Modeling of Spatially Referenced Meteorological and Landscape Factors Influencing the Probability of Pathogen Isolation from Natural Environments

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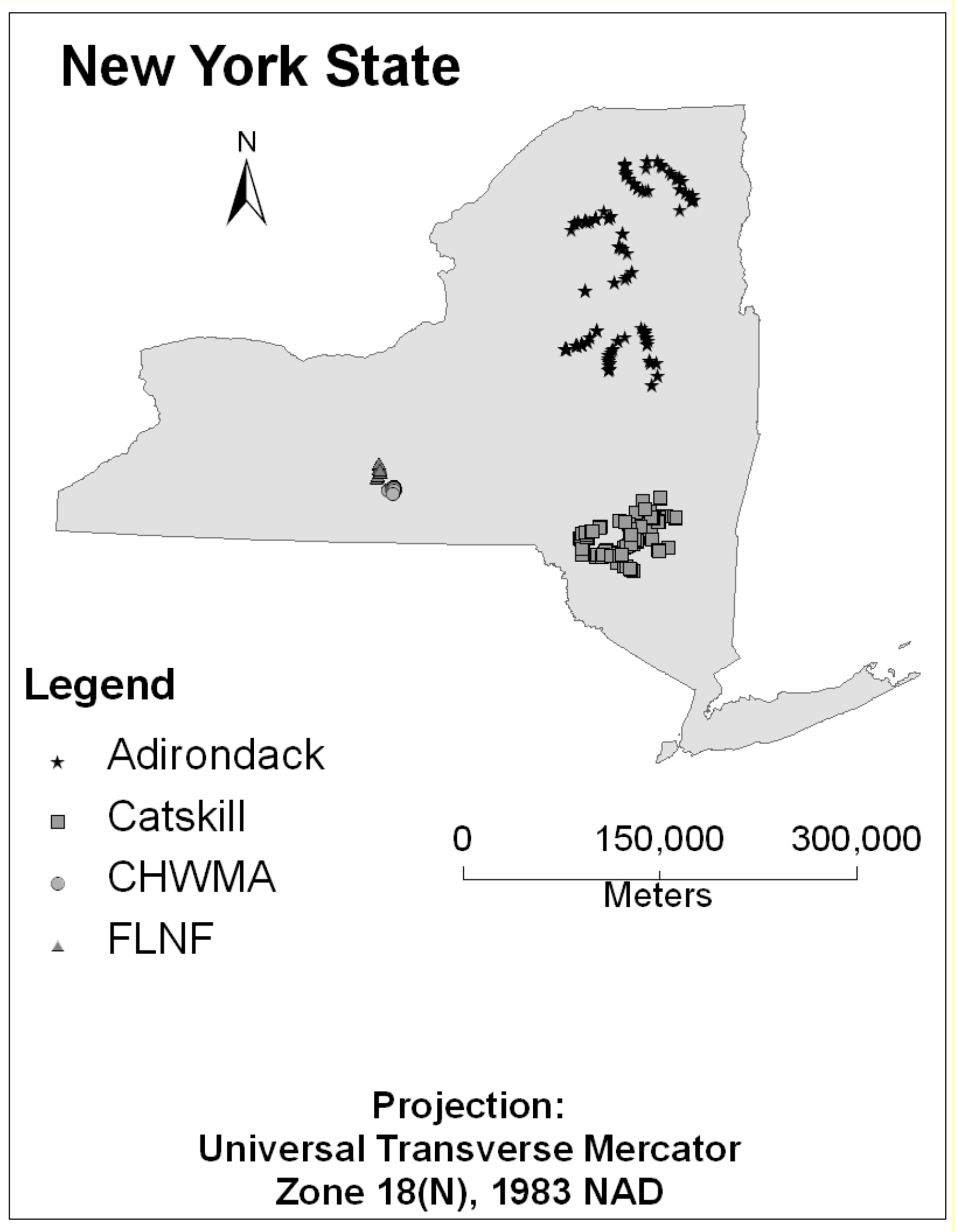

Figure 1. Study area. CHWMA= Connecticut Hill Wildlife Management Area; FLNF=Finger Lakes National Forest.

1 BACKGROUND

Changes in climate in coming decades will likely cause important changes in the incidence and distribution of diseases caused by pathogens with free-living stages (e.g., *Listeria monocytogenes*, *Salmonella*, *Escherichia coli*, and *Cryptococcus gattii*).

Our **objective** was to develop a methodological framework to study spatially referenced meteorological and landscape factors affecting the probability of pathogen isolation from a location.

