Risk assessment of vector-borne diseases for Public Health governance

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Abstract

Objectives. In the context of public health, risk governance (or risk analysis) is a framework for the assessment and subsequent management and/or control of the danger posed by an identified disease threat. Generic frameworks in which to carry out risk assessment have been developed by various agencies. These include monitoring, data collection, statistical analysis and dissemination. Due to the inherent complexity of disease systems, however, the generic approach must be modified for individual, disease-specific risk assessment frameworks.

Study design. The analysis was based on the review of the current risk assessments of vector-borne diseases adopted by the main Public Health organisations (OIE, WHO, ECDC, FAO, CDC etc…).

Methods. Literature, legislation and statistical assessment of the risk analysis frameworks.

Results. This review outlines the need for the development of a general public health risk assessment method for vector-borne diseases, in order to guarantee that sufficient information is gathered to apply robust models of risk assessment. Stochastic (especially spatial) methods, often in Bayesian frameworks are now gaining prominence in standard risk assessment procedures because of their ability to assess accurately model uncertainties.

Conclusions. Risk assessment needs to be addressed quantitatively wherever possible, and submitted with its quality assessment in order to enable successful public health measures to be adopted. In terms of current practice, often a series of different models and analyses are applied to the same problem, with results and outcomes that are difficult to
compare because of the unknown model and data uncertainties. Therefore, the risk assessment areas in need of further research are identified in this article.

*Keywords*: risk governance, risk assessment, public health governance, vector-borne diseases, statistical analysis.
1. Introduction

Public Health (PH) can be defined as the activities engaged in by governments and organisations to prevent disease and to ensure a healthy population. This includes the assessment and monitoring of the health of communities and populations at risk, intervention, education, and formulation of public policies, and encompasses all issues that may be detrimental to health. In terms of Public Health, risk has been defined by medical epidemiologists and health organizations as “the probability of disease developing in an individual in a specified time interval.” More generally, the Society for Risk Analysis (SRA) defined risk as “the potential for realization of unwanted, adverse consequences to human life, health, property, or the environment; estimation of risk is usually based on the expected value of the probability of the event occurring times the consequence of the event given that it has occurred.” In econometrics, risk is quantified by the “absolute value of expected losses.” Notice that in these latter two definitions the probabilistic concept of risk is conflated with some idea of the (fixed or calculable) economic cost outcome should that risk be realised.

PH risk governance is a framework that includes risk assessment (or risk estimation), risk management and risk communication. In this manuscript we focus on one category of public health challenges, the risk assessment of vector-borne diseases (human and/or animal illness transmitted by arthropods) which, at least in the tropics, have a huge impact on human health and well-being (for example, WHO estimated there were 627,000 deaths among 207 million cases of malaria in 2012). Emerging vector-borne diseases are of increasing concern in Europe and North America (West Nile virus, chikunguya, malaria and dengue for instance) some with autochthonous cases.
Especially in the case of vector-borne diseases, because of their complexity, the metric used for risk is not uniquely defined. Often risk is synonymous with vector or host suitability, the basic reproduction number $R_0$, vector capacity, vector presence/absence, prevalence or incidence of the disease or many others. The same diversity is found in model selection, data resolution, the predictor variables, their transformation, and the input parameters (e.g. models coefficients applied to different areas/events) used to model risk, even for the same disease (e.g. for Lyme disease). Hence a deep understanding of the various metrics and models used for estimating risk is of primary importance, especially when previously obtained parameters, values and models are applied outside the domain of the original model fitting (e.g. in the case of newly emerging diseases).

The goal here is to integrate risk assessment or estimation theory (and models) for vector-borne diseases with the present regulatory, and sometimes mandatory, system of risk governance, as defined by the main health organizations.

2. Risk governance in international public health organizations and some national agencies.

Table 1 presents some key contributions to general risk-related policy over the last fifty years. From the initial basic statements of risk governance guidelines, procedures have developed into clear conceptual frameworks allowing a standard approach to be adopted. Most recently the complementary roles of quantitative and qualitative methods have been directly addressed along with the understanding that an estimation of uncertainty is vital to any risk analysis.
The concept of risk governance as a combination of risk assessment, risk management and risk communication (or “translating knowledge”\textsuperscript{16} into advice for informative/legal actions\textsuperscript{17}) originated in the 1960s and 1970s when concerns were raised over environmental carcinogens and food additives\textsuperscript{18 19 20 21 22}. Subsequently risk governance concepts were formulated by individual scientists\textsuperscript{19}, and by national and international agencies\textsuperscript{20}, with a concentration on cancer and harmful chemicals\textsuperscript{21, 22}. In the 1990s, risk assessment became mandatory in Europe for environmental, epidemiological and food health threats (i.e. Council Directive 89/391/ECC, the Decision No 2119 of 1998/EC, the European Commission Regulation 178/EC of 2002), was enshrined within the European Union Risk Assessment System and was managed by DG SANCO.

