Generic approaches for Risk Assessment of Infectious animal Disease introduction (G-RAID)

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Abstract

The objective of the G-RAID project was the mutual exchange of knowledge between the consortium members on the development of generic risk assessment (RA) tools for animal disease incursion. Seven generic RA tools were compared considering objectives, inputs, algorithms and outputs. All tools were designed for rapid risk assessment and could assess the incursion risk for multiple diseases and pathways. Specific objectives of the tools, however, varied from immediate response to new disease events to prioritization of diseases and horizon scanning, resulting in different approaches to evaluate the incursion risk of infectious animal diseases. Cross-validation was explored as a method to validate the generic RA tools. All tools were applied to a case study for African swine fever (ASF) in which the incursion risk for the Netherlands and Finland was assessed for the 2017 situation and two hypothetical scenarios with ASF cases reported in Germany. The generic RA tools were parameterized using the same global databases for disease occurrence and trade in live animals and animal products. Disease-related parameters, however, could not be standardized because of the different levels of detail included in the model calculations. A comparison of absolute results of the tools was not possible, because output parameters represented different endpoints, varied from qualitative probability levels to quantitative numbers, and were expressed in different units. Therefore, relative risks across countries and scenarios were calculated for each tool and compared. The risk assessment tools largely agreed upon the ranking of countries and scenarios based on relative risks and would thus indicate similar priorities for risk management. As such, the cross-validation increased the credibility of results obtained with the generic RA tools. The cross-validation also contributed to the internal validation and further development of the tools. Results from the G-RAID project were disseminated to risk assessors and risk managers at a one-day symposium.

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Generic risk assessment tools

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Summary

Increasing globalization and international trade contribute to rapid expansion of animal diseases, as illustrated by the recent outbreaks of African swine fever (ASF) and lumpy skin disease (LSD) in Europe. Introduction of exotic animal diseases into naive livestock populations can result in large-scale epidemics with serious economic and socio-ethical impact. Hence, preparedness is warranted to prevent, detect, and control outbreaks of exotic animal diseases. To make decisions on risk management of exotic animal disease threats, it is necessary to know which animal diseases pose the highest threats and should therefore deserve more attention.

Risk assessment is a useful tool for prioritization of diseases with respect to their incursion risk, the results of which can be used to assign resources for prevention and surveillance to those diseases posing the highest risk or to identify targets for additional research. Most commonly, risk assessments are developed to assess the risk for a single disease and introduction pathway. In recent years, several generic risk models or frameworks have been developed that can be applied to assess the incursion risk of multiple animal diseases and pathways. The G-RAID consortium brought together researchers from across Europe, who have been developing such generic tools, with the objective of facilitating a mutual exchange of knowledge on the development, assets, and drawbacks of such tools. In particular, the aim was to: 1) exchange expertise and experience in generic import risk modelling; 2) investigate options for standardization of input data and algorithms; and 3) explore methods for validation.

Seven generic risk assessment (RA) tools were developed in recent years by the consortium members: SPARE, COMPARE, MINTRISK, RRAT, IDM, NORA and SVARRA. All seven tools were built to be flexible with respect to the animal diseases to be evaluated, although MINTRISK focused specifically on vector-borne diseases. All tools were designed for rapid risk assessment, although the assessment will in general take more time if a specific disease has not been evaluated with the tool before. The total number of diseases and pathways evaluated so far with each tool greatly varies, as does the level of resources (expertise, data, time) needed to complete the assessment. Output of the tools is also different, with some of the tools providing the risk assessor with a detailed quantitative estimate of the risk, whereas others provide a semi-quantitative risk score or a qualitative description of the risk.

The seven generic RA tools were mostly developed independently and with different objectives in mind, resulting in different modelling approaches (from qualitative to quantitative), different endpoints (e.g. entry into the country, exposure of native animals, first infection, epidemiological or economic consequences) and different output parameters (probabilities, numbers). NORA and SVARRA were specifically developed to be used in response to disease events, e.g. a new outbreak of an epizootic disease in Europe. These tools aim to rapidly assess the incursion risk of such a new disease for the target region and consider the specific situation at that time. All other tools assess a continuous incursion risk based on annual data for trade patterns and disease outbreaks. These tools will signal an increase in the risk of incursion for a specific disease over time rather than assessing the increased risk resulting from a specific disease event.

Most of the RA tools of G-RAID can be classified as semi-quantitative (MINTRISK, RRAT, IDM and NORA), using both quantitative and qualitative input data to estimate the incursion risk of animal diseases. The input data of these tools are often converted into risk scores which are then used as an input to the model; the results are also mostly presented in the form of risk scores or qualitative descriptions of risk levels. Two RA tools of G-RAID are fully quantitative models (SPARE, COMPARE). These tools use only quantitative input data to calculate the risk and return a quantitative estimate of the incursion risk. One RA tool is a purely qualitative tool (SVARRA). While quantitative input data may be used to inform the tool, no calculations are performed to arrive at the final risk estimate, which is presented using well-defined qualitative terminology.

All tools use input data on disease prevalence in the areas of origin, movements from the areas of origin to the target regions such as international trade, exposure to susceptible species, and disease-related parameters. Data on disease prevalence, international trade, and susceptible species are mainly derived from global databases such as WAHIS (OIE), EMPRES-i (FAO), TRACES (EU), Comtrade (UN) and
Eurostat (EU), with different choices being made among the tools mainly due to availability and accessibility issues. Some tools have built-in algorithms to transform the raw data from these global databases into input parameter values. Data on disease-related parameters were mostly obtained from scientific literature and expert opinion. Harmonization of input data across the tools appeared to be difficult due to different levels of detail in the calculations. Nevertheless, a need was felt to have a repository with data on disease parameters and other parameters commonly used in risk assessment that relate to disease transmission or exposure rates.

All seven generic RA tools are primarily based on the OIE import risk assessment framework. They all use methodology based on the Binomial model to assess the probability of entry of new pathogens, combining information on pathway numbers with probabilities of infection based on prevalence levels. However, the level of detail included in the algorithms varied widely among the tools. All tools that evaluate epidemiological consequences (COMPARE, MINTRISK, IDM) use the basic reproductive number $R_0$ as the basis for estimating epidemic growth.

Cross-validation, in which model results are validated by comparing them to results of other models that addressed the same question, was explored as a method for validation of generic RA tools. To this end, all seven tools were applied to a case study for ASF in which the incursion risk for both the Netherlands and Finland was assessed for the 2017 situation and two hypothetical scenarios in which ASF cases were reported in wild boar and/or domestic pigs in Germany. Where possible the same data were used across the tools. Results were compared using the relative risk across countries and scenarios for the three pathways most in common between the tools; trade in live animals, trade in animal products, and wild boar movements. A full comparison of the absolute results of the different generic RA tools for the ASF case study was not possible because of the previously mentioned differences in methodologies (modelling approaches, endpoints, output parameters, pathways considered).

