Species distribution modeling of a new invasive mosquito: A Bayesian approach

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Introduction

The spread of **infectious diseases** associated with changes in geographical distribution of a vector species has a critical impact on human health [1]. Indeed, many invasive species are vectors of zoonoses. Bloodsucking arthropods represent the majority of organisms capable of transmitting infectious diseases to humans. Among them, **mosquitoes** have been one of the most successful **invasive vector groups** since the 20th century, and represent the bridge-vector of many of the highest impacting anthropozoonoses. Several invasive *Aedes* species are now established in Europe, and Italy is one of the most heavily infested European countries. Among them, *Aedes koreicus* has spread throughout northern Italy since 2011 [2]. This species shares many ecological features with other *Aedes* invasive species, *Ae. japonicus* and *Ae. albopicus*; vectors of several infectious diseases. Thereby, monitoring and **modelling** *Ae. koreicus* distribution is critical to understand the invasion process, with the ultimate goal of predicting its **potential distribution range** and to develop effective control strategies.

Figure 1: *Ae. koreicus*

References

[1] Crowl TA, Crist TO, Parmenter RR, Belovsky G, Lugo AE. *The spread of invasive species and infectious disease as drivers of ecosystem change*. Front Ecol Environ. 2008, 1;6(5):238-46.

[2] Capelli G, Drago A, Martini S, Montarsi F, et al. *First report in italy of the exotic mosquito species Aedes (Finlaya) koreicus, a potential vector of arboviruses and filariae*. Parasite Vector. 2011, 28;4(1):188.

[3] Metz M, Rocchini D, Neteler M. *Surface Temperatures at the Continental Scale: Tracking Changes with Remote Sensing at Unprecedented Detail*. Remote Sensing. 2014, 28;6(5):3822-40.

[4] Roiz D, Neteler M, Castellani C, Arnoldi D, Rizzoli A. *Climatic Factors Driving Invasion of the Tiger Mosquito (Aedes albopictus) into New Areas of Trentino, Northern Italy*. PLoS ONE. 2011, 15;6(4):e14800.

Materials and Methods

Ae. koreicus presence was investigated through 67 BG-S and 12 CDC-light traps, 280 ovitraps and larval surveys from May to September 2013-2014 (Fig1). **Bioclim**, seasonal **NDVI**, **NDWI** and two further temperature-based variables (including average temperature of mosquito population growing season; ATGS) were used as predictors. All predictors were derived from **remote sensing** at 250m resolution (MODIS and CMORPH [3]). The intial set of variables was filtered using correlation analyses and scientific information. A logistic regression with **Bayesian** framework was implemented using R and JAGS. **Informed priors** derived from literature on *Ae. albopictus* were used for overall annual and average temperature of the coldest month [4]. DIC was used to select the best model. Size and direction of parameter estimates were assessed using 30000 **MCMC iterations**.

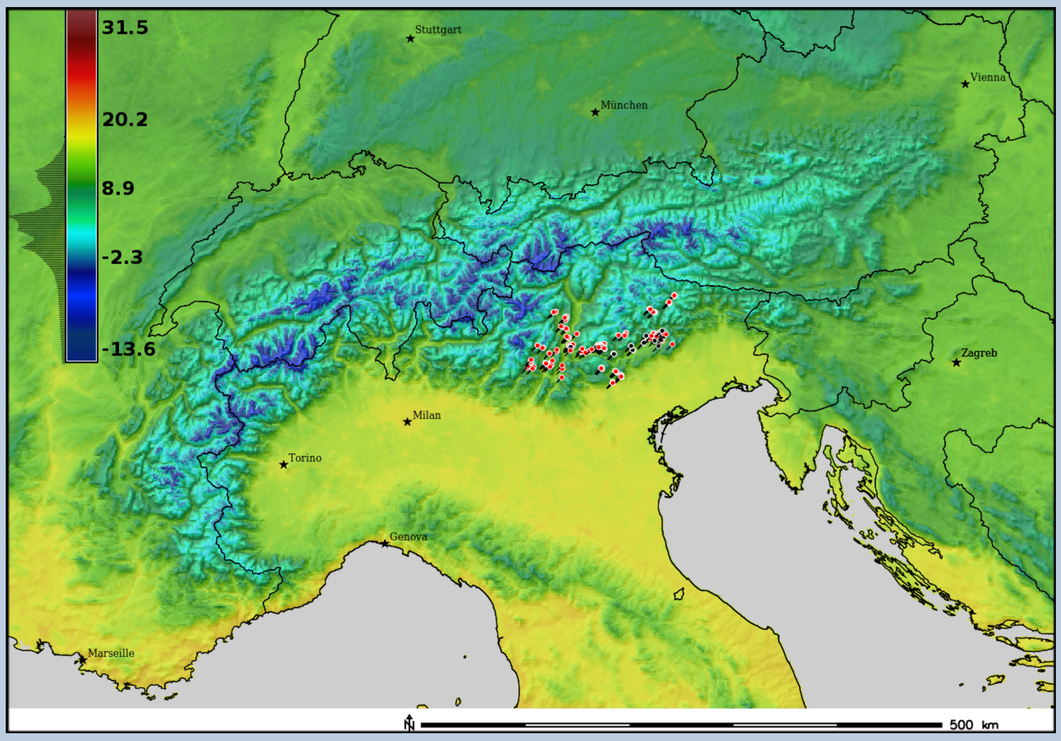

Figure 2: Trap locations with Bio1 as background.

