Bayesian variable selection in modelling geographical heterogeneity in malaria transmission from sparse data : an application to Nouna Health and Demographic Surveillance System (HDSS) data, Burkina Faso

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)

ID 3121421
Author(s) Diboulo, Eric; Sié, Ali; Diadier, Diallo A; Voules, Dimitrios A Karagiannis; Yé, Yazoume; Vounatsou, Penelope
Author(s) at UniBasel Vounatsou, Penelope ;
Year 2015
Title Bayesian variable selection in modelling geographical heterogeneity in malaria transmission from sparse data : an application to Nouna Health and Demographic Surveillance System (HDSS) data, Burkina Faso
Journal Parasites and vectors
Volume 8
Pages / **Article-Number** 118
Keywords Bayesian, Zero-inflated, Negative binomial, Stochastic search variable selection, Entomological inoculation rate, Burkina Faso, Sub-Saharan Africa, Nouna HDSS, Lag time
Quantification of malaria heterogeneity is very challenging, partly because of the underlying characteristics of mosquitoes and also because malaria is an environmentally driven disease. Furthermore, in order to assess the spatial and seasonal variability in malaria transmission, vector data need to be collected repeatedly over time (at fixed geographical locations). Measurements collected at locations close to each other and over time tend to be correlated because of common exposures such as environmental or climatic conditions. Non- spatial statistical methods, when applied to analyze such data, may lead to biased estimates. We developed rigorous methods for analyzing sparse and spatially correlated data. We applied Bayesian variable selection to identify the most important predictors as well as the elapsing time between climate suitability and changes in entomological indices.; Bayesian geostatistical zero-inflated binomial and negative binomial models including harmonic seasonal terms, temporal trends and climatic remotely sensed proxies were applied to assess spatio-temporal variation of sporozoite rate and mosquito density in the study area. Bayesian variable selection was employed to determine the most important climatic predictors and elapsing (lag) time between climatic suitability and malaria transmission. Bayesian kriging was used to predict mosquito density and sporozoite rate at unsampled locations. These estimates were converted to covariate and season-adjusted maps of entomological inoculation rates. Models were fitted using Markov chain Monte Carlo simulation.; The results show that Anophele. gambiae is the most predominant vector (79.29%) and is more rain-dependant than its sibling Anophele. funestus (20.71%). Variable selection suggests that the two species react differently to different climatic conditions. Prediction maps of entomological inoculation rate (EIR) depict a strong spatial and temporal heterogeneity in malaria transmission risk despite the relatively small geographical extend of the study area.; Malaria transmission is very heterogeneous over the study area. The EIR maps clearly depict a strong spatial and temporal heterogeneity despite the relatively small geographical extend of the study area. Model based estimates of transmission can be used to identify high transmission areas in order to prioritise interventions and support research in malaria epidemiology.

Publisher Bio Med Central
ISSN/ISBN 1756-3305
edoc-URL http://edoc.unibas.ch/dok/A6381839

Full Text on edoc Available;
Digital Object Identifier DOI 10.1186/s13071-015-0679-7
PubMed ID http://www.ncbi.nlm.nih.gov/pubmed/25888970
ISI-Number WOS:000351903500003
Document type (ISI) Journal Article