336.

[5] R. Rosà, V. Tagliapietra, M. Manica, D. Arnoldi, H.C. Hauffe, C. Rossi, F. Rosso, H. Henttonen, A. Rizzoli, Changes in host densities and co-feeding pattern efficiently predict tick-borne encephalitis hazard in an endemic focus in northern Italy, Int. J. Parasitol. 49 (2019) 779–787, https://doi.org/10.1016/j.ijpara.2019.05.006.

[6] F. Cagnacci, L. Bolzoni, R. Rosà, G. Carpi, H.C. Hauffe, M. Valent, V. Tagliapietra, M. Kazimirova, J. Koci, M. Stanko, M. Lukan, H. Henttonen, A. Rizzoli, Effects of deer density on tick infestation of rodents and the hazard of tick-borne encephalitis. I: empirical assessment, Int. J. Parasitol. 42 (2012) 365–372, https://doi.org/10.1016/j.ijpara.2012.02.012.

[7] F. Dagostin, V. Tagliapietra, G. Marini, G. Ferrari, M. Cervellini, W. Wint, N. S. Alexander, M.G. Zuccali, S. Molinaro, N. Fiorito, T. Dub, D. Rocchini, A. Rizzoli, High habitat richness reduces the risk of tick-borne encephalitis in Europe: a multi-scale study, One Health 18 (2024) 100669, https://doi.org/10.1016/j.onehlt.2023.100669.

[8] E. Martello, E.L. Gillingham, R. Phalkey, C. Vardavas, K. Nikitara, T. Bakonyi, C. M. Gossner, J. Leonardi-Bee, Systematic review on the non-vectorial transmission of tick-borne encephalitis virus (TBEv), Ticks Tick-Borne Dis. 13 (2022) 102028, https://doi.org/10.1016/j.ttbdis.2022.102028.

[9] D. Ruzek, T. Avšič Županc, J. Borde, A. Chrdle, L. Eyer, G. Karganova, I. Kholodilov, N. Knap, L. Kozlovskaya, A. Matveev, A.D. Miller, D.I. Osolodkin, A. K. Överby, N. Tikunova, S. Tkachev, J. Zajkowska, Tick-borne encephalitis in Europe and Russia: review of pathogenesis, clinical features, therapy, and vaccines, Antivir. Res. 164 (2019) 23–51, https://doi.org/10.1016/j.antiviral.2019.01.014.

[10] European Centre for Disease Prevention and Control, Tick-borne encephalitis, in: ECDC (Ed.), Annual Epidemiological Report for 2022, ECDC, Stockholm, 2024.

[11] J. Van Heuverswyn, L.K. Hallmaier-Wacker, J. Beauté, J. Gomes Dias, J. M. Haussig, K. Busch, J. Kerlik, M. Markowicz, H. Mäkelä, T.M. Nygren, H. Orlíková, M. Socan, J. Zbrzeźniak, M. Žygutiene, C.M. Gossner, Spatiotemporal Spread of Tick-Borne Encephalitis in the EU/EEA, 2012 to 2020, Eurosurveillance 28, 2023, https://doi.org/10.2807/1560-7917.ES.2023.28.11.2200543.

[12] D. Da Re, G.F. Gilson, Q. Dalaiden, H. Goosse, R. Bødker, L.J. Kjær, N.H. Ogden, R. Rosà, S.O. Vanwambeke, Northward expansion of the thermal limit for the tick Ixodes ricinus over the past 40 years, Parasit. Vectors 18 (2025) 449, https://doi.org/10.1186/s13071-025-07084-4.

[13] S. Bhatt, P.W. Gething, O.J. Brady, J.P. Messina, A.W. Farlow, C.L. Moyes, J. M. Drake, J.S. Brownstein, A.G. Hoen, O. Sankoh, M.F. Myers, D.B. George, T. Jaenisch, G.R.W. Wint, C.P. Simmons, T.W. Scott, J.J. Farrar, S.I. Hay, The global distribution and burden of dengue, Nature 496 (2013) 504–507, https://doi.org/10.1038/nature12060.

[14] D. Erazo, L. Grant, G. Ghisbain, G. Marini, F.J. Colón-González, W. Wint, A. Rizzoli, W. Van Bortel, C.B.F. Vogels, N.D. Grubaugh, M. Mengel, K. Frieler, W. Thiery, S. Dellicour, Contribution of climate change to the spatial expansion of West Nile virus in Europe, Nat. Commun. 15 (2024) 1196, https://doi.org/10.1038/s41467-024-45290-3.

[15] Z. Farooq, J. Rocklöv, J. Wallin, N. Abiri, M.O. Sewe, H. Sjödin, J.C. Semenza, Artificial intelligence to predict West Nile virus outbreaks with eco-climatic drivers, Lancet Reg. Health 17 (2022) 100370, https://doi.org/10.1016/j.lanepe.2022.100370.