The RA tools largely agreed upon the direction of the relative risks and thus on prioritization of countries and scenarios. All tools concluded that the ASF risk of trade in live animals was lower to Finland than the Netherlands in the baseline scenario (2017), and that the risk of wild boar movements to Finland was equal to or higher than the Netherlands. Furthermore, all tools concluded that the presence of ASF in Germany (hypothetical scenarios) had little or no impact on the ASF risk to Finland, but did increase the ASF risk to the Netherlands. It was therefore concluded that the cross-validation contributed to the credibility of the results obtained with the generic RA tools. It also led to an increased understanding of all tools within the consortium and as such to their internal validation and future development.

Results from the G-RAID project were disseminated at a one-day symposium that was attended by 17 people, both risk managers and risk assessors, from 10 different EU member states. Participants were actively involved in discussions on modelling approaches, data requirements and risk communication during three interactive workshop sessions. The most important conclusions from the symposium were:

- The major advantage of generic RA tools is the speed with which they can produce results;
- It is preferable for generic RA tools to include a consequence assessment in order to provide an accurate representation of the incursion risk;
- There is no uniform definition of semi-quantitative risk assessment;
- There is a need for dialogue between risk assessor and risk manager throughout the risk assessment process;
- The message from the risk assessor to the risk manager should not merely convey the results of the risk assessment, but include information on assumptions, limitations and uncertainties of the risk assessment;
- An international risk assessment community or platform to share and discuss data accessibility, availability and quality would be of benefit to future risk assessments;
- Publication of negative results, e.g. from experimental or surveillance studies, should be encouraged as these can provide useful information for risk assessment studies;
- There is unlikely to be a “One Data” solution that will be adhered to by all data providers.
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1. Introduction

1.1. Background and Terms of Reference

This grant was awarded by EFSA to: Wageningen Bioveterinary Research, The Netherlands (WBVR) (coordinator); Animal and Plant Health Agency, UK (APHA); Finnish Food Authority, Finland (Ruokavirasto); National Veterinary Institute, Sweden (SVA); National Veterinary Institute, Technical University of Denmark, (DTU-VET); Institute of Food and Agricultural Research and Technology, Spain, (IRTA-CReSA).

Grant title: Generic approaches for Risk Assessment of Infectious animal Disease introduction (G-RAID)
Grant number: GP/EFSA/AFSCO/2017/01

The terms of reference for this grant were the mutual exchange of knowledge between the consortium members on the development, assets, and drawbacks of the generic risk assessment frameworks and models that were developed by the consortium members. In particular, the aim was to:

- Exchange expertise and experience in generic import risk modelling
- Investigate options for standardization of input data and algorithms
- Explore methods for validation

1.2. Scope of the report

Increasing globalization and international trade contribute to rapid expansion of animal diseases, as illustrated by the recent outbreaks of bluetongue (BT), African swine fever (ASF), lumpy skin disease (LSD), equine infectious anaemia (EIA) and peste des petits ruminants (PPR) in Europe. Introduction of exotic animal diseases into naïve livestock populations can result in large-scale epidemics with serious economic and socio-ethical impact. Hence, preparedness is warranted to prevent, detect, and control outbreaks of exotic animal diseases. Import risk assessment is a useful tool to inform risk managers on exotic animal disease threats providing information on e.g., relevant pathways, regions at risk, or those diseases that pose the highest threat. Results can be used to assign resources for prevention and surveillance to those pathways, regions, or diseases that pose the highest risk or to identify targets for additional research or to inform specific risk management actions. Data required for such import risk assessments includes the worldwide distribution of diseases, infectiousness of hosts, contamination of and survival in products and material, and the numbers of hosts and commodities that are being moved from infected areas to the target regions.

Most commonly, risk assessments are developed as bespoke models to assess the risk for a single disease and introduction pathway. In recent years, several generic risk models or frameworks have been developed that can easily be applied to assess the incursion risk for multiple diseases (Havelaar et al., 2010; Roberts et al., 2011; ANSES, 2012; De Vos et al., 2016; EFSA, 2017; Kyyrö et al., 2017; Roelandt et al., 2017; Simons et al., 2019; Taylor et al., 2019). In contrast to bespoke models, generic risk assessment (RA) tools allow for a more rapid response to a variety of newly emerging or re-emerging diseases.

Generic RA tools are faced with three major challenges: (i) the need for extensive and real-time databases on global disease presence and movements of humans, animals, and products, (ii) the use of algorithms to combine all input data into either a qualitative or a quantitative risk estimate, and (iii) the validation of results. The objective of the G-RAID project is the mutual exchange of knowledge between the consortium members on the development, assets, and drawbacks of the generic RA frameworks and models that have been developed in recent years by the consortium members. In particular, the aim was to:

- Exchange expertise and experience in generic import risk modelling
• Investigate options for standardization of input data and algorithms
• Explore methods for validation

Expertise and experience in generic RA tools were exchanged during three project meetings and a one-day symposium. At the first project meeting (April 2018), seven generic RA tools (Table 1) developed by the consortium members were presented and discussed in detail with respect to their objectives, input data, algorithms and output. The outcome of this meeting was used to explore options for standardization of input data and algorithms.

To explore methods for validation of generic RA tools, cross-validation was applied in which results of different models addressing the same risk question are compared. The seven generic RA tools were applied to a single case study. The selected case study focused on the risk to the Netherlands and Finland from ASF virus for a number of disease scenarios. The scenarios investigated were: (1) the ASF disease situation as of December 2017 (baseline); (2) a hypothetical outbreak in wild boar in Germany in December 2017 and (3) a hypothetical outbreak in wild boar and domestic pigs in Germany in December 2017. Results for all of the tools were presented during the second project meeting (November 2018), after which a comparison was made based on relative risks obtained by the tools for countries and scenarios.

Results from the G-RAID project were disseminated at a one-day symposium (May 2019). Three interactive workshop sessions were organized to actively involve the participants in discussions on modelling approaches, data requirements and risk communication. The input obtained at this symposium was further discussed during the third project meeting (May 2019).

This report presents an overview of the generic RA frameworks and models developed by the consortium members and discusses the similarities and differences observed, with a focus on input data and algorithms (Sections 3.1 to 3.4). The report describes the results of the case study on ASF, which was used to explore the opportunities for cross-validation of the generic RA tools (Section 3.5). Furthermore, the main conclusions derived from the discussions during the symposium are given (Section 3.6).
### Table 1: Summary of the seven generic RA tools included in G-RAID.

