MOSQUITOES

Spatial modelling of the potential temperature-dependent transmission of vector-associated diseases in the face of climate change: main results and recommendations from a pilot study in Lower Saxony (Germany)

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Abstract The sustained climate change is going to modify the geographic distribution, the seasonal transmission gate and the intensity of the transmission of vector-borne diseases such as malaria or the bluetongue disease. These diseases occur nowadays at higher latitudes or altitudes. A further rise in ambient temperature and rainfall will extend the duration of the season in which mosquito vectors are transmitting pathogens. The parasites transmitted by the vectors also benefit from increasing temperatures, as both their reproduction and development are then accelerated, too. Thus, it seemed prudent to examine potential effects on the seasonal transmission gate due to the ongoing and predicted climate changes. Lower Saxony (northwest Germany) is a former malaria region with highest incidences of *Anopheles atroparvus* and tertian malaria along the coastal zones before malaria had finally become extinct in the early 1950s. Nevertheless, the *Anopheles* mosquitoes which transmit the malaria pathogens have still been present in Lower Saxony up to now. This together with the climate change-related implications gave reason to investigate whether a new autochthonous transmission could take place if the malaria pathogen is introduced again in Lower Saxony. Thus, the potential spatial and temporal structure of temperature-driven malaria transmissions was mapped using the basic reproduction rate (R_0) and measured and predicted air temperatures (1947–1960, 1961–1990, 1985–2004, 2020, 2060, 2100, each best case and worst case scenario). This paper focuses on both the summarizing of the results from this risk modelling approach and on the conclusions to be drawn. The recommendations highlight the need to link vector monitoring as one of the key elements of an epidemiological monitoring with the environmental monitoring.

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Background

The WHO (2004) evaluated the potential of early warning systems based on climate variations to enhance global surveillance and response to epidemic-prone diseases. Among others, this should be reached by achieving safe and healthy human environments, protected from biological, chemical, and physical hazards and secure from the adverse effects of global and local environmental threats. Two of several technical strategies are vector control and prevention and containment of epidemics. Nevertheless, the first appearance of bluetongue disease, a biting midge-borne viral infection of ruminants, in the early summer month in 2006 in Germany struck farmers, veterinary departments, and superior authorities, as well as disease and pest control managers completely unprepared. During the summer and autumn months of the past year, the virus spread across the Netherlands, Belgium, Germany, France, and Luxembourg and was eventually identified at more than 2,000 farms where numerous cattle and sheep fell ill or even perished. According to the limited epizootic knowledge on bluetongue disease, the management of the crisis was of minor success. Particularly with respect to the vectors of bluetongue disease, information is rather restricted; thus, vector control hardly is possible. Basic data regarding distribution, ecology, and behavior of the various species of biting midges in Germany is lacking. In the face of climatic changes and related ecological implications, it is essential to initiate a vector monitoring program and connect it with environmental monitoring program and

epidemiological surveillance (Baylis et al. 1998; Becker et al. 2008; Kampen et al. 2007).

The increased accuracy of climate predictions and improvements in understanding more and more the interactions between weather and infectious disease has motivated attempts to develop models which predict changes in the incidence of epidemic-prone infectious diseases. Such models are designed to provide early warning of impending epidemics which, if accurate, would be essential for epidemic preparedness and prevention (WHO 2004). Such models should be integrated into the ongoing environmental and epidemiological monitoring and designed by using geographic information systems and surface geodata. The monitoring data should be used to calculate predictive geographic information system (GIS) maps of the distribution of relevant vectors in space and time as well as to perform risk assessments (Estrada-Pena 1998; Glass et al. 1994; Kitron 2000; Kampen et al. 2007; Wakefield et al. 2000; Waller et al. 2007; Wilson 1998; Wilson et al. 1990).