[16] E. Arsevska, T. Hengl, D.A. Singleton, P.-J.M. Noble, C. Caminade, O.A. Eneanya, P. H. Jones, J.M. Medlock, K.M. Hansford, C. Bonannella, A.D. Radford, Risk factors for tick attachment in companion animals in Great Britain: a spatiotemporal analysis covering 2014–2021, Parasit. Vectors 17 (2024) 29, https://doi.org/10.1186/s13071-023-06094-4.

[17] D. Porretta, V. Mastrantonio, S. Amendolia, S. Gaiarsa, S. Epis, C. Genchi, C. Bandi, D. Otranto, S. Urbanelli, Effects of global changes on the climatic niche of the tick Ixodes ricinus inferred by species distribution modelling, Parasit. Vectors 6 (2013) 271, https://doi.org/10.1186/1756-3305-6-271.

[18] M. Walter, J.R. Vogelgesang, F. Rubel, K. Brugger, Tick-borne encephalitis virus and its European distribution in ticks and endothermic mammals, Microorganisms 8 (2020) 1065, https://doi.org/10.3390/microorganisms8071065.

[19] R. Uusitalo, M. Siljander, T. Dub, J. Sane, J.J. Sormunen, P. Pellikka, O. Vapalahti, Modelling habitat suitability for occurrence of human tick-borne encephalitis (TBE) cases in Finland, Ticks Tick-Borne Dis. 11 (2020) 101457, https://doi.org/10.1016/j.ttbdis.2020.101457.

[20] A.M. Friedsam, O.J. Brady, A. Pilic, G. Dobler, W. Hellenbrand, T.M. Nygren, Geo-spatial characteristics of 567 places of tick-borne encephalitis infection in southern Germany, 2018–2020, Microorganisms 10 (2022) 643, https://doi.org/10.3390/microorganisms10030643.

[21] C.B. Zeimes, G.E. Olsson, M. Hjertqvist, S.O. Vanwambeke, Shaping zoonosis risk: landscape ecology vs. landscape attractiveness for people, the case of tick-borne encephalitis in Sweden, Parasit. Vectors 7 (2014) 370, https://doi.org/10.1186/1756-3305-7-370.

[22] European Union, Regulation (EC) No 1059/2003 of the European Parliament and of the Council of 26 May 2003 on the Establishment of a Common Classification of Territorial Units for Statistics (NUTS). http://data.europa.eu/eli/reg/2003/1059/oj/eng, 2003. (Accessed 11 April 2022).

[23] M.A.H. Braks, S.E. Van Wieren, W. Takken, H. Sprong (Eds.), Ecology and Prevention of Lyme Borreliosis, Wageningen Academic Publishers, Wageningen, 2016.

[24] F. Dagostin, V. Tagliapietra, G. Marini, C. Cataldo, M. Bellenghi, S. Pizzarelli, R. R. Cammarano, W. Wint, N.S. Alexander, M. Neteler, J. Haas, T. Dub, L. Busani, A. Rizzoli, Ecological and environmental factors affecting the risk of tick-borne encephalitis in Europe, 2017 to 2021, Eurosurveillance 28 (2023), https://doi.org/10.2807/1560-7917.ES.2023.28.42.2300121.

[25] J. Feranec, Project CORINE land cover, in: European Landscape Dynamics: CORINE Land Cover Data, 2016, pp. 9–14, https://doi.org/10.1201/9781315372860.

[26] Copernicus Climate Change Service, ERA5-Land Hourly Data From 2001 to Present, 2019, https://doi.org/10.24381/CDS.E2161BAC.

[27] S.E. Randolph, R.M. Green, M.F. Peacey, D.J. Rogers, Seasonal synchrony: the key to tick-borne encephalitis foci identified by satellite data, Parasitology 121 (2000) 15–23, https://doi.org/10.1017/S0031182099006083.

[28] Z. Wan, S. Hook, G. Hulley, MODIS/Terra Land Surface Temperature/Emissivity Daily L3 Global 0.05Deg CMG V061, 2021, https://doi.org/10.5067/MODIS/MOD11C1.061.

[29] W. Wint, 2022_WeightedMammal_HostDistributionModels, 2024, https://doi.org/10.5281/ZENODO.12799371.

[30] Open Street Maps, downloaded from: https://www.openstreetmap.org/#map=6/54.910/-3.432, 2017. (Accessed March 2017).

[31] A.J. Tatem, WorldPop, open data for spatial demography, Sci. Data 4 (2017) 170004. www.worldpop.org. https://doi.org/10.1038/sdata.2017.4.

[32] J. Elith, J.R. Leathwick, T. Hastie, A working guide to boosted regression trees, J. Anim. Ecol. 77 (2008) 802–813, https://doi.org/10.1111/j.1365-2656.2008.01390.x.

[33] G. Ridgeway, D. Edwards, B. Kriegler, S. Schroedl, H. Soutworth, B. Greenwell, B. Boehmke, J. Cunningham, gbm: Generalized Boosted Regression Models. R Package Version 2.1.3, Available from: https://cran.r-project.org/package=gbm, 2017.

[34] M. Lang, M. Binder, J. Richter, P. Schratz, F. Pfisterer, S. Coors, Q. Au, G. Casalicchio, L. Kotthoff, B. Bischl, mlr3: a modern object-oriented machine learning framework in R, JOSS 4 (2019) 1903, https://doi.org/10.21105/joss.01903.