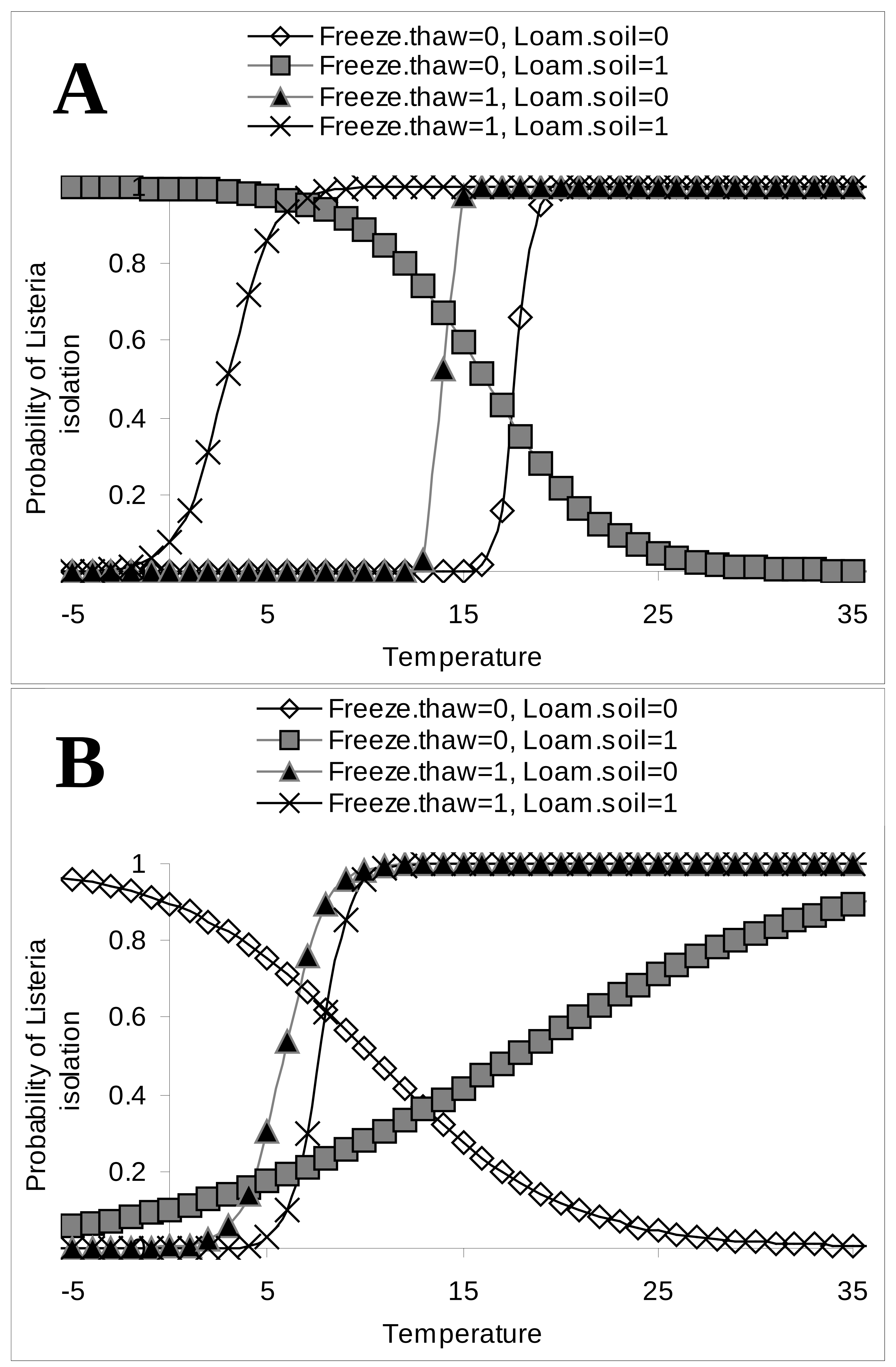

Figure 2. The probability of *Listeria* isolation from the vegetation layer in the northernmost (panel A) and southernmost (panel B) part of the study area for different levels of average temperature over the five days before sample collection, loam soil (“Loam.soil”) and freeze/thaw cycle occurring three days before sample collection (“Freeze.thaw”).

2 MATERIALS AND METHODS

Data on isolation of ***Listeria* spp.** from the natural environment collected in New York state, USA (Figure 1) were used as a model system. For each sampled location we obtained potentially relevant spatially referenced covariates grouped under soil properties, precipitation, ambient temperature, alternating freezing and thawing temperatures and geographic position. **Logistic Regression** (LR) and **Classification Tree** (CT) methods were applied and their successes in predicting *Listeria* presence in the environment were compared.