Mapping the potential temperature-dependent tertian malaria transmission in Lower Saxony

Background and goal

Plasmodium vivax has a major adverse impact on global health accounting for 70–80 million clinical cases annually. It is responsible for more than 50% of malaria outside Africa, notably in Southeast Asia and Central and South America, and particularly on the Indian subcontinent. When introduced in non-endemic areas such as, nowadays, northwest Germany, tertian malaria requires special attention because diagnosis often is complicated since symptoms may occur several months after arrival from endemic areas. Since 1999, the introduction of tertian malaria in Europe has been monitored by the TropNetEurop surveillance network. From this monitoring, Mühlberger et al. (2004) concluded that malaria is a severe disease all over Europe. *P. vivax* could be identified to be the second most frequent cause of introduced malaria in Europe, except France, accounting for up to 40% of the annual cases in single countries.

The latest incidences of autochthonous malaria in Germany were reported by Weyer (1956). Whereas in the face of the current climate change research on vector-borne diseases and investigations on the population density and distribution of *Anopheles* were conducted in some European countries (Eritja et al. 2000; Kubica-Biernat 1999; Romi et al. 1997; Schaffner 1998), in Germany only poor data sets are available (Maier et al. 2003). This gap together with the rise of air temperatures and the correlated ecological changes as indicated by plant phenology throughout Ger-

many (Schröder et al. 2005) gave reason to investigate whether the former malaria region Lower Saxony is at risk of a new outbreak due to the increasing air temperatures and whether higher temperatures could prolong the seasonal transmission gate of the tertian malaria pathogen which from 1985 to 2004 lasted for 2 and 3 months, respectively.

Risk assessment requires models to support decision-making processes. Such models should combine various sources of data regarding different aspects of the disease dynamics and link these aspects with external causes or covariates serving as driving forces or as surrogates for just them. According to Hoshen and Morse (2005), most of the malaria transmission models today can be classified as follows: (1) Statistical models compare malaria transmission variables with local conditions (Killeen et al. 2000). (2) Rule-based models determine the regions in which malaria transmission is possible (Snow et al. 1998). (3) Dynamic models relate malaria transmissions to constant climate conditions (Bailey 1982). Models connecting malaria transmission and changing climate which may serve for preventive decision-making based on weather forecasts seem to be missing. Therefore, this pilot study picked up the recommendations given by Gemperli et al. (2006), Gimnig et al. (2005), Hendrickx et al. (2004), Kleinschmidt et al. (2000), Martens and Thomas (2005), and WHO (2004) and aimed at partially filling the gap. Achieving this, a mathematical model of the reproduction rate of *P. vivax* transmitted by *Anopheles atroparvus* was combined with a multivariate ecoregionalization, geostatistical surface estimation, and a GIS taking a former malaria region in Germany as an example. This paper is focused on both a summary of the results presented in more detail elsewhere (Schmidt and Schröder 2007; Schröder 2006; Schröder and Schmidt 2007; Schröder et al. 2007a, b) and on recommendations for future work in this field.

Materials and methods

The estimation of the geographical distribution of malaria vectors needs to correlate their incidences with habitat characteristics and their life stages quantitatively. To this end, all the historical *Anopheles* findings and malaria cases documented in the literature were localized and mapped in a GIS. They were supplemented by *Anopheles* findings since 1985 documented in the digital BOG-archive (Archiv Biologische Oberflächengewässer, Schröder et al. 2007a, b) or published by Wilke et al. (2006). Apart from several factors that affect the aquatic juvenile stages of *A. atroparvus*, one of the main driving forces for development is temperature. The lengths of the seasonal transmission gate were computed by use of temperature values in terms of lower development thresholds, the optimum temper-

atures, and the upper limits above which no further progress is possible were taken over from Jetten and Takken (1994). This information is essential for the subsequent identification of areas at risk. The development of the malaria pathogens inside of the vector mosquito is predominantly influenced by temperature, too. Malaria is caused by infection with an intracellular protozoan parasite of the genus *Plasmodium*. Human beings are commonly infected by *Plasmodium falciparum*, *P. vivax*, *Plasmodium ovale*, or *Plasmodium malariae*. *P. vivax* causes tertian malaria which was dominant in northwest Germany (Mühlens 1930). The modelling was performed by using data referring to *P. vivax* published by Jetten and Takken (1994).

