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MODELLING RISK OF TICK EXPOSURE IN SOUTHERN SCANDINAVIA USING MACHINE LEARNING TECHNIQUES, SATELLITE IMAGERY, AND HUMAN POPULATION DENSITY MAPS

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Vector-borne diseases such as Lyme disease and tick-borne encephalitis have become more common in recent decades and present a real health problem in many parts of Europe. Risk assessment, control, and prevention of these diseases require a better understanding of vector abundance as well as risk factors determining human exposure to ticks. There is a great need for analyses and models that can predict how vectors and their associated diseases are distributed and how this relates to high risk areas for human exposure.

As a part of the ScandTick Innovation project, we surveyed ticks at approximately 30 sites (forests and meadows) in each of Denmark, southern Norway and south-eastern Sweden. At each site we measured presence/absence of ticks, and used the data obtained along with environmental satellite images to run Boosted Regression Tree machine learning algorithms to predict overall spatial distribution (probability of presence) in southern Scandinavia. Together with the predicted distribution maps, we used human density maps to determine areas with high risk of exposure to ticks.

For nymphs, the predicted distribution found corresponded well with known distributions of ticks in Scandinavia, with more widespread distribution in Denmark compared to Norway and Sweden. In the Norwegian region, probability of presence was markedly higher nearer the coastline and the

data shows a latitudinal boundary in the Swedish region above which probability of presence was low or close to zero. Presence of larvae was much more clustered in the observed data, which was also reflected in the predicted distribution maps for the region. Whereas the predicted distribution of larvae was mostly even throughout Denmark, larvae were primarily around the coastlines in Norway and Sweden. When combining these distribution maps with human population density maps and accounting for area accessibility, we could assess the proportion of the population living in areas where ticks were present. Our data showed that although ticks are found in a limited proportion of the total region area (particularly for Norway and Sweden), areas with high population densities tend to overlap with these zones.

Machine learning techniques allow us to predict for larger areas without having to perform extensive sampling all over the region in question, and we were able to produce models and maps with high predictive value. The results from these models help us pinpoint areas with high risk of exposure to ticks and thus potentially tick-borne diseases.

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