<table>
<thead>
<tr>
<th>Generic RA tool: acronym</th>
<th>Generic RA tool: full title of associated project / tool</th>
<th>Quantitative /Semi-quantitative /Qualitative</th>
<th>Origin</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>SPARE</td>
<td>Animal Health and Welfare ERA-Net (ANIHWA) project “Development of a SPatial risk assessment framework for Assessing exotic disease incuasion through Europe</td>
<td>Quantitative</td>
<td>Animal and Plant Health Agency (APHA)</td>
<td>Defra, UK(a); Simons et al., 2017; Simons et al., 2019</td>
</tr>
<tr>
<td>COMPARE</td>
<td>EU H2020 project COllaborative Management Platform for detection and Analyses of (Re-) emerging and foodborne outbreaks in Europe.</td>
<td>Quantitative</td>
<td>Animal and Plant Health Agency (APHA)</td>
<td>Taylor et al., 2019</td>
</tr>
<tr>
<td>MINTRISK</td>
<td>Method for INTEGRated RISK assessment of vector-borne diseases</td>
<td>Semi-quantitative</td>
<td>Wageningen University &amp; Research (WBVR)</td>
<td>De Vos et al., 2012; De Vos et al., 2016; EFSA AHAW Panel, 2017; EFSA, 2017</td>
</tr>
<tr>
<td>RRAT</td>
<td>Rapid Risk Assessment Tool</td>
<td>Semi-quantitative</td>
<td>Wageningen University &amp; Research (WBVR)</td>
<td>De Vos et al., 2018</td>
</tr>
<tr>
<td>IDM</td>
<td>International Disease Monitoring tool for risk of incursion</td>
<td>Semi-quantitative</td>
<td>Animal and Plant Health Agency (APHA)</td>
<td>Roberts et al. 2011, EFSA, 2017</td>
</tr>
<tr>
<td>NORA</td>
<td>NOpea RiskinArviointityökalu</td>
<td>Semi-quantitative</td>
<td>Finnish Food Authority (Ruokavirasto)</td>
<td>Evira(c), Kyyrö et al., 2017</td>
</tr>
<tr>
<td>SVARRA</td>
<td>Rapid Risk Assessment tool for introduction of exotic disease to the Swedish animal population</td>
<td>Qualitative</td>
<td>National Veterinary Institute (SVA)</td>
<td>Swedish Board of Agriculture, EFSA, 2017</td>
</tr>
</tbody>
</table>

(a) Funded by Defra as part of a EU ERANET project (ANIHWA)
(b) Ministry of Agriculture, Nature and Food Quality
(c) New name as of January 2019: Ruokavirasto
2. Data and Methodologies

2.1. Methodologies

A total of seven generic frameworks or models to assess the incursion risk of infectious animal diseases were developed independently in recent years by the consortium members (Table 1). More detailed information on each of the generic RA tools is provided in Section 3.1 and Appendix A. Each of the RA tools was reviewed and compared with special attention to (i) the input parameters and the databases used to estimate the inputs, such as global disease presence and movements of humans, animals, and products, and (ii) the type of algorithms used to combine all input data into an overall risk estimate, either qualitatively or quantitatively.

Validation of the generic RA tools was carried out by cross-validation. All tools were used to assess the probability of incursion for a selected case study on African swine fever. Wherever possible, the same input data were used in all tools (Section 2.2.1). Table 2 provides the case study scenarios that were evaluated by each of the seven tools for both Finland and the Netherlands. In addition, one consortium member developed a bespoke model for this case study (IRTA; a description of the modelling approach is given in Appendix A).

A direct comparison of absolute results obtained by the seven generic RA tools and the bespoke model was not possible, because endpoints for the incursion risk varied from the probability of entry to the probability of establishment. In addition, the tools had different output parameters and evaluated different numbers and types of introduction pathways. Results of the case study were therefore compared by calculating relative risks by country and scenario for the three pathways that were evaluated by almost all tools (legal trade in live animals; trade in animal products; wild boar movements). Observed similarities and differences were investigated, leading to a better understanding of the tools and their algorithms.

Three outputs of the risk assessment were compared across the tools:

1. Relative risk across the pathways to identify for each tool the pathways that contributed most to the ASF incursion risk; by country and scenario.
2. Relative risk for the Netherlands compared to Finland in the baseline scenario (S1) for each tool and pathway.
3. Relative risk for the hypothetical scenarios (S2 and S3) compared to the baseline scenario (S1) for each tool and pathway.

In order to calculate the relative risks for SVARRA, a log-scale was assumed to convert the qualitative risk levels to numerical values: Negligible (Neg)=1, Neg-Very Low (VL)=3, VL=10, Low (L)=100, etc.). All other RA tools produced numerical results, either representing absolute risk estimates or semi-quantitative risk scores. Negligible or zero results in quantitative or semi-quantitative tools were set equal to $10^{-10}$ to allow the calculation of the relative risks. The value of $10^{-10}$ was based on the lowest results that were calculated by the tools (7×$10^{-10}$ for the risk of the live animal trade pathway to Finland as calculated by RRAT). For these quantitative or semi-quantitative tools, calculated relative risks could be extremely high with values varying from $10^{-10}$ to 1, whereas for other semi-quantitative tools (especially IDM), relative risks could never be higher than the ratio of the maximum score possible in the tool to its minimum score.

A one-day international symposium was organised to disseminate the results of the G-RAID project to risk managers and risk assessors. The symposium consisted of (1) lectures on generic risk assessment and more specifically the RA tools and results from G-RAID and (2) three interactive workshops on modelling approaches, data requirements and risk communication. The ultimate aim of the symposium was to contribute to harmonization of generic RA tools across Europe and to ensure that such generic RA tools are tailored to the needs of the risk managers.
### Table 2: Selected case study for the cross-validation of the seven RA tools.