Measurements on air temperature from 1947 to 2004 were collected from 54 meteorological stations of the German National Meteorological Service (Deutscher Wetterdienst, DWD) covering Lower Saxony. These site-specific data were integrated into the GIS and transformed to surface data by use of geostatistics (Webster and Oliver 2001). The resulting temperature maps were updated according to the climate change scenarios of the IPCC (2001) and used as input for the calculation of the basic reproduction rate R_0 (see below). The results were spatially differentiated in terms of ecologically defined land units (Schröder et al. 2006). The geostatistical surface estimations enabled the spatial link of the temperature data with the *Anopheles* findings and associated malaria incidences until the early 1950s and with the *Anopheles* findings documented in the BOG archive since 1985 (Schröder and Schmidt 2007).

The air temperature maps were used for modelling the potential of temperature-induced malaria transmission in Lower Saxony according to the basic reproduction rate R_0. This is the average number of secondary infections assuming a single infected individual is introduced into a potential host population in which each member is susceptible. If $R_0 \geq 1$, the disease will proliferate indefinitely; if $R_0 < 1$, the disease will die out (Martens et al. 1999).

$$R_0 = \frac{m*a^2*b*p*n}{-\ln(p)*r}$$

m relative density of adult female *Anopheles*
a frequency of feeding on a person expressed as a daily rate
ma   number of bites per person per day (product was set to 1, Lindsay and Thomas 2001)
a h/u
h proportion of mosquito blood meals taken from people and not from animals, also expressed as HBI (the model assumes a mean value of 0.42 for indoor-resting mosquitoes, Jetten and Takken 1994)

u length (in days) of the gonotrophic cycle (interval between mosquito blood meal and oviposition)
u $f_1/(T-g_1)$
f_1 thermal sum, measured in degree days (36.5 at a lower threshold of 9.9 °C, Jetten and Takken 1994)
T average air temperature
g_1 threshold below which development ceases (9.9 °C, Jetten and Takken 1994)
b proportion of female mosquitoes with developing parasites after taking an infected blood meal (as no value could be found in the literature for German *Anopheles*, a mean value was calculated out of records from England and the Netherlands. Thus, the assumed value for Germany is 0.14)
p daily survival probability of an adult female mosquito (the model considers a median mortality rate for *A. atroparvus* of 0.029/day, thus $p=0.97$/day, Jetten and Takken 1994)
n period of parasite development in the adult female mosquito in days: sporogonic cycle
n $f_2/(T-g_2)$
f_2 thermal sum, measured in degree days (105 at the lower threshold of 14.5 °C, Jetten and Takken 1994)
g_2 minimum temperature required for parasite development in mosquitoes (14.5 °C, Jetten and Takken 1994)
R rate of recovery of humans from infection [the usual assumption is that the duration of each infection is therefore $1/r$ days. According to Lindsay and Thomas 2001, it is assumed that an infection is present for 60 days, resulting in a value for $1/r$ of 0.0167/day]

The calculations were performed for the periods 1947–1960, 1961–1990, and 1985–2004 as well as for the future according to the best case (b.c.) and worst case (w.c.) scenarios 2020, 2060, and 2100 (IPCC 2001).

Results

The geostatistical estimation resulted in air temperature maps, maps on areas at risk of malaria outbreak, and maps on the duration of the seasonal transmission gates of the tertian malaria pathogen due to recent and future monthly mean temperatures. Each of the maps was subdivided into natural landscapes by intersection with the map on ecoregions published by Schröder et al (2006). Accordingly, the results from the spatial modelling of the reproduction rate of *P. vivax* transmitted by *A. atroparvus* could be ecoregionalized. The following paragraphs focus on the transmission gate and compare the periods 1947–1960, 1961–1990, and 1985–2004 as well as the possible future conditions in 2020, 2060, and 2100. These results were

presented as maps and tables by Schmidt and Schröder (2007), Schröder and Schmidt (2007), Schröder et al. (2007a, b).