[35] R. Valavi, J. Elith, J.J. Lahoz-Monfort, G. Guillera-Arroita, BLOCK CV : an R package for generating spatially or environmentally separated folds for *k* -fold cross-validation of species distribution models, Methods Ecol. Evol. 10 (2019) 225–232, https://doi.org/10.1111/2041-210X.13107.

[36] B. Leroy, R. Delsol, B. Hugueny, C.N. Meynard, C. Barhoumi, M. Barbet-Massin, C. Bellard, Without quality presence–absence data, discrimination metrics such as TSS can be misleading measures of model performance, J. Biogeogr. 45 (2018) 1994–2002, https://doi.org/10.1111/jbi.13402.

[37] A. Jiménez-Valverde, Insights into the area under the receiver operating characteristic curve (AUC) as a discrimination measure in species distribution modelling, Glob. Ecol. Biogeogr. 21 (2012) 498–507, https://doi.org/10.1111/j.1466-8238.2011.00683.x.

[38] G. Ghisbain, W. Thiery, F. Massonnet, D. Erazo, P. Rasmont, D. Michez, S. Dellicour, Projected decline in European bumblebee populations in the twenty-first century, Nature 628 (2024) 337–341, https://doi.org/10.1038/s41586-023-06471-0.

[39] D. Da Re, M. Gilbert, C. Chaiban, P. Bourguignon, W. Thanapongtharm, T. P. Robinson, S.O. Vanwambeke, Downscaling livestock census data using multivariate predictive models: sensitivity to modifiable areal unit problem, PLoS One 15 (2020) e0221070, https://doi.org/10.1371/journal.pone.0221070.

[40] D. Da Re, E. Tordoni, A. Naranjo-Cigala, M.A. Padrón-Mederos, M. González, C. González-Montelongo, J.R. Arévalo-Sierra, Assessing the impacts of land use and climate change on the distribution patterns of *Ulex europaeus* L. (Fabaceae) in the Canary Islands, Biol Invasions 26 (2024) 4363–4379, https://doi.org/10.1007/s10530-024-03452-w.

[41] R Core Team, R: A Language and Environment for Statistical Computing, R Foundation for Statistical Computing, Vienna, Austria, 2022. https://www.R-project.org/.

[42] G. Dobler, S. Tkachev, Chapter 11: General epidemiology of TBE, in: Tick-Borne Encephalitis - The Book, 2023, https://doi.org/10.33442/26613980_11-6.

[43] A. Stoefs, L. Heyndrickx, J. De Winter, E. Coeckelbergh, B. Willekens, A. Alonso-Jiménez, A.-M. Tuttino, Y. Geerts, K.K. Ariën, M. Van Esbroeck, Autochthonous cases of tick-borne encephalitis, Belgium, 2020, Emerg. Infect. Dis. 27 (2021) 2179–2182, https://doi.org/10.3201/eid2708.211175.

[44] E. Botelho-Nevers, A. Gagneux-Brunon, A. Velay, M. Guerbois-Galla, G. Grard, C. Bretagne, A. Mailles, P.O. Verhoeven, B. Pozzetto, S. Gonzalo, S. Fafi-Kremer, I. Leparc-Goffart, S. Pillet, Tick-borne encephalitis in Auvergne-Rhône-Alpes region, France, 2017–2018, Emerg. Infect. Dis. 25 (2019) 1944–1948, https://doi.org/10.3201/eid2510.181923.

[45] T.M. Kreusch, M. Holding, R. Hewson, T. Harder, J.M. Medlock, K.M. Hansford, S. Dowall, A. Semper, T. Brooks, A. Walsh, K. Russell, O. Wichmann, A Probable Case of Tick-Borne Encephalitis (TBE) Acquired in England, July 2019, Euro Surveillance: Bulletin Europeen Sur les Maladies Transmissibles = European

Communicable Disease Bulletin 24, 2019, https://doi.org/10.2807/1560-7917.ES.2019.24.47.1900679.
[46] I. Nebogatkin, O. Onishchuk, H. Oleksandr, W. Erber, T. Vuković-Janković, TBE in Ukraine, in: Tick-Borne Encephalitis - The Book, 2023, https://doi.org/10.33442/26613980_12b34-6.
[47] R.A. Bille, K.E. Jensen, R. Buitenwerf, Global patterns in urban green space are strongly linked to human development and population density, Urban For. Urban Green. 86 (2023) 127980, https://doi.org/10.1016/j.ufug.2023.127980.
[48] P.A. Nuttall, Climate change impacts on ticks and tick-borne infections, Biologia 77 (2022) 1503–1512, https://doi.org/10.1007/s11756-021-00927-2.
[49] B. Kriz, M. Daniel, C. Benes, M. Maly, The role of game (wild boar and roe deer) in the spread of tick-borne encephalitis in the Czech Republic, Vector-Borne Zoonotic Dis. 14 (2014) 801–807, https://doi.org/10.1089/vbz.2013.1569.