<table>
<thead>
<tr>
<th>Scenario number</th>
<th>Scenario title</th>
<th>Scenario narrative and risk question</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Current Situation as of December 2017</td>
<td>It is 31 December 2017. Forty-three new cases of African swine fever in Europe were reported on 29 December 2017 (according to EMPRES-i), forty-two of which involved wild boar in Poland, Russia, Ukraine and Czech Republic. One case involved domestic pigs in Ukraine. In total, there have been 1,451 separate reports of African swine fever in Europe this year (according to EMPRES-i). Given these new cases and the history of cases in Europe in 2017, as well as trade patterns in 2017, what is the predicted probability of introduction, probability of exposure, and probability of first infection for 2018 for the Netherlands and Finland, for all pathways that you consider and as an overall probability?</td>
</tr>
<tr>
<td>2</td>
<td>Wild boar Cases in Germany</td>
<td>It is 31 December 2017. Assume the exact same number of cases and locations of ASF within Europe as Scenario 1. However, as well as the cases in Scenario 1, there have also been cases of ASF in wild boar in Germany, reported on 30 December 2017. Specifically, there have been 10 separate cases of wild boar found dead, infected with ASF in the Munster region of Germany (NUTS code DEA3). Given these new cases in Germany and the history of cases in Europe, what is the predicted probability of introduction, probability of exposure, and probability of first infection for 2018 for the Netherlands and Finland, for all pathways that you consider and as an overall probability?</td>
</tr>
<tr>
<td>3</td>
<td>Wild boar and domestic pig cases in Germany</td>
<td>It is 31 December 2017. Assume the exact same number of cases and locations of ASF within Europe as Scenario 1. However, as well as the cases in Scenario 1, there have also been cases of ASF in wild boar (same as in Scenario 2) and in domestic pigs in Germany, reported on 30 December 2017. Specifically, as per Scenario 2, there has been 10 separate cases of wild boar found dead, infected with ASF in the Munster region of Germany (NUTS code DEA3). And there has been one outbreak on a single commercial mixed (breeding and fattening) farm in the same region (Munster) with 2500 pigs on it, 18 of which were found infected and all 2500 have now been slaughtered.</td>
</tr>
</tbody>
</table>
Given these new cases in Germany and the history of cases in Europe, what is the predicted probability of introduction, probability of exposure, and probability of first infection for 2018 for the Netherlands and Finland, for all pathways that you consider and as an overall probability?

2.2. Data

The data required for each generic RA tool are very similar, although specific data sources used may vary. This may be due to access to different data sources, the preference for quantitative data, or the requirements of the algorithms in the RA tools. The data required by the tools can be divided into four types: (1) prevalence in area of origin, (2) movement from one area to another, (3) exposure to susceptible species and (4) disease-related parameters. Sources of these data types are discussed in more detail below.

**Prevalence in area of origin:** All tools use global reports on disease occurrence to infer a qualitative, semi-quantitative or quantitative estimate of prevalence. WAHIS (OIE, 2019) is the primary data source for these disease reports, but EMPRES-i (FAO, 2019a), ADNS (Animal Disease Notification System; EU, 2019a), official reports from the European Commission and COM-mail (notifications by the EU Commission to the member states) are also used across the tools.

**Movement from one area to another:** This category of data input is relevant to the entry stage of the risk assessment and focuses for each pathway on how many animals/products/humans etc. will reach the target region from the area of origin, regardless of whether or not it is infected. Sources of data include global databases such as TRACES (Trade Control and Expert System; EU, 2019b), Comext (Eurostat, 2019a) or Comtrade (UN, 2019), although national statistics may also be considered by some tools.

**Exposure to susceptible species:** This category of data input relates to the exposure and first infection of susceptible animals (including wild animals) and establishment within susceptible populations in the target region. Data sources include Eurostat for the number of animals and farms at country or region level in EU member states (Eurostat, 2019b) or density maps of livestock provided by FAO (FAO, 2019b). National livestock databases are also used, if available. Other data sources include published literature and expert opinion.

**Disease-related parameters:** This category of data input includes all parameters specific to the disease such as: transmission probabilities, duration of the latent and infectious periods, decay rate in
products, etc. This category also includes parameters related to the impact of the disease. Disease-related parameters are primarily obtained from the published literature and, if necessary, expert opinion. Tables 1 – 4 in Appendix B compare and contrast the different input data sources used in the seven generic RA tools.

2.2.1. Data for the ASF case study

Wherever possible, each RA tool used the same data in the case study for ASF. Sources of data included the following:


**Movement from one area to another:** All of the RA tools considered multiple trade routes. Each of the RA tools used the Eurostat Comext trade data for 2017: [https://ec.europa.eu/eurostat/data/bulkdownload](https://ec.europa.eu/eurostat/data/bulkdownload). However, the product codes included in the tool depended on pathway and tool and may not have been the same across all tools.

**Exposure to susceptible species:** Maps on pig density (FAO, 2019b) and wild boar abundance (Alexander et al., 2016) were used as an input by COMPARE (Figure 1). The other tools did not need data at this spatial scale, but did use national data on susceptible populations for both wild boar and pigs.

**Disease-related parameters:** Parameters within the risk assessment specific to ASF varied between the tools. The parameters were mostly estimated by literature searches or expert opinion. Parameter values were shared among the consortium members to enable harmonization of input data over the RA tools, if similar input parameters were used.
Figure 1: Map indicating (A) pig density (head/km²) and (B) wild boar abundance in Europe at a 1km² spatial scale. Wild boar abundance is measured on a semi-quantitative scale between 0 and 4 with 0 indicating no boar in that location and 4 indicating locations with highest estimated abundance. Data on pig density were derived from FAO (2019b). Data on wild boar distributions were derived from Alexander et al. (2016).
3. Assessment

3.1. Overview of the generic risk assessment tools

All seven RA tools (Table 1) were built to be flexible with respect to the animal disease or diseases to be evaluated, although MINTRISK focused specifically on vector-borne diseases. All tools were designed for rapid risk assessment, although the assessment will in general take more time if a specific disease has not been evaluated with the tool before. The total number of diseases evaluated so far with each tool greatly varies, as does the level of resources (expertise, data, time) needed to complete the assessment. Output of the tools is also different, with some of the tools providing the risk assessor with a detailed quantitative estimate of the risk, whereas others provide a semi-quantitative risk score or a qualitative description of the risk. Qualitative risk assessment is defined here as having outputs that are descriptive outputs rather than numerical, for example Very low, Low, Moderate, etc. Likewise, the outputs from the tools that are quantitative are numerical estimates, e.g. a probability or number of contaminated consignments. The semi-quantitative risk assessments provide a numerical risk score as an output. Scales of the risk scores can vary. In these risk assessments, qualitative or quantitative input data are often converted into risk scores which are then used as a model input. A more detailed overview of the RA tools is given in Appendix A.

The RA tools vary greatly in the number and type of pathways considered, which include: live animals, products of animal origin, germplasm, vectors, wildlife, human travel, transport, feed and bedding, laboratory material and airborne spread. Table 3 provides a summary of which RA tools include which of the above pathways. Each of the tools are then considered below and key attributes are summarised.

Table 3: Summary of the pathways included in the seven generic RA tools included in G-RAID.