The fundamentals of risk governance are similar in the various frameworks of Table 1 and based on the concepts defined by the Red Book and by the CODEX of the FAO/WHO\textsuperscript{23}. With these documents the division of risk governance into risk assessment, risk management and risk communication becomes the standard form for risk governance for any type of risk.

None of the frameworks presented in Table 1 imposes a specific method of risk assessment. Indeed, a unique risk assessment method for Public Health risk governance does not yet exist. The following section outlines the current statistical approaches to risk assessment as a contribution to developing such a method. It concentrates on vector-borne diseases because although these have historically been neglected in many risk assessment frameworks they are likely to become increasingly important in temperate regions in the future.

To date, risk assessment of vector-borne and other diseases for Public Health applications has depended heavily upon the modellers and what they can and cannot do with the data available. The choice of the model depends on the aetiology of the disease in question. For example, when aetiology is unknown, studies are usually population-based (e.g. smoking/pollutants related cancers). Usually very large sample sizes are required to remove obvious biases and to reveal what are often very low incremental probabilities of disease risk. In most vector-borne diseases the aetiology is well established. Insect or tick ‘vectors’ pick up infections (i.e. become infected) when they take blood from infectious vertebrate hosts. The vectors in turn become infectious (i.e. capable of transmitting the infection to another vertebrate host) only after a period of incubation which may take several days (insects) or even months (ticks) and is referred to as extrinsic incubation period (EIP). Hence a minimum of three species are involved in vector-borne disease transmission (host, vector and pathogen). In fact such transmission often involves numerous and complex vector and zoonotic (domestic and wild animal) components. In these cases even if risk assessment can be more individual-based, or based on identifiable sub-groups, for example focussed only on those people living where vectors can be found, the number of parameters and variables needed would be greater than is typically used in other sorts of public health models. More complex systems need more research investment to reach the same level of understanding but vector-borne diseases have been neglected in comparison with other diseases (e.g. cancer), probably because of their lack of importance in the developed world.
In 2006, and following an outbreak of the mosquito-borne disease chikungunya (CHIK) in Asia, destination of many tourists and others from Europe, the European Centre for Disease Prevention and Control (ECDC) conducted a CHIK risk assessment for Europe. The risk assessment was based on the knowledge that infected and infectious travellers were returning to Europe, in some cases to places where a known vector of chikungunya, the Asian tiger mosquito *Aedes albopictus*, had already established (in Europe, this mosquito was first reported in Albania in 1979, and in Italy in 1990). By studying the current numbers of recorded cases in endemic areas as well as imported cases and the presence of local vector species, the ECDC concluded there was a risk of local acquisitions of CHIK virus in Europe, although the magnitude of this risk could not be determined. Quantitative models were not applied because of the lack of knowledge of the response of the virus to the environmental conditions of a new geographic area, the preventative measures on the parts of both travellers and health professions, the potential of further spread in southern Europe of *Ae. albopictus* and finally the competence of local mosquitoes to transmit the virus. In 2009, following a large outbreak of CHIK in Italy in 2007 and after a subsequent large-scale entomological survey, the ECDC published a first risk map for *Ae. albopictus* in Europe, based on a random forest model and multi-criteria analysis applied to entomological and environmental datasets. As in all other cases, however, a risk map of a putative vector is not the same as a risk map of the disease it transmits. ‘Anophelism without malaria’ (i.e. the occurrence of the vector *Anopheles* without the malaria) is a familiar concept to malariologists, and a similar effect is likely to apply to all other vector-borne diseases.
Disease pathogens potentially transmitted by many different mosquito species are even less likely to be described by risk maps of just one, or even several of their vector species. For example, the European Union has made several attempts to assess the risk to Europe of Rift Valley fever (the transmission of which in Africa involves several different mosquito species) but, due to the complexity of the disease epidemiology and the difficulties in the transmission parameterization, the risk assessments were predominantly qualitative.  