3 RESULTS AND DISCUSSION

Precipitation and alternating freezing and thawing temperatures prior to sample collection, loam soil, water storage to a soil depth of 50 cm, slope gradient and cardinal direction to the North were **key predictors** for *Listeria* isolation from a spatial location. Different combinations of factors affected the probability of *Listeria* isolation from the soil, vegetation and water layers of a location, indicating that the three layers represent **different ecological niches for *Listeria***. Figure 2 shows predictions for the vegetation layer obtained from the LR model, while Figures 3 and 4 show the best CTs for the soil and water layers, respectively. The **predictive power of CT was comparable to that of LR** (Table 1).

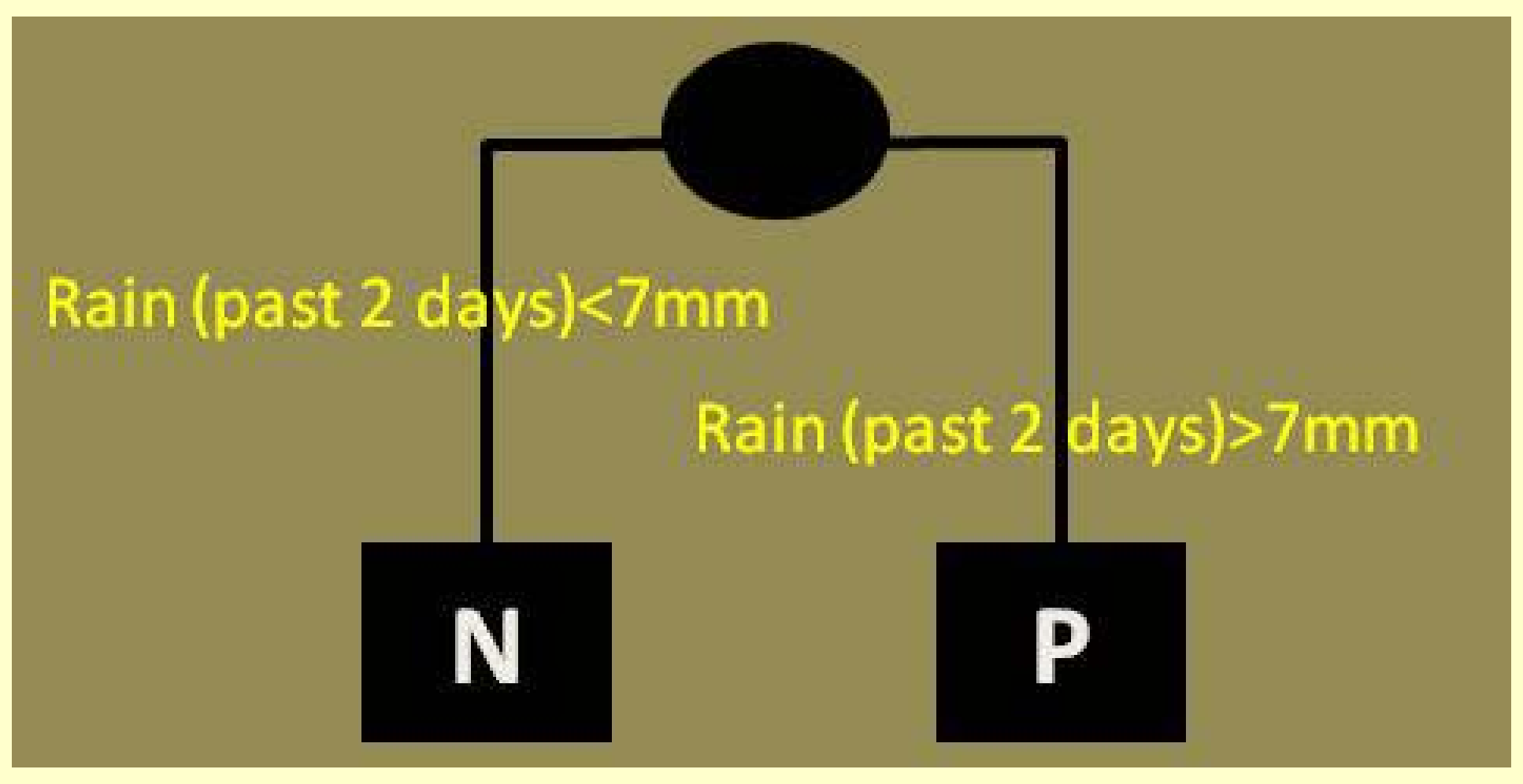

Figure 3. Classification tree for *Listeria* isolation from the soil layer.