<table>
<thead>
<tr>
<th>Pathway(a)</th>
<th>SPARE</th>
<th>COMPARE</th>
<th>MINTRISK(b)</th>
<th>RRAT</th>
<th>IDM</th>
<th>NORA</th>
<th>SVARRA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Live animals</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Products of animal origin</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Germplasm</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Vectors (insects/ticks)</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Wildlife dispersion</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Human travel</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Transport (fomites)</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Feed and bedding</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Laboratory material</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
<td></td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>Airborne spread</td>
<td>X</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

(a) Definitions of pathways vary between the tools
(b) Pathways in MINTRISK are user-defined and consequently MINTRISK can do any pathway the risk assessor considers relevant for the risk question addressed
(c) Living genetic resources such as semen, ova and embryos that are maintained for the purpose of animal breeding

3.1.1. Quantitative risk assessment tools

3.1.1.1. SPARE

SPARE was developed as part of the Animal Health and Welfare ERA-Net (ANIHWA) project "Development of a SPatial risk assessment framework for Assessing exotic disease incuRision through Europe (SPARE)". It has been built as a generic framework in R (R Core Team, 2019) that can be used to evaluate the incursion risk of theoretically every pathogen that OIE reports on from any country in the world. SPARE is an overarching model that makes rapid use of available metadata to identify pathways of potential risk for classes of disease transmission (e.g. vector-borne). SPARE is a deterministic model calculating the probability of entry of specific pathogens. The output of SPARE feeds
into other models, also developed as part of the project, to assess the probability of establishment and epidemic spread. Inputs and outputs of SPARE are purely quantitative. So far, the model has been used to assess the incursion risk for EU member states. SPARE was parameterized for three case studies to cover the most important introduction pathways; classical swine fever (trade in live animals and animal products), bluetongue (windborne vector dispersion), and classical rabies (trade in pets and wild animal dispersion). The model aims to provide valuable information for risk assessors in the first instances of a disease outbreak, where typically information on imports, routes of entry, and potential for spread is undertaken on a case-by-case basis. It will also allow for an objective and systematic evaluation to inform risk-based animal health and zoonotic surveillance activities.

**Summary information:**
- **Objective:** Early warning of disease incursion risks
- **Output type:** Quantitative
- **Output parameter:** Number of entries per year
- **Software:** R
- **Uncertainty/variability:** Not considered
- **Pathways:** Live animals, Products of animal origin, Vectors (insects/ticks), Wildlife dispersion, Human travel

### 3.1.1.2. COMPARE

COMPARE was developed as part of the EU H2020 project COllaborative Management Platform for detection and Analyses of (Re-) emerging and foodborne outbreaks in Europe (COMPARE). COMPARE is a stochastic model that aims to identify hotspots for incursion of disease taking into account the probability of entry, and first infection, and subsequent spread to new areas. COMPARE has been built as a generic framework in R that works at different spatial resolutions, for different diseases including zoonotic diseases, and for different pathways. COMPARE is a purely quantitative model that incorporates variability directly, while using quantitative input data and providing quantitative results. Results of COMPARE can be used to target surveillance as well as allowing comparisons to be made across diseases and pathways. At the time of writing, COMPARE has been parameterized to estimate the probability of first infection for African swine fever and lumpy skin disease for Europe. An additional module estimating the subsequent spread to new areas (epidemiological consequences) once the disease is introduced into the target region is under construction. As part of the COMPARE project, this tool will also be used to evaluate the incursion risk of Zika virus and avian influenza.

**Summary information:**
- **Objective:** Identification of hotspots for risk-based surveillance
- **Output type:** Quantitative
- **Output parameter:** Annual probability
- **Software:** R
- **Uncertainty/variability:** Variability
- **Pathways:** Live animals, Products of animal origin, Vectors (insects/ticks), Wildlife dispersion, Human travel
3.1.2. Semi-quantitative risk assessment tools

3.1.2.1. MINTRISK

The Method for INTegrated RISK assessment of vector-borne diseases (MINTRISK) is a web-based calculation tool written in Visual Studio and C# that can be used to evaluate the incursion risk of vector-borne diseases, taking into account the probability of entry, probability of transmission, probability of establishment, extent of spread, likelihood of persistence, and the impact of disease. MINTRISK aims to ensure completeness and consistency in risk assessment of vector-borne diseases and its results can be used for comparison and prioritization purposes. In theory, the tool could also be used to assess the incursion risk of non-vector-borne diseases; however, results will be less good because some questions and algorithms are less relevant for these diseases. MINTRISK does not have a pre-filled database and the tool can incorporate any vector-borne disease pathway the risk assessor considers relevant for the incursion risk. The tool consists of questions that are to be answered qualitatively by the risk assessor. However, each qualitative answer category (usually from very low to very high) has been translated into a quantitative scale to guide the risk assessor. Furthermore, for some of the key questions, there is an option of entering an exact number instead of a qualitative answer. In answering the questions, the risk assessor is also asked to indicate his/her uncertainty. MINTRISK is a stochastic tool, that allows the uncertainty indicated by the risk assessor to be included in the model calculations. The qualitative answers are converted into quantitative distributions, incorporating the estimate and its uncertainty, and then calculations are performed quantitatively. The output of MINTRISK consists of three risk scores to give an indication of the rate of introduction, the expected epidemic size and the economic impact. These risk scores and their uncertainty intervals are communicated both qualitatively (words) and semi-quantitatively (numbers) with corresponding explanation.

Summary information:
- **Objective**: Comparison and prioritization of vector-borne diseases
- **Output type**: Semi-quantitative
- **Output parameter**: Risk score (0 to 1)
- **Software**: C#, Visual Studio
- **Uncertainty/variability**: Uncertainty
- **Pathways**: Pathways in MINTRISK are user-defined and consequently MINTRISK can do any pathway the risk assessor considers relevant for the risk question addressed

3.1.2.2. RRAT

The Rapid RA Tool (RRAT) has been built as a relational database in R with a pre-filled databank in SQlite. This tool was developed to enable quick and real-time assessment of the incursion risk of exotic livestock diseases for the Netherlands. RRAT assesses the probability of entry resulting in a first infection (primary case) with the aim to rank diseases, areas of origin, and/or pathways for their incursion risk. Results of RRAT can be used to prioritize diseases for risk management and early warning and to identify high-risk trade flows. The main tables in RRAT provide information on disease occurrence worldwide, the level of trade for each pathway of introduction, and disease-related parameters to assess the relevance of each pathway. These tables are linked to calculate a semi-quantitative score for the incursion risk of different diseases, the results of which allow for prioritization. Calculations in RRAT are deterministic and do not account for spatial variation in risk. So far, RRAT has been parameterized to assess the incursion risk by legal trade in live animals, germplasm, and products of animal origin.

