DTU Library

Modelling tick abundance using machine learning techniques and satellite imagery

Kjær, Lene Jung; Korslund, L. ; Kjelland, V.; Slettan, A.; Andreassen, Å. K.; Paulsen, K. M.;
Christensson, M.; Kjellander, P.; Teräväinen, M.; Soleng, A.; Edgar, K. S.; Lindstedt, H. H.; Schou,
Kirstine Klitgaard; Bødker, Rene

[Link back to DTU Orbit](#)

Modelling tick abundance using machine learning techniques and satellite imagery. Kjær, L. J.[1], Korslund, L.[2], Kjelland, V.[2], Slettan, A.[2], Andreassen, Å. K.[3], Paulsen, K. M.[3], Christensson, M.[4], Kjellander, P.[4], Teräväinen, M.[4], Soleng, A.[5], Edgar, K. S.[5], Lindstedt, H. H. [5], Schou, K. K.[1], Bødker, R[1].

[1]Department for Diagnostics and Scientific Advice, Technical University of Denmark, National Veterinary Institute, Copenhagen, Denmark

[2]Department of Natural Sciences, University of Agder, Agder, Norway
[3]Department of Virology, Norwegian Institute of Public health, Oslo, Norway
[4]Department of Ecology; Wildlife Ecology Unit, Swedish University of Agricultural Sciences, Grimsö, Sweden
[5]Department of Pest Control, Norwegian Institute of Public health, Oslo, Norway

Recently, focus on tick-borne diseases has increased as diseases such as Lyme disease and tick-borne encephalitis have become more widespread and represent a real health problem in many parts of Europe. Effective control and prevention of these diseases requires a better understanding of the factors affecting the vectors. There is a great need for analyses and models that can predict how vectors and their associated diseases are distributed now and possibly in the future.

As a part of the ScandTick Innovation project, we surveyed and collected ticks at approximately 30 sites in each of Denmark, southern Norway and south-eastern Sweden. At each site we measured presence/absence and relative tick abundance using north- and east- facing line transect, where number of larvae, nymphs and adult females and males were counted at eight 50 m transects. We used the data obtained along with environmental satellite images to run Boosted Regression Tree machine learning algorithms to predict overall distribution (presence/absence of ticks) and relative tick abundance of nymphs and larvae in southern Scandinavia. For nymphs, the predicted abundance had a positive correlation with observed abundance and the spatial variation found corresponded well with known abundance and distributions of ticks in Scandinavia, with higher abundance and more widespread distribution in Denmark compared to Norway and Sweden. Because abundance was strongly correlated with forested habitats the risk areas were much larger in Sweden and Norway compared to Denmark. In both the Norwegian and Swedish regions, abundance was markedly higher nearer the coastline. Presence of larvae was much more clustered in the observed data, which was also reflected in the predicted abundance and distribution maps for the region. Whereas the predicted distribution of larvae was mostly even throughout Denmark, it was primarily around the coastlines in Norway and Sweden. Abundance was fairly low overall except in some fragmented patches corresponding to forested habitats in the region.

Machine learning techniques allow us to predict for larger areas without having to perform extensive sampling all over the region in question. The results from these models can be used in epidemiological models and can help us determine areas under risk of disease transmission and help us interpret human incidence data. Next step will be to analyze the collected ticks for pathogens and using the same machine learning techniques to develop prevalence maps of the ScandTick region.