From 1947 to 1960, areas with potential malaria transmission over 2 months per year cover 81.7% of the territory of Lower Saxony. A 3-month transmission gate would have been possible on 16.1% of the land area. The regions characterized by a 3-month risk are larger than those of 1-month or of no transmission. From 1961 to 1990, malaria transmission would have been possible over 3 months (21.8%), whereas the predominant seasonal transmission gate accounts for 2 months (74.9%). The regions with a possible *P. vivax* spread of 3 months were almost identical to those in the previous period, but the spots became larger. From 1985 to 2004, just one very small area could be identified where no transmission was possible. The rest of Lower Saxony was characterized by a potential seasonal transmission gate of 2 months (74.5%). Areas with a 3-month transmission potential covered 25% of Lower Saxony. The b.c. scenario 2020 is based on a predicted temperature increase of about 0.3°C when compared to the mean value temperatures from 1961 to 1990. The areas where no transmission of tertian malaria would be possible together with the areas of a potential 1-month seasonal transmission gate represent less than 1% of the territory. The remainder of the country is expected to be divided equally in transmission areas of 2 and 3 months. In the 2020 w.c. scenario, expecting an average air temperature rise of 0.9 °C when compared to the mean value temperatures from 1961 to 1990, malaria might be transmittable for 4 months (0.1% of the land area) for the first time. Additionally, in the whole territory of Lower Saxony, transmission is expected to be possible, and a seasonal transmission gate of 3 months prevails (93.9%). Only 6.0% of Lower Saxony may remain, representing zones with a seasonal transmission gate of 2 months. The 2060 b.c. scenario equals the 2020 w.c.: the average temperature rise since the 1961 to 1990 period is expected to be 0.9°C. The IPCC (2001) presumes an average worst case temperature rise of 3.3°C in 2060 when compared to the mean temperatures from 1961 to 1990. The transmission map of that year reveals that 5 months of transmission would dominate in Lower Saxony (94.3% of the land area). In the highlands and along the coastal zone, the transmission could be possible during 3 to 4 months. The 2100 b.c. scenario estimates a minimum climate warming of 1.4 °C when compared to the mean value temperatures from 1961 to 1990 and includes September as the fourth month with transmission of malaria. The seasonal transmission gate in most areas is expected to be possible during 3 months (76.6%). Regions with 4-month transmission cover 21.4% of Lower Saxony. Assuming the worst case, the temperature would rise to 5.8°C in 2100 when compared to the

mean value temperatures from 1961 to 1990. Then, Lower Saxony would be divided into two parts with differing seasonal transmission gates. The western part reveals a predicted seasonal transmission gate of 6 months (55.8% of the land area). A 5-month seasonal gate of malaria transmission is expected to cover 44.2% of Lower Saxony.

Discussion and conclusions

The pilot study on the potential temperature-dependent transmission of malaria in Lower Saxony could reveal that recent anopheline larvae findings in Lower Saxony could be matched with past endemic malaria zones. Using the basic reproduction rate (R_0), it could be demonstrated that during the periods 1947–1960, 1961–1990, and 1985–2004 in most parts of Lower Saxony, the temperature-dependent seasonal transmission gate was 2 months. Regarding the future, the seasonal transmission gate might take 3 (2020 w.c., 2100 b.c.) and 5 or 6 (2100 w.c.) months from May to October. Therefore, studies on the breeding site preferences of different Anophelinae species should contribute to a spatially more specific application of the basic reproduction rate.