Similar problems arise with diseases of veterinary importance, especially those of high economic impact such as bluetongue (BT), which provoked an extensive legislative response (Directive 75/EC of 2000, EC Regulation 178 of 2002, Commission Decision 393/EC of 2005, Regulation 1266/EC of 2007; Decision, 367/EC, Regulation 394/EC of 2008, Regulation 1304/EC of 2008, Decision 655/EC of 2008, Decision 19/EC of 2009, Regulation 1156/EC of 2009); or foot-and-mouth in the UK in 2001. In both cases control activities against the diseases were eventually informed by predictive risk models each of which subsequently came in for a certain amount of criticism because of the ways in which the models were formulated (including the assumptions on which the models were based), and the values of the models parameters used.

These examples show the difficulties in applying model-based solutions to human and non-human, vector-borne and directly transmitted disease outbreak emergencies when only inadequate or incomplete data are available. This will inevitably be the case with emerging diseases (for example chikungunya, Rift Valley fever and West Nile virus in
Europe) but may also apply even to neglected but long-established diseases, such as Lyme disease.\textsuperscript{8,15}

The examples clearly show that, in the face of an imminent public or veterinary health threat, control agencies have little time to worry about the characteristics of disease models. Instead, they must be seen to be doing something to combat the diseases, whether or not this is informed by quantitative models. Sometimes this involves excessive application of the precautionary principle, for example the localised and repeated use of insecticide which although it diminishes disease risk may not eliminate it entirely but certainly does create other environmental and health risks.\textsuperscript{30} The greater the impact of an event, or the longer its duration, the more likely an inappropriate control (either too much or too little; the precautionary approach encourages the former) will be applied. Policy must therefore encourage the development of robust models in advance of any new threat and, ideally, these models should be tested during simulation exercises,\textsuperscript{15} as was done in 2004 in the aftermath of the 2001 foot-and-mouth outbreak in the UK and following no fewer than three independent reports into the outbreak\textsuperscript{31} and one Department of Health longitudinal study on the health and social impacts of it.\textsuperscript{32}

But what should these robust models look like, and how may they be developed? The final section explores some of the options.


The distinction made in the previous section, between models for diseases without or with known aetiologies, highlights the dichotomy between statistical and biological approaches to disease modelling. Statistical models look for statistical associations
between a dependent variable (e.g. the number or percentage of disease cases) and a suite of independent variables that may be either correlated with risk, indicators of risk or causal drivers of risk (the distinction between these three different types of independent variables is not obvious at the start of many studies but tends to become clearer over time, as was the case with lung cancer). The statistical model of risk therefore seeks robust statistical descriptions of levels of risk based on the measured levels of the independent variables. Various kinds of regression and odds ratio models can be employed here.

In contrast to statistical models, biological models consist of components, each of which captures one or other important biological feature of the know infection pathway. For example, a model for the extrinsic incubation period (defined above) will incorporate temperature as a causal variable determining the duration of the EIP. During the EIP, however, the insect may die either from abiotic (temperature, rainfall) or biotic (predation) effects each of which may be incorporated into full biological models of disease transmission. Characteristic of many biological systems are thresholds (pathogens will not develop at all below a threshold temperature), break-points (mortalities may be low at low densities and then increase above a certain level of abundance of competitors, parasites or predators of the vectors) and non-linearities (insect mortality rates increase at increasing rates at the upper end of their thermal tolerance ranges). The ideal biological model must therefore be able to describe all aspects of each and every threshold, break-point and non-linearity at all points of the transmission pathway and this is often beyond the limits of our present knowledge and capabilities. Instead, relatively simplistic but still biologically-based models can go a long way towards describing the overall characteristics of diseases, if not their finer points. Classic examples of simple but powerful biological models for
vector-borne diseases involve calculation of the key epidemiological variable, R0, the
disease’s basic reproductive number, or the number of secondary cases arising in an
totally susceptible population from one case of the disease at the present time. This index
can be used to predict if a vector-borne disease can establish after introduction in a certain
area and under certain climatic and environmental conditions. It has several advantages
over statistical methods, such as the clear biological and epidemiological interpretation of
its values, and the flexibility for simulating different scenarios. However, even the
relatively simplified R0 equation requires estimates of many different parameters and the
knowledge of the relevant biological processes involved (for example, the R0 equation for
insect vectors is quite different from that for ticks). In addition, theoretical studies show
that R0 is related to disease prevalence at equilibrium (i.e. the former might therefore be
used to predict the latter). But it is a moot point as to how often diseases are in fact in
equilibrium, and therefore how often the R0 approach is applicable; vector-borne diseases
are often seasonal and many emerging and re-emerging vector-borne diseases of interest are
clearly not in equilibrium.