Summary information:
- **Objective**: Identification of high priority exotic notifiable diseases
- **Output type**: Semi-quantitative
• **Output parameter**: Risk score (0 to 1)
• **Software**: R, SQLite
• **Uncertainty/variability**: Not considered
• **Pathways**: Live animals, Products of animal origin, Germplasm

### 3.1.2.3. IDM

The International Disease Monitoring tool for risk of incursion (IDM) is a semi-quantitative RA tool in Excel to rank diseases for their incursion risk to the United Kingdom (UK). The tool includes mostly exotic notifiable diseases, but it is possible to add any new or emerging disease. IDM is a pre-populated tool defining certain risk pathways for each disease and is regularly updated to take into account changes in trade patterns and disease occurrence. The tool is manually fed with information on disease outbreaks, trade volumes, pathways, and where international trade rules and disease control measures are in place. All input parameters are given semi-quantitative risk scores that serve as input into the calculations. Output of IDM is presented as semi-quantitative risk scores for each disease. Although IDM is deterministic, the uncertainty in input parameters can easily be explored by what-if analysis. The emphasis in IDM is on the probability of entry, but the tool also considers the probability of exposure. Consequences are largely ignored, assuming that all notifiable diseases will have large consequences once introduced. However, the risk scores in the final graph have been colour coded to give an indication of the expected $R_0$ value. IDM was developed to provide an evidence base for the most high priority exotic notifiable diseases and the risk of their incursion for the UK. The tool compares different pathways (trade of live animals, products and germplasm, vectors, wildlife and transport) for different diseases to give a comparative risk score and help policy makers decide on areas for prioritisation. It deliberately does not take account of any national rules or risk management measures in place at the border or inland (such as post-import testing or quarantine) as the original purpose of the tool was to feed another UK prioritisation tool (Gibbens et al. 2016). However, IDM is regularly used to communicate to risk managers why we have national rules in place. IDM uses regional rather than country level for the areas of origin, thereby avoiding political boundaries for the transboundary animal diseases.

**Summary information:**

- **Objective**: Identification of high priority exotic notifiable diseases
- **Output type**: Semi-quantitative
- **Output parameter**: Risk score (0 to 60)
- **Software**: Excel
- **Uncertainty/variability**: Not considered
- **Pathways**: Live animals, Products of animal origin, Germplasm, Vectors (insects/ticks), Wildlife dispersion, Transport (fomites), Laboratory material

### 3.1.2.4. NORA

The Finnish rapid RA tool NOpea RiskinArviointityökalu (NORA) is a semi-quantitative RA tool in Excel to estimate the incursion risk of exotic notifiable diseases for Finland and has been parameterized for African swine fever, lumpy skin disease, chronic wasting disease, foot and mouth disease, and bluetongue at the time of writing. NORA was developed to be quick to use and to provide consistency in order to support risk management decisions. NORA can be used in situations where there is a change in the disease status of highly infectious animal diseases in neighbouring countries or in countries with significant interactions with Finland and can therefore be used to inform risk management decisions, e.g. NORA identified an increased risk to Finland due to the presence of ASF in Estonia and therefore additional posters were placed at the borders. NORA consists of questions to evaluate the contribution of different pathways to the probability of entry resulting in a first infection, and statements to evaluate the economic impact. These questions and statements are to be answered by the risk assessor. A total
of nine introduction pathways are considered in NORA that are assigned weighted scores based on their contribution to the evaluated disease. Weighting of pathways is based on expert opinion. The output of NORA comprises semi-quantitative risk scores for the combined probability of entry and exposure, the economic consequences, and for the overall risk. These risk scores are converted into a qualitative risk estimate with a corresponding explanation. Calculations in NORA are deterministic and do not account for uncertainty or variability. The tool has a user-friendly interface and, but no underlying database as the data are imported manually by the assessor.

Summary information:
- **Objective**: Rapid risk assessment to respond to new disease events
- **Output type**: Semi-quantitative
- **Output parameter**: Risk score (0 to 1)
- **Software**: Excel
- **Uncertainty/variability**: Not considered
- **Pathways**: Live animals, Products of animal origin, Germplasm, Vectors (insects/ticks), Wildlife dispersion, Human travel, Transport (fomites), Feed and bedding, Airborne spread

### 3.1.3. Qualitative risk assessment tools

#### 3.1.3.1. SVARRA

The Rapid RA tool for introduction of exotic diseases to the Swedish animal population (SVARRA) is a qualitative RA tool (initially developed as a MS Word document) that uses a pre-defined template with corresponding instructions to evaluate the risk of incursion of exotic diseases. The objective of SVARRA is to ensure that a systematic, structured, transparent and well documented qualitative risk assessment can be produced within a very short timescale. SVARRA was developed to be used in response to disease events (e.g. a new outbreak of an epizootic disease in Europe) to evaluate the possible change in the incursion risk for Sweden. The tool was first developed for AI and ASF; it has, however, now been adapted to be more generic. Furthermore, it was translated into English for the G-RAID project, so that it is available to a wider public. Also, the MS Word table of SVARRA was transferred to MS Excel to automate some of the steps in the risk assessment. SVARRA assesses the probability of entry and exposure to Swedish animals via several pathways including trade in live animals, imports of animal products and germplasm, indirect transmission routes, vectors, and wildlife. SVARRA does not have an underlying database, and no calculations are required to perform the risk assessment. Standardized definitions for probability and uncertainty levels are provided to guide the risk assessor. A risk matrix is used to combine the probabilities of entry and exposure into a single probability estimate. Consequences are not taken into account since introduction of exotic disease are expected to have major impact.

Summary information:
- **Objective**: Rapid risk assessment to respond to new disease events
- **Output type**: Qualitative
- **Output parameter**: Qualitative probability level
- **Software**: Word, Excel
- **Uncertainty/variability**: Uncertainty
- **Pathways**: Live animals, Products of animal origin, Germplasm, Vectors (insects/ticks), Wildlife dispersion, Human travel, Transport (fomites), Feed and bedding
3.2. **Input data used by the generic risk assessment tools**

All seven tools use a large quantity of data to inform their generic risk assessments including global databases, national statistics, published literature and expert opinion. For the two quantitative tools, SPARE and COMPARE, the preference is to use the data as-is or within a sub-model that informs a parameter of the larger risk assessment. In RRAT, the input of many of the parameters is quantitative, but because some of the probabilities are semi-quantitative scores based on risk classes, the final output is semi-quantitative. For the final four tools, the data are used to inform the choice of scores, whether those are defined as “very low” to “very high” as in MINTRISK and SVARRA, or from 0 – 5 such as in IDM.

For the most part, the data required for each tool are very similar, although specific data sources used may vary. This may be due to availability of or access to different data sources, the preference for quantitative data, or the requirements of the algorithms in the risk assessments. The majority of the data required for the risk assessments can be broken down into 4 categories: 1) prevalence in area of origin 2) movement from one area to another; 3) exposure to susceptible species; 4) disease-related parameters. We outline each of these in more detail below. Tables 1 – 4 in Appendix B summarise the sources of the data used by each RA tool for each of the four data types.