The investigation revealed areas in Lower Saxony that are susceptible for a new tertian malaria outbreak transmitted by *A. atroparvus* due to their high summer mean temperatures. The calculations corroborate that although malaria is not an endemic disease in Germany, the risk of an autochthonous transmission does exist (Krüger et al. 2001). Pathogens of the respective malaria types could be introduced by infected travelers and in mosquitoes from endemic areas. Germany reported 150, i.e., 24.3% of all European cases of tertian malaria in 1999–2003 (Mühlberger et al. 2004). Reiter (2000) and Small et al. (2003) concluded that non-climatic factors are underestimated and, therefore, should be examined closer. However, as there is no explicit evidence so far that climate warming will not influence the distribution of malaria, there is a need for research in areas like Lower Saxony that are located in potential future risk zones. Some European countries like the U.K. and Italy have already undertaken studies in that field, concluding that climate warming would increase the malaria transmission potential (Lindsay and Thomas 2001). In Germany so far, there is no systematic risk assessment, which in close contact with environmental and epidemiological monitoring aims at identifying hot spot areas where vector-borne diseases are likely to happen. A better understanding of the malaria transmission in a given area helps to design or to optimize both monitoring and control program. GIS have already been applied for malaria surveillance as well as for malaria prevention (Gimnig et al. 2005; Kitron et al. 1994). This pilot study could prove geostatistics and GIS to be

powerful tools for the mapping of spatial patterns of potential malaria transmissions and for assessing the associated ecological factors in terms of an ecological land classification. Referring to the compilation given by Takken et al. (2005), the approach presented might be classified as sophisticated and competitive.

The model applied in this investigation is based on the basic reproduction rate (R_0), which is well established in malaria transmission risk assessments (Dietz 1993; Lindsay and Thomas 2001; Martens et al. 1999; Snow et al. 1999). However, the formula has also some deficits. The relationship between climate and transmission potential of malaria is still only partly understood. Furthermore, in addition to meteorological factors, disease transmission dynamics are influenced by many other factors with regard to the hosts, to the vectors, and other members of the affected ecosystems and interactions between them (Martens et al. 1999). Certain variables which can play a significant role in the complex dynamic process of disease spread were excluded like, e.g., precipitation, humidity, availability of mosquito breeding sites, and other ecological factors determining the developmental process of the vector mosquitoes and also hygiene and medical care. If temperature was the only relevant parameter, malaria would not have been eradicated in Europe, as demonstrated by the risk modelling. It would be wrong to confuse the modelling results with reality. The modelling results should rather be considered as an approximation and a useful tool to determine areas at risk and a precondition to control them (Smith and McKenzie 2004). The impact of climate change poses enormous challenges to scientists because of the considerable amount of complexity and uncertainty: The same environmental change may induce quite different effects in different places or times. Thus, there is a strong need for investigations on the short- and long-term dynamics of complex systems, and this requires an interdisciplinary approach integrating, among others, the fields of biogeography, ecology, and both medical and social sciences.

The prediction of environmental change and the resulting health impacts encounters several difficulties. Some of them are of scientific nature and refer to a deficient understanding of the actual processes. Some of the uncertainties are related to the modeling of the relation between the increase of temperature and humidity on the one hand and mosquito breeding, survival, and biting behavior on the other. Furthermore, uncertainties pertain to what can be foreseen about future emissions of greenhouse gases. Finally, uncertainty may be caused by data compilation. Several models have been developed to describe a specific bioclimatic envelope for malaria. Those of them which match the presence of a particular species with a discrete range of temperature and precipitation parameters can be used to project the effect of climate change on the spatial patterns of vector distribution (Lindsay et al. 1998). As demonstrated in this investigation and those of Hay et al. (2002) and Patz et al. (2002), grid maps interpolated from meteorological data often provide the basis for modeling the interrelationship between vectors, vector-borne diseases, and climate. However, such approaches cannot include all factors that affect the distribution of species. For example, local barriers and interactions between species are important factors that determine whether species colonize suitable habitats (Davis et al. 1998). Martin and Lefebvre (1995) could estimate the changes in malaria risk based on moisture and minimum and maximum temperatures required for parasite development. The modeling results fit well with the distribution of malaria in the 19th century and the 1990s. Rogers and Randolph (2000) found that malaria will increase in some areas and decrease in others by 2050.