An alternative approach for vector-borne diseases is therefore to fall back on the sorts
of statistical methods applied to diseases of unknown aetiology. This would appear to be a
backward step (why ignore all the information we have on causal pathways in the
transmission of vector-borne diseases?) but it may be the only approach we can take when
we are unclear about key aspects of transmission, all of which must be understood for the
biological approach to succeed. For example, West Nile virus in the USA infects at least
100 species of mammals and birds and is potentially transmitted by up to 70 or more
different mosquito species; what chance, ever, is there of being able to quantify the myriad
interactions there might be between this number of vectors and hosts? In such a context, statistical models ignore many of the details of biological transmission and look for direct correlations between environmental variables and vector or disease outcomes. This approach clearly ‘short-circuits’ the often tortuous biological pathways involved in transmission, and depends for its success on close, predictable and unchanging links between predictor and predicted variables. That this approach is often successful is due entirely to the sensitivity of many vector-borne diseases to climate (most of the parameters of the R0 equation for vector-borne diseases are vector-related and hence sensitive to climate and environment). Risk assessments here are based on modelled correlations between the vector’s distribution and or abundance, or past disease presence/incidence, and sets of environmental variables. In the first case (based on vector distribution/abundance), analyses are excellent predictors of risk to individuals. It is, however, difficult to translate them into measures of human disease incidence or prevalence, both population-level measures of risk. In the second (based on past incidence/prevalence) the risk assessment is clearly based on the past exposure of the local human population to disease risk, something that is affected not just by the absolute risk in each area, but by the amount of human exposure to that risk, dependent on both human population density and behaviour. The resulting risk assessment, therefore involves the often unacknowledged component of human behaviour, which is sometimes more important than human population in determining disease incidence or prevalence.

Commercial trade and human travel add additional levels of complexity. Examples here include the connectivity/mobility analysis of humans (e.g. air travel, and goods) in which risk is often calculated from a crude or probabilistic combination of suitable
habitat in the arrival area for the pathogen or vector (brought in by tourism or trade) and the
rate at which such importation occurs.

As a result of the application of the above approaches, risk can be expressed as
incidence, prevalence, occurrence, cumulative cases (as for the West Nile Virus map used
by CDC) or, alternatively, as other metrics that generally represent a portion of the disease
transmission process, for example the probability of pathogen establishment according to
the probability of introduction\textsuperscript{24, 35}, the probability of contact between host and vectors but
not humans\textsuperscript{36} or between host capacities (a rate of vector infection from the host species),
vector-host feeding preferences and, finally, human biting rates per vector\textsuperscript{37}. Risk metrics
are hence based on the information available (see the attempt of\textsuperscript{38} to produce a uniform
scheme) and are rarely expressed as a probability (apart from the few examples given here),
which is the canonical form for risk as defined for public health (see the introduction
section).

The statistical and mechanistic approaches to risk modelling and prediction are many
and varied, including discriminant analysis, generalized linear models (e.g. logistic
regression, autoregressive regression, Poisson models etc…), generalized additive models,
mixed models, tree based classifications, fractals, spectral density, wavelets, agent based,
cellular automata, maximum entropy, multicriteria analysis, community models among
others\textsuperscript{12, 24, 36, 39, 40}. Examples of applications of these models can be found in the
quantitative risk assessment as defined by the World Organisation for Animal Health (OIE)
(Terrestrial Animal Health Code\textsuperscript{41}); WHO (numerical approaches to the quantification of
risk\textsuperscript{42}); International Risk Governance Council (IRGC)\textsuperscript{43}; EFSA\textsuperscript{44}; International
It is well established that different models often give different outputs (e.g. the dengue models compared in [47]), hence a procedure for their validation and comparison is needed.