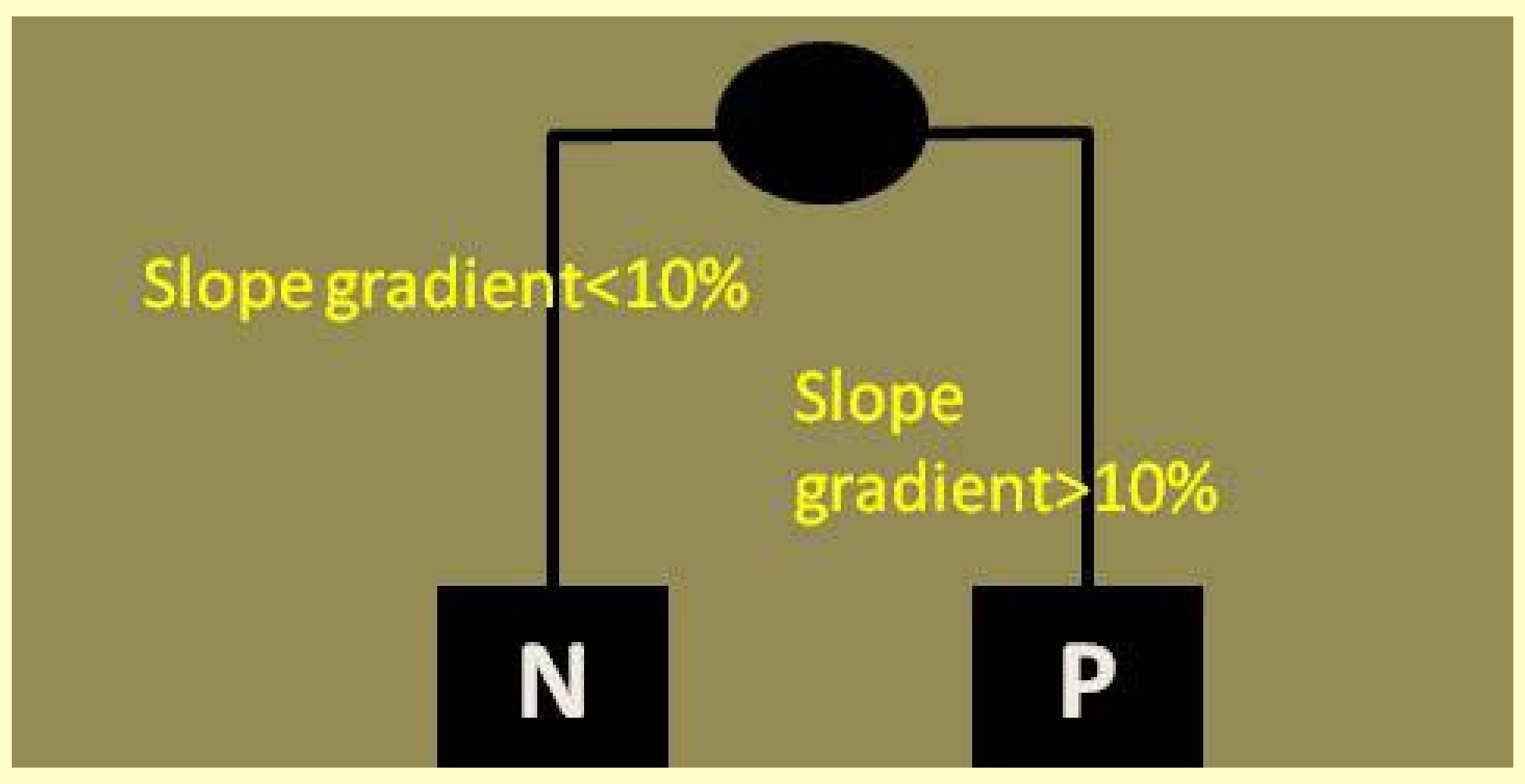

Figure 4. Classification tree for *Listeria* isolation from the water layer.

Table 1. Predictive performance of Logistic Regression (LR) and Classification Tree (CT) models

	Soil		Vegetation		Water	
	LR	**CT**	**LR**	**CT**	**LR**	**CT**
Sensitivity (Se)	0.28	0.51**	0.91	0.86	0.57	0.55
Specificity (Sp)	0.94**	0.77	0.34	0.43*	0.89	0.76
LR v. CT, p-value	<0.001		0.002		0.06	

*p-value ≤ 0.01; ** p-value ≤ 0.001

4 CONCLUSIONS

Our study demonstrated the utility of the developed modeling framework in analysis of a pathogen’s spatial distribution with the purpose of identifying predictors of the pathogen’s presence in the environment. That knowledge could be used to forecast microbial occurrence in response to changes in weather patterns anticipated in the coming years and, accordingly, to propose control strategies to reduce human and animal environmental exposure.