### 3.2.1. Prevalence in area of origin

All tools use global reports on disease occurrence to infer a qualitative, semi-quantitative or quantitative estimate of prevalence. However, SVARRA primarily uses these global disease reports as an alert mechanism to initiate the risk assessment process. OIE is the primary data source for these disease reports, but EMPRES-i (FAO, 2019a), ADNS (EU, 2019a), FAO, EC reports and COM-mail (notifications by the EU Commission to the member states) are also used across the tools.

For SPARE, COMPARE and RRAT, the actual raw data are not used as direct inputs in the risk assessment but instead used in a sub-model to estimate the prevalence. This is due to known discrepancies with the raw disease data. For example, there is likely to be underreporting of disease cases, especially in wild populations, and there are many cases of disease or freedom from disease not being reported. Each of these three RA tools deals with these uncertainties and variabilities in different ways, although for some pathways, COMPARE uses output of SPARE for estimated prevalence.

Some of the seven RA tools include mitigation measures, such as trade restrictions and testing before export, in the assessment of prevalence. The data for the mitigation measures depend on national or EU legislation, while test sensitivity primarily comes from published literature. Finally, most tools consider (for some pathways at least) the probability that an animal/product that was infected/contaminated, when it left the exporting country, will still be infected when it reaches the target region. This is estimated via statistics on travel times/distances and duration of infection or decay in products.

### 3.2.2. Movement from one area to another

This input data category is relevant to the entry stage of the risk assessment and for each pathway focuses on how many animals/products etc. will reach the target region from the area of origin, regardless of whether or not the animals/products are infected. As stated in Section 3.4.2 on the algorithms, most of the tools consider a Binomial model, \( N \times p \), for entry, where \( N \) is the total number of animals/products entering and \( p \) is the prevalence. Therefore, each tool needs to estimate the value of \( N \) and all do this predominantly using global databases. For legal trade in live animals or products, all of the tools use one or more of TRACES (EU, 2019b), Comext (Eurostat, 2019a) or Comtrade (UN, 2019), although national statistics may also be considered for some tools. It is generally believed that within Europe, TRACES is the most reliable global data source including the widest range of relevant
product types of animal origin. However, the choice of which global database to use is primarily driven by data accessibility. For example, within TRACES it is only possible to access the trade data relevant to your own country. Of particular relevance is the fact that the trade data sources do not completely concur, and risk assessment results using the different data sources may not yield the same results, which could be most relevant for the more quantitative tools. For movement of wild terrestrial animals, birds and vectors, and illegal trade, global databases are obviously not possible to obtain. However, most tools incorporate global databases of travel statistics or population abundance maps in order to either model or estimate a score for how much illegal trade or wild animal movement there is. For example, in SPARE the amount of illegal meat products entering each country in the EU is modelled using global databases on passenger travel, air freight and maritime containers entering each country, UK national statistics on the proportion of these that bring in illegal meat, and the average amount of illegal meat each passenger/freight/container would bring. Similarly, IDM uses national databases for the UK border to estimate a score for the number of trucks entering the UK from each region, as trucks can be a contamination source.

The primary difference between the tools, with regard to this category of data input, is the pathways, which each tool incorporates (Table 3). For example, only some of the tools consider the movement of humans (e.g. via air travel) and fomites (e.g. via transport lorries) between countries. This is either due to choosing to focus on only some pathways, or because the tool is still under construction and other pathways may be added later. However, when considering pathways in common, most of the tools use the same set of data sources in similar ways (for more details, see Appendix B).

3.2.3. Exposure to susceptible species

This category of data input relates to stages of the risk assessment following entry; the exposure and first infection of susceptible animals and establishment within susceptible populations. For this category of data input, there is more variation between the seven tools; partly because these risk assessment stages are not included for all tools, but also because many contrasting choices are made to model contact between susceptible animals and infected animals/products. In tools where these steps are included, data are needed to determine if any detection at import could occur, whether contact is possible with the native animal population, how many susceptible animals could be in contact with the infectious animal/product, and if different classes of susceptible animals need to be considered. For example, SVARRA splits the susceptible animals into four classes to distinguish between domestic animals at farms with low and high biosecurity levels, and wildlife populations that are either fenced or not. COMPARE is the only tool that uses quantitative data directly for these inputs, with data sources including Eurostat for the number of animals and farms at country or region level (Eurostat, 2019b) or density maps of livestock provided by FAO (FAO, 2019b). However, NORA uses their national farm registry as an indirect input to determine abundance of susceptible animals, and MINTRISK uses national databases if available. Other data sources indirectly used by the other tools includes published literature and expert opinion of expected transmission according to the basic reproductive number $R_0$.

3.2.4. Disease-related parameters

This data category includes all parameters specific to the disease such as: transmission probabilities, duration of the latent and infectious periods, decay rate in products etc. The seven tools differ in whether or how they incorporate these disease parameters; however, all of them use primarily published literature and expert opinion to find the relevant parameter values. Whilst disease-related parameters are necessary at all stages of the risk assessment, it is most important when considering probability of first infection, establishment and epidemiological consequences. COMPARE, MINTRISK and IDM use the basic reproductive number ($R_0$), within their algorithms in order to summarise these disease-related parameters. Both MINTRISK and IDM use published literature or expert opinion to estimate $R_0$. COMPARE breaks $R_0$ down into its component parts (which will be different depending on disease and...
3.3. Algorithms used by the generic risk assessment tools

Each of the seven generic RA tools was built independently, although results of SPARE to assess the prevalence of disease in areas of origin are used as input into COMPARE and there was collaboration between these two tools in the development of algorithms for wild animal dispersion. The risk assessment steps included in the generic RA tools differ (Figure 3). All tools evaluate the probability of entry of a pathogen, and, to differing extents, the probability of exposure of the native animal population, apart from SPARE, which only evaluates the probability of entry. Only two generic tools, MINTRISK and NORA, also evaluate the economic impact of disease once introduced. SPARE and COMPARE generate quantitative results, whereas MINTRISK, RRAT, NORA and IDM provide semi-quantitative risk scores, and SVARRA provides purely qualitative probability estimates. Despite all these differences, the basic principles underlying the algorithms to arrive at the risk estimate are similar across all tools. A more detailed description of the algorithms in the seven generic RA tools is given below. In summary, all tools evaluate the probability of entry using the Binomial model and the basic reproductive number $R_0$ to assess epidemiological consequences, if included in the tool.

3.3.1. Quantitative risk assessment tools

3.3.1.1. SPARE

SPARE consists of two modules. The first module estimates the prevalence of a specific pathogen in each species in each country of the world based on OIE data. The second module estimates the probability of entry into all EU member states via different pathways.