A further complication, which is often ignored in vector and disease risk mapping, is that of spatial dependency of the disease, which arises for two main reasons. Firstly, simple geographic proximity means that epidemiological outcomes often depend on disease events occurring in nearby locations (e.g. pathogen transmission may occur between areas that are close to each other, or infected vectors might fly, or infected humans move, between them). Secondly the environmental conditions that favour the occurrence of a vector or disease in one area are likely to be similar in nearby areas and so promote the occurrence of the same disease in those areas, too. Whatever the cause of spatial dependency is, it may be used to improve the predictions of vector-borne disease models to render them truly spatial. Spatial dependency is included in models in many different ways, from the simple auto-logistic regression approach of considering the occurrence of the species only in the most adjacent grid squares to the more complex approach of using the techniques of kriging and cokriging (directly or combined with deterministic models). The unwary biologist or modeller should be warned that kriging and cokriging often applies only to predicting errors from a modelled ‘mean’ surface, the latter imagined to be constant or trending in a simple way (e.g. dependent on environmental variables) [48]. The biological interest is therefore really in the trend surface rather than in the kriging results [49]. Kriging thus contributes an important and usually neglected component to risk maps; the prediction of errors indicating the variability of the modelled result at different points in space (and time, with spatio-temporal
models), and hence the statistical significance of the trend. The size of such errors
generally depends upon the amount and variability of the data available; errors are
minimized when there is a sufficient amount of local data, all with similar mean values
(which is not always the case for vector-borne diseases such as malaria) 50.

Today we are still experiencing risk maps 51, 52 based simply on the un-modelled
distribution of diseases, pathogens or conditions, or real-time data from online warning
systems and media sources (Table 2), or from informal exchanges between public health
professionals ("Event-based" surveillance) 53. Despite increasing use of disease mapping,
for which often quality cannot be evaluated, it is urgent to define a policy for disease risk
mapping assessment (within the risk governance framework) in order to obtain products of
similar statistical quality.

Uncertainty is a common feature of risk assessment of meteorological events and
earthquakes, but it is usually not applied in vector-borne disease risk mapping. In the past,
uncertainty was obtained from sensitivity analyses by simply varying (within fixed ranges)
the values chosen for the parameters and variables. Rarely do sensitivity analyses consider
variation of more than one parameter/variable at a time. Interactions between variables may
be investigated using hyper-cube sampling of variables, but gives no real indication of the
likely variability of each of the parameters in the field 54.

Today, the most successful models use a Bayesian approach to predicting both the level of
risk and the uncertainty of that prediction 55. This approach is usually applied when
knowledge of the process is available and converted into distributional forms, but is also
used for hypothesis testing and uncertainty measurement. These new Bayesian approaches
are ideal for the relatively small datasets often found in epidemiology, for which the
frequentist approaches are unable to include prior knowledge although they are robust for small sample size. Frequentist studies are based on the hypothetical question “Given ten thousand versions of reality, on how many occasions would we observe an outcome as extreme as that shown by the data?” If the occasions are very few, then the result is likely to be ‘significant’, i.e. it is unlikely to be a member of the ten thousand versions of reality generated by the hypothesis being tested. Unfortunately, however, there is only one version of reality and so the above question remains a hypothetical one. The one version of reality, that we do have, generates the data that we record. These data may have been produced by a variety of different mechanisms which we can test in the Bayesian modelling approach to answer the question; “Given this particular dataset, is hypothesis/model A more likely than hypothesis/model B?” Not only do Bayesian statistics allow us to distinguish between alternative hypotheses, they also involve estimation of the errors of the different parameters involved, allowing the output models not only to predict mean risk, but also the errors and uncertainties of those mean risks. From the practical point of view, the main differences between the Bayesian and the more traditional frequentist approach are the use of prior and posterior distributions. The latter is the main output of the Bayesian approach and expresses as a probability, the weighted average of the prior (a priori knowledge) and the data (through its likelihood) via the Bayesian theorem.

