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Mapping spatial variations of tick abundance in heterogeneous agricultural landscapes to build a simulator prototype of tick abundance

Gwenaël Vourc'h¹, David Abrial¹, Albert Agoulon², Olivier Plantard², Thierry Hoch² ¹UMR EpiA, ²UMR BIOEPAR











CONTEXT

- The tick *Ixodes ricinus* is widespread in Europe and transmits various pathogens (bacteria, virus and protozoa). It is the vector of the bacteria *Borrelia burgdorferi sensu lato*, the causative agents of Lyme borrelioses.
- Its abundance and the related tick-borne disease risk depend on global factors (climate) but also on local conditions of temperature and humidity which influence its survival as well as wild and domestic animal densities.
- Agriculture landscapes may be heterogeneous, especially bocage areas corresponding to mosaics of habitats, and tick densities may be contially highly variable in such areas

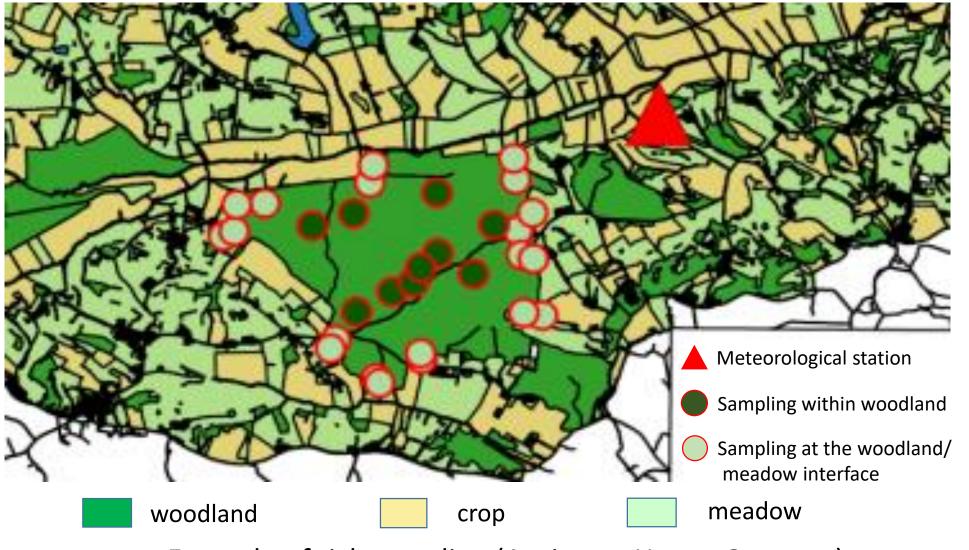
may be spatially highly variable in such areas.

OBJECTIVE

In this context, the OSCAR project was set up and aimed to develop a mapping simulation tool of tick abundance according to the characteristics of a bocage agricultural landscape. First, a statistical model of collected tick densities was fitted considering biotic and abiotic variables. This model was then included in a simulation tool that could be applied to other similar areas.

DATA

- Samplings of *Ixodes ricinus* nymphs were carried out in agricultural landscapes in two areas (in Ille-et-Vilaine and Haute-Garonne) during the tick spring peak, for three consecutive years.
- Habitats were geo-referenced, allowing to distinguish between woodland, meadows, roads, crops and buildings, which influence tick presence differently.
- Tick sampling on vegetation was carried out in the most favourable environments for ticks (woodland, woodland edges, hedges bordering meadows).
- Meteorological data (air temperature, relative humidity) from stations near these areas were recorded.



Example of tick sampling (Aurignac, Haute-Garonne)

MODEL

Explanatory variables were distinct depending on the habitat (woodland vs woodland edge or hedgerow) since some variables were not applicable in woodland. A GLMM was fitted on the tick densities (Y_i) considering a binomial negative distribution:

$$Y_i \sim BN(\mu_i, \psi)$$
 and $\log(\mu_i) = X_i\beta + \delta_i X_i^{(F)}\beta^{(F)} + (1 - \delta_i)X_i^{(O)}\beta^{(O)} + \iota$

 μ_i is the mean of the negative binomial distribution law for the spatial units *i*. $X_i^{(F)}$ is a set of fixed effects, associated to parameters $\beta^{(F)}$, specific to forest and $X_i^{(O)}$ is another set, associated to $\beta^{(O)}$ specific to other sampling unit.

