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Areas at risk of zoonoses - Considering ecological knowledge of both pathogen and vector in modelling vector-borne diseases

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Background

Current developments in the spread of zoonoses in Europe emphasize the importance and urgency of well-informed projections concerning their expectable future development. To identify current and future areas at risk of zoonoses a combination of ecological knowledge and statistical species distribution models is required. Here, we use an ensemble modelling approach implemented in the biomod2 package of R (see Methods below).

Within a pilot project of the German Research Platform for Zoonoses ('Zoonosis RISKTOOL') we developed current and future risk maps for Dengue and West Nile with special focus on the cold tolerance of the vectors *Aedes albopictus* and *Aedes japonicus* and the extrinsic incubation period (EIP) of the pathogens.

Results: Climatic suitability for Aedes albopictus and Dengue



Methods

- Correlative species distribution model
- Bioclimatic variables of Worldclim (5' resolution, global scale)
- Ensemble modelling approach as implemented in biomod2 R-package
- Generalized Linear Model (GLM), Boosted Regression Tree (BRT), Random Forest (RF), Maximum Entropy (MAXENT)
- Pseudo-absences/background selection (maximum distance for Ae. albopictus, randomly for Ae. japonicus)
- Future projections until 2030, 2050 and 2070 for five climate models and two emission scenarios (rcp4.5, rcp8.5)
- · Intersection with EIP of Dengue virus and cold tolerance of the vector's eggs
- See also the poster of Nils Tjaden for more details on the modelling framework

Further References

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