Martens et al. (1999) developed a model that is basically similar to the approach applied for modeling the temperature-dependent increase of the potential malaria transmission in Lower Saxony: climate-change scenarios were linked with the formula for the basic reproduction rate (R_0) to calculate the epidemic potential of a malaria-vectoring mosquito population. The basic reproduction rate is defined as the number of new cases of a given disease that will arise from one case when introduced into a nonimmune host population during a single transmission cycle (Anderson and May 1991). Model variables that are sensitive to temperature include mosquito density, feeding frequency, survival, and extrinsic incubation period. The extrinsic incubation period, i.e., the development of the parasite in the mosquito, is of particular importance. The minimum temperature for parasite development is the limiting factor for malaria transmission in many areas.

Malaria incidence is strongly influenced by geography and prevailing climate. However, malaria incidences correlate with per capita income, too. Apportioning malaria causality between environment and socioeconomic conditions is therefore problematic (Martens and Thomas 2005). The problem of modeling the impacts of global change processes on human health is that it has to cope with a variety of processes that operate on different temporal and spatial levels and differ in complexity: Modeling has to link processes that differ by nature, such as physical processes, monetary processes, social processes, and policy processes. Furthermore, modeling has to deal with the fundamental problem of predicting across temporal and spatial scales. Despite such limitations of modeling, models draw attention to the climate change-related impacts and point out the relative importance of the factors. This could help to increase the understanding of the impacts of climate change and to identify gaps in data and knowledge needed to improve the analysis of these effects.

Recommendations

Global change is likely to affect human and animal health via complex interactions that may affect a vector-borne disease: the mosquito vector, the parasite, human hosts, climate, topography, vegetation, aquatic habitats, demography, health care, and socioeconomic status. Whether the pilot study would have been focused not on malaria but on dengue or leishmaniasis, the conclusions and recommendations would not have been much different. Environmental change such as climate change will affect the incidence of vector-borne diseases remarkably. The uncertainty of these impacts results from the level of change as well as from the spatial and temporal patterns. Until recently, it seemed difficult to provide concrete evidence that environmental change had caused a significant positive impact on a vector-borne disease, leading to increased cases of disease. Takken et al. (2005) provided evidence that environmental degradation, accelerated by increased precipitation, and higher temperatures favor vector-borne diseases. Hence, it is expected that transmission will increase in those countries which are too poor to provide adequate health care. By contrast, malaria is unlikely to return to former endemic countries as, for example, Germany because of the high standard of living and because environmental measures prevent a return of malaria endemicity, even under climate change (Rogers and Randolph 2000).

It is generally accepted that transmission of many infectious diseases is affected by climatic conditions. Diseases caused by pathogens which spend part of their life cycle outside of human or other warm-blooded hosts are particularly climate-sensitive. Some of these diseases are among the most important global causes of mortality and morbidity, particularly in low-income societies in developing countries. In many environments, these diseases occur as epidemics, possibly triggered by changes in climatic conditions favoring higher transmission rates. Following Takken et al. (2005), global environmental changes will cause both increases and decreases in the areas appropriate for vector-borne diseases transmission, but a bunch of factors will determine the susceptibility of respective countries for these diseases. Assessments on the spatial and temporal patterns should be elaborated from both an environmental and a socioeconomic point of view.