RESULTS

The predicted number of mean questing nymphs was:

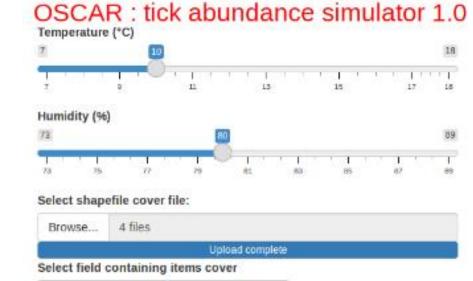
 $\log (\mu_i) = \delta_i (0.07 \times TEM_i + 2.34 \times WOP_i + 1.56 \times ROD_i)$

+ $(1 - \delta_i) (0.07 \times TEM_i + 0.02 \times HUM_i + 0.73 \times WOP_i - 2.26 \times BUP_i - 2.62 \times WOD_i) + v$

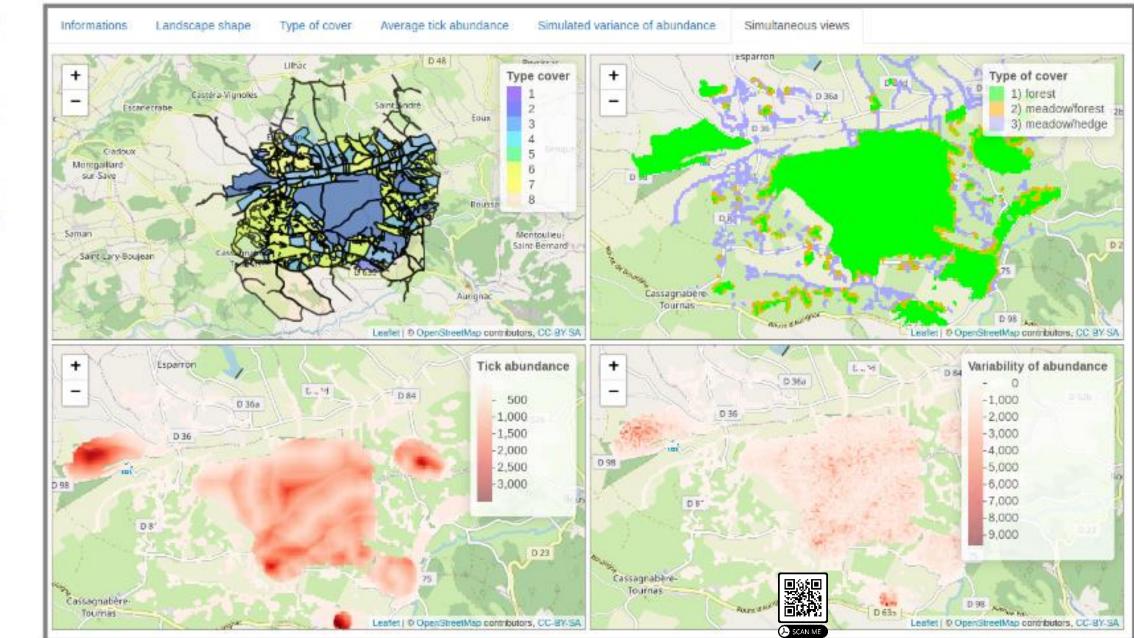
Model fitting led to the following variables being considered significantly influential on tick densities:

- in woodland: temperature (TEM), woodland perimeter (WOP) and distance to road (ROD),
- at woodland edge or hedgerow: temperature, humidity (HUM), woodland and building (BUP) perimeters and distance to woodland (WOD). The identified explanatory variables are consistent with our knowledge of *Ixodes ricinus* ecology.

The model has been included in a tool (R Shiny application) that allows to simulate tick density for areas where an abundance estimation is possible, provided that a numerical description of the



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landscape is available.

https://oscar-abondance.sk8.inrae.fr/

CONCLUSION

This tool is to our knowledge the first simulation tool that could be applied to a mapped landscape made up of different habitats. However the model should be restricted to landscapes with similar habitat characteristics. The genericity of the approach still needs a validation step on other areas.



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