A third model category exists in Public Health applications, based on expert opinions, or other experience, and referred to as participatory models. An example is the vaccination-advice map for yellow fever based on expert opinion that decided specific thresholds for certain environmental variables thought to be key to transmission (for
example, elevation, land cover etc…)\(^1\). This map categorises risk into four classes: endemic, transitional, low risk and no risk\(^1\). Vaccination is “recommended” for those areas that are classified as endemic and transitional, and also for low risk areas if a prolonged stay is expected. In brief, this semi-quantitative risk assessment is the result of a complex process involving data acquisition, data analysis and data discussion in which modellers, national experts and epidemiologists are involved\(^6\). The role of the health practitioner using such a map is to merge the information given by the guidelines with individual characteristics of the person to be exposed to the disease risk (age, gender, medical history, vaccination history) and trip information (destination, departure date, duration of the travel, purpose of travel)\(^2\). Whilst the final decision here (to vaccinate or not) is based on a subjective weighing of the evidence by the medical practitioner or health agency involved, this decision is likely to be better informed if based upon more accurate, quantitative risk maps. The unplanned surveillance and control in Sudan, for areas that are recognised of endemic transmission for yellow fever, may have contribute to the recent uncontrolled outbreaks in Sudan, which required a mass-vaccination treatment of the population\(^3\).

In summary, while risk governance is a framework that is very homogeneous between international organisations and scientists\(^1\), the risk assessment component is not standardised, and often not defined at all. For example, in the OIE terrestrial code a list of statistics necessary for risk assessment is given without mention of their uncertainty. EFSA describes the full risk assessment framework, which includes uncertainty, but is not flexible enough to be adapted for general use. Other agencies require semi-quantitative approaches
with a strong stakeholder component (IRGC and WHO). The seminal work of 1 adapted
the IRGC risk governance framework to the case of vector-borne diseases for which they
provide generic, but not methodological, guidelines for a pre-assessment and appraisal of
the risk. Apart from the useful indication on the data requested for public health utility, the
authors did not however, explore the issues related to the existing variability in the data,
methods and outputs used for risk estimation. Risk assessment for vector-borne diseases
was only defined in its general aspects, and a framework which guarantees high quality
disease mapping and comparable analyses, was missing.

5. Conclusions.

Risk governance is the main component of PH measures (prevention, management,
surveillance and communication) and is scientifically and legally defined. Although the
same basic framework is followed, each risk assessment tends to be uniquely determined by
the details of the particular disease under study, the data available for it and the region and
time period over which those data were collected. In a recent review on the impact of
drought on vector-borne diseases for UK 64, the authors underlined the undefined risk
associated with climate change and human adaptation due to the lack of relevant data 65. In
addition, the competence of existing or newly introduced insect vectors in Europe to
transmit diseases that are currently confined mostly to the tropics 36,11,66 are unknown as
they ways in which they are transported 24,35,37. At present time, when different models
and analyses are applied to the same problem, they often produce results that are difficult to
compare quantitatively because of unknown model and data uncertainties.
Hence, new dynamic and flexible approaches are required, determined by the Public Health framework and the inherent complexity and unique characteristics of each system being investigated.

Anthropological, zoological or entomological (or a combination of these) disease risk assessment needs to be addressed quantitatively, wherever possible, and submitted with a quality assessment in order to evaluate tolerability and adaptability of the risk; and to enable successful public health measures to be adopted, since simple interventions are often impossible (for many vector-borne diseases there is no available treatment or vaccine).

Successful application of control measures in the future depends on the reliability of the uncertainty estimations. Even if uncertainty sometimes cannot be reduced, it is important for policy-makers to have an accurate estimate of it to support action if the risk estimates warrant it, in order to avoid over- and under-estimations of risk.

In conclusion we make the following recommendations for the future:

1) A standard risk assessment within a risk governance framework for vector-borne diseases as proposed by should be produced and accepted, that includes experiences and lessons from the various agencies involved in risk assessment (e.g. OIE, FAO, EFSA, WHO, SANCO) and from OneHealth actions;

2) A comparative review should be carried out of Public Health model selection decisions and model evaluations (as done by for species’ distributions);

3) Quantitative approaches should be used in participatory analyses leading to risk assessment.
435 4) In conformity with the definition of risk in public health, risk should be expressed
436 as a probability;
437 5) All models used for making Public Health decisions should include estimates of
438 model uncertainty 75;
439 6) The spatial and temporal validity of models (i.e. up to what distances and times
440 are the model error levels acceptable) should always be assessed;
441 7) Finally, data should routinely be gathered that can contribute to Public Health
442 preparedness for future outbreaks of vector-borne and other diseases.
443 preparedness for which quality and availability of the data need to be assessed for
444 future emergencies.

445

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451

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454 decision to submit the manuscript for publication.