WHO (2004) evaluated the potential of climate-based disease early warning systems (EWS) as an instrument of improving preparedness for, and response to, epidemics. Climate-sensitive diseases were identified as being of major public health importance. Thus, WHO (2004) evaluated the current state of the art in climate-based modeling of these diseases, as well as future requirements and recommendations. Climate-based disease EWS go back to Gill (1921, 1923). Nowadays, in times of climate change and since climate and other environmental data, GIS and other tools required to link these observations with disease data have become widely available, there is clear justification for investigating the potential of climate-based EWS regarding their usefulness in planning of control interventions. Following WHO (2004), no large scale EWS is yet in place, but for some diseases, such as malaria and Rift Valley fever, early warning systems based on climatic conditions are going to be used in selected locations to alert ministries of health to the potential for increased risk of outbreaks and to improve epidemic preparedness. However, the use of such models is just beginning, and experience with their use is limited for several reasons: Affordable and accessible data as well as analytical tools have become widely available just recently. Therefore, the development of EWS is at a relatively early stage. As few studies have been published, there are no generally agreed criteria for accessing predictive accuracy. Most EWS have not been tested in locations outside of the original study area, focus solely on climate factors, and do not encompass other influences. Therefore, it is difficult to evaluate quality and utility of existing systems. High-quality, long-term disease and environmental data must be available for the development of models relating climate and other environmental factors to infectious disease. Up to now, disease and climate modeling has been restricted to discrete datasets for relatively small areas. This is useful for methodological reasons, but there are relevant questions left concerning the extent to which findings from these studies can be generalized spatially and the assessment of the prediction accuracy. Predictive models should be tested in locations covering a broad range of ecological conditions. Non-climatic influences on variations in disease rates should be investigated, too.

EWS should be developed according to the principles of public health surveillance (Brookmeyer and Stroup 2004; Teutsch and Churchill 1994; Waller and Gotway 2004) as an internet-based geographical information system (WebGIS) using open source software.

The open source initiative (OSI) specifies the concept of open source by several criteria (Williams 2002). The access to the source code has to be free without any constraints in terms of circulation of the software to third parties or certain users and the range of use. The license does not allow the discrimination of anyone. The software mostly is available and downloadable via the internet, and modifications of the source code have to be transferred under the same terms of use. It is allowed to use parts of the source code in other free software products. It is only allowed to use the concept open source if the software is protected by one of the license models of the OSI. The most commonly used license of the Free Software Foundation is the GNU Public Licence. It is not allowed to demand money for the

acquisition and the use of the software. This does not include a fee for the installation or user-based modifications of the software.

Nowadays, open source is an alternative compared to proprietary software but without any warranty for the function of the software. Users are not only people at home; offices and also companies and public authorities are using open source software in all fields of information technology. Examples are operating systems for servers like Linux and server-based software like http servers or content management systems and desktop software like GRASS GIS, JUMP, or Open Office. Proprietary software products have their own licenses and copyrights. Very often, the users obtain a license for a year and have to pay the charges annually. The circulation of the software mostly is forbidden, and the source code is hidden because it is the commercial basis (Spath and Günther 2005).

The standards of the Open Geospatial Consortium (OGC) are considered as well as the access to spatial and measured data and metadata of the disease surveillance and environmental monitoring programs. The standards of the OGC constitute the base of interoperable networks for spatial data infrastructures and additional attribute data located anywhere in the world. They are designed by using ISO-, CEN-, and other standards as basis and implemented into the most GIS software (Korduan and Zehner 2008). The most important standards of the OGC are the open web services (OWS) which are interfaces for a standardized access to remotely located geodata (Müller and Augstein 2005). The client/server-model describes web services as operations which provide information in different formats (mime-types; Peng and Tsou 2003). Client requests are handled by the server returning standardized contents. The communication between client and server is effected by HTTP-get/post-variables (Dreesmann 2004). At least a web map service is needed to enable geodata access. Another example for OWS is the web feature service (WFS) which provides vector-based geodata instead of raster data, like a web map service (WMS) does. The catalogue service offers metadata management (Müller and Augstein 2005). The simple features implementation specifications (e.g., SQL) define interfaces which provide a transparent access to geodata in heterogeneous and data publishing systems. Another and surely interesting standard for WebGIS is the web processing service (WPS) which allows the standardized use of online GIS functions, for example, with the open source software GRASS GIS.

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