Results and Discussion

79 traps out of 359 were positive for *Ae. koreicus*. The best model comprised ATGS, Annual Precipitation and autumn NDWI. Convergence was reached for all the MCMC outputs (Gelman diagnostic). No strong correlation was found among the posterior distributions (Fig3) which showed how *Ae. koreicus* invaded range is mostly driven by **humidity** (Fig4). While higher amount of annual precipitation characterises the invaded area, a wet environment during autumn seems to constrain spreading. ATGS showed a lower effect, moreover its posterior distribution showed a different shape than its prior (based on *Ae. albopictus*), potentially underpinning a **lower dependence from temperature**.

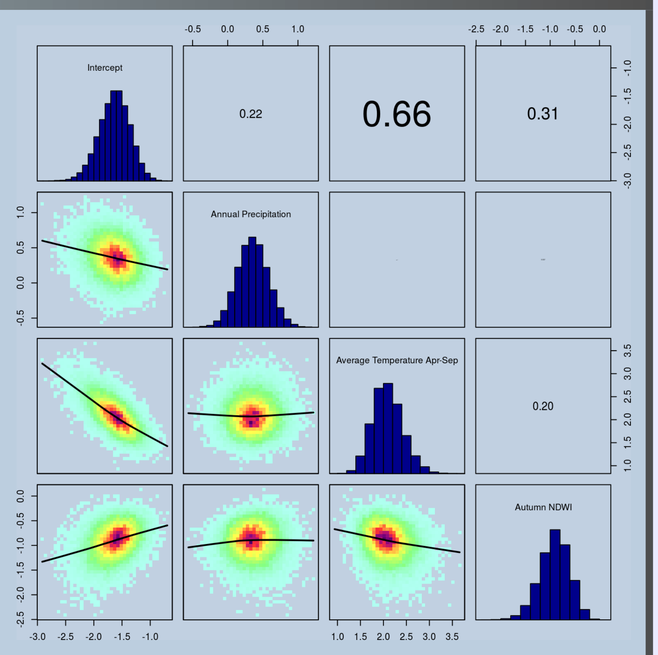

Figure 3: Correlation matrix of posterior distributions

Therefore *Ae. koreicus* may **invade** a different niche, characterised by a colder climate than *Ae. albopictus*. Since the mountainous morphology of the study area, the arrival of this potential mosquito vector at **higher altitude** may be inferred. As there is a lack of information about the ecology of new invasive species, Bayesian statistics, through the integration of **prior knowledge**, allows more robust model parameter estimates. Furthermore, **remote sensed predictors** allow a continous temporal and spatial coverage at detailed spatial resolution. Therefore, we conclude that Bayesian statistics coupled with remote sensing represents a powerful tool to improve SDM of new invasive species.

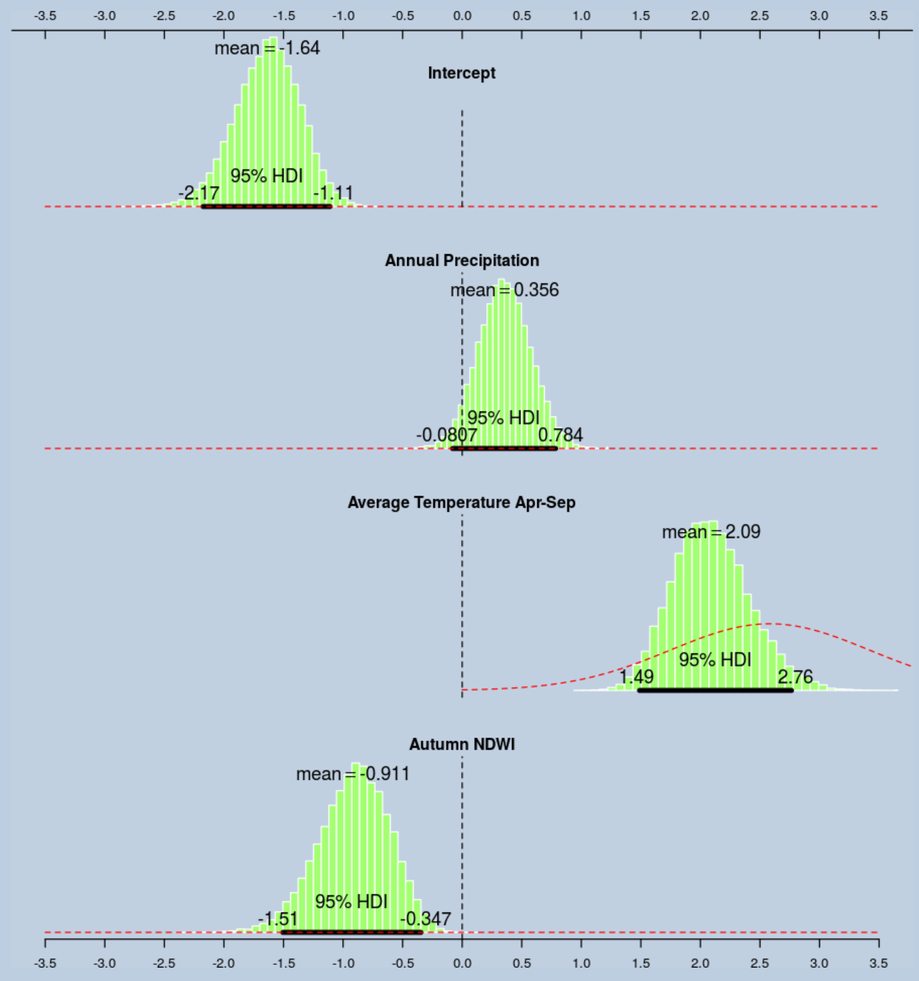

Figure 4: Posterior distributions