455

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457 subjects.
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85. Team HW. Travax-Travel Health-HP. 2006.


Table 1. Main documents defining risk analysis for public health purposes.

<table>
<thead>
<tr>
<th>Year</th>
<th>Agency</th>
<th>Document</th>
</tr>
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<tbody>
<tr>
<td>1981</td>
<td>The Society for Risk Analysis (SRA)</td>
<td>Vision Statement</td>
</tr>
<tr>
<td>1983</td>
<td>National Research Council of the US (NRC)</td>
<td>Red Book</td>
</tr>
<tr>
<td>1995</td>
<td>Food and Agriculture Organisation of United Nations (FAO)</td>
<td>Risk analysis and food: the experts’ view</td>
</tr>
<tr>
<td>2002</td>
<td>European Commission</td>
<td>Regulation 178/2002</td>
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<tr>
<td>2005</td>
<td>European Commission</td>
<td>Regulation 851/2004</td>
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<tr>
<td>2005</td>
<td>International Risk Governance Council (IRGC)</td>
<td>White paper on risk governance (towards an integrative approach)</td>
</tr>
<tr>
<td>2007</td>
<td>European Commission</td>
<td>White paper on the health strategy for years 2008-2013</td>
</tr>
<tr>
<td>2009</td>
<td>National Research Council of the US (NRC)</td>
<td>Science and Decisions: Advancing Risk Assessment</td>
</tr>
<tr>
<td>2012</td>
<td>European Food Safety Authority</td>
<td>Guidance on risk assessment for animal welfare</td>
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Table 2. Surveillance and risk communication websites with a focus on vector-borne diseases.

<table>
<thead>
<tr>
<th>Organisation</th>
<th>Description</th>
<th>Website</th>
<th>Reference</th>
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<tbody>
<tr>
<td>CDC</td>
<td>Arbonet is a site for displaying vector-borne disease maps based solely on recorded cases of each disease (i.e. not on models). Maps are updated continuously as new surveillance data are acquired.</td>
<td><a href="http://www.cdc.gov/ncidod/dvbid/westnile/USGS_frame.html">http://www.cdc.gov/ncidod/dvbid/westnile/USGS_frame.html</a></td>
<td>86</td>
</tr>
<tr>
<td>ProMed</td>
<td>An internet reporting system aimed at providing early warning of global threats to human health</td>
<td><a href="http://www.promedmail.org/">http://www.promedmail.org/</a></td>
<td>87</td>
</tr>
<tr>
<td>HealthMap</td>
<td>An online cartographic resource maintained by the Computational Epidemiology Group of the Children's Hospital, Boston, U.S.A. The site offers real-time surveillance of emerging health threats around the world. It uses an algorithm that monitors eleven sources of news and reports, among them</td>
<td><a href="http://healthmap.org/en/">http://healthmap.org/en/</a></td>
<td>88</td>
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<tr>
<td></td>
<td>Description</td>
<td>Website</td>
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<td>ProMED-mail, Google News, WHO, OIE and ECDC.</td>
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<td>BioCaster</td>
<td>Real-time surveillance website that tracks over 1700 RSS feeds and plots emerging health events in Google Maps.</td>
<td><a href="http://born.nii.ac.jp/_dev/">http://born.nii.ac.jp/_dev/</a></td>
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<tr>
<td>EpiSPIDER</td>
<td>Identifies potential outbreaks by screening news reports and Twitter feeds (only English texts) with a naive Bayesian classification service, then refining the output with web-based text miners.</td>
<td><a href="http://www.epispider.org/">http://www.epispider.org/</a></td>
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<td>FAO</td>
<td>EMPRES-i is a global animal disease information system based on a collection of official (e.g. governmental) and unofficial (e.g. personal contacts, NGOs) sources and displayed on Google Maps</td>
<td><a href="http://empres-i.fao.org/eipws3g/">http://empres-i.fao.org/eipws3g/</a></td>
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<td>OIE</td>
<td>WAHID provide access to the data held by OIE on past, present and immediate animal disease notification.</td>
<td><a href="http://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home">http://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home</a></td>
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<td>Google</td>
<td>Google Flu trends uses regional search engine results relating to influenza to detect possible outbreaks.</td>
<td><a href="http://www.google.org/flutrends/">http://www.google.org/flutrends/</a></td>
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