The prevalence of a pathogen in a specific country and species ($P_c$) is based on data on the number of reported cases ($E$), the animal species population in that country ($N$), a generic underreporting factor ($U$), and the probability that an outbreak occurs ($P$). This probability is based on the number of historical outbreaks in that country and the time that has passed since these outbreaks. Prevalence is then calculated as:

$$P_c = \frac{E}{N} \times U \times P$$
For the purposes of trade, the prevalence is corrected for the probability that an animal is infected at the point of export \( (P_s) \) and the proportion of cases that occurs before detection of an outbreak \( (P_d) \). The corrected prevalence is calculated as:

\[
P_{c1} = P_c \times P_s \times P_d
\]

The risk for each pathway is calculated by multiplying the corrected prevalence with the total number of pathway units originating from this specific country \( (N_p) \). The results from different products contributing to the same pathway are summed. The risk is thus expressed as the expected number of introduction events per year for each pathway and is calculated as:

\[
R = P_{c1} \times \sum N_p
\]

For windborne spread of vectors, a different approach is used. So far, this has only been implemented for midges (bluetongue). First, all countries that can contribute to this risk for a specific EU member state were identified based on the maximum distance that vectors can travel by wind (here: 300 km). Then, the risk is calculated as the probability that at least one infected vector would be released, taking into account the number of outbreaks \( (N) \) based on OIE data and the relative livestock density in the regions, from where vectors might originate, the prevalence in vectors \( (P_v) \), which was set equal to the prevalence in livestock, and the probability of survival of the vector \( (P_s) \), which depends on the distance and the percentages of water and land that need to be crossed. Temperature and wind direction have not been considered here. Risk for vector-borne incursions is then calculated as:

\[
R = 1 - (1 - P_s \times P_v)^N
\]

Here, the risk is thus expressed as the probability of at least one introduction event per year.

The model does not allow for a comparison of the risk between pathways, since the pathways are expressed in different units (e.g. animals vs tons of products) and do not include the probability of exposure of the native population of the importing country. The model, however, does calculate the viral load per consignment. This can be used as input for an exposure assessment (results of this model are used by other partners in the SPARE project to perform an exposure assessment and not included here).

### 3.3.1.2. COMPARE

COMPARE is a stochastic model that aims to identify hotspots for incursion of disease taking into account the probability of entry, initial infection, and onward spread. The probability of first infection for a target region is calculated by initially computing how many infected units will reach this region. This is based on a Binomial distribution to simulate the number of infected units reaching this region. The Binomial distribution includes an estimate of prevalence from each area of origin \( (p) \) and the number of units \( (N) \) from each area of origin entering the target region. The prevalence estimates are based either on data derived from SPARE or estimated directly from OIE reports (depending on the pathway), while the numbers of traded units are extracted from global databases or modelled using indirect data sources. The number of infected units reaching the target region \( (I) \) is thus simulated as:

\[
I = Bin(N,p)
\]
Then, another Binomial distribution is used to simulate the number of infected units entering the target region ($J$), accounting for the probability of detection ($P_D$):

$$J = Bin(I,(1 - P_D))$$

COMPARE uses the basic reproductive number ($R_0$) to model the probability of survival, contact, and initial transmission. Within the equation for $R_0$ is a calculation of how many susceptible animals in the target region may be in contact with the infectious animal entering, although the calculation will be different for different pathways. The number of new infections ($N_I$) is then calculated for each simulation by assuming a Poisson process with $JR_0$ simulated number of infected units entering the target region, each with a likelihood of infecting $R_0$ susceptible animals:

$$R = 1 - e^{-R_0 \times J}$$

$$N_I = \sum_{j=1}^{J} Pois(R_0)$$

The probability of at least one infection, $R$, is then given by the proportion of the simulations where infection occurs. The probability of at least one infection by any pathway is subsequently calculated by multiplying the risks per pathway in the following equation:

$$Risk = 1 - \prod (1 - R)$$

COMPARE will also include the epidemiological consequences, i.e., the probability that the target region will spread the disease to other regions. This is still under development but will also be based on the $R_0$ estimate as well as geographical location and other factors. The overall risk calculated with COMPARE will then be a multiplication of the probability of first infection and the probability of subsequent spread.

### 3.3.2. Semi-quantitative risk assessment tools

#### 3.3.2.1. MINTRISK

MINTRISK provides three main risk scores to evaluate the incursion risk of vector-borne diseases: rate of introduction, epidemic size, and impact of disease. The rate of introduction gives the expected annual number of introductions resulting in successful establishment for each pathway. To this end, the rate of entry ($Entry$) is multiplied with the probability of establishment ($Est$). The rate of entry is based on the import volumes ($V$), the probability of infection based on prevalence data from the areas of origin ($P_{inf}$), and the probabilities that the infection will survive transport ($P_{surv.transport}$) and preventive measures in place ($P_{surv.PM}$), and is calculated as:

$$Entry = V \times P_{inf} \times P_{surv.transport} \times P_{surv.PM}$$

The probability of establishment considers the steps needed to complete at least one transmission cycle from vector to host to vector, or from host to vector to host. If the probability of transmission, which is expressed as the optimal reproduction ratio ($R_{opt}$) for the target region, is $< 1$, the rate of introduction
is, however, limited to ensure that it will never be higher than the optimal reproduction ratio. This restriction was included in MINTRISK to consider the probability of transmission in this step. The rate of introduction (Intro) is then calculated as:

\[ \text{Intro} = \begin{cases} \text{Entry} \times \text{Est} & \text{if } R_{\text{opt}} \geq 1 \\ \text{Min} \left( R_{\text{opt}}, \text{Entry} \times \text{Est} \right) & \text{if } R_{\text{opt}} < 1 \end{cases} \]

Pathways are to be defined by the risk assessor and are either related to host animals, vectors, or, if the disease is zoonotic, humans. Based on the risk scores for the rate of introduction, the risk assessor is asked to select three pathways for inclusion in the next steps of the risk assessment.

The output “Epidemic size” provides the expected number of infected animals (or herds) depending on the extent of spread in the first vector season and the likelihood that the infection will persist during the adverse season. The extent of spread in the first vector season (Inf\text{Total}) is based on the effective reproduction ratio (R\text{eff}) in the affected region, the number of infection generations in one vector season (IG\text{Season}), and the expected time until detection of disease expressed in number of infection generations (IG\text{Det}) and is calculated as:

\[ \text{Inf}_{\text{Total}} = \begin{cases} \sum_{i=1}^{\text{IG}_{\text{Season}}} \text{R}_{\text{eff}} \\ \sum_{i=1}^{\text{IG}_{\text{Det}}} \text{R}_{\text{eff}} \times \left( 1 + \sum_{i=1}^{\text{IG}_{\text{Det}}} \text{R}_{\text{CM}} \right) & \text{if } \text{IG}_{\text{Det}} \geq \text{IG}_{\text{Season}} \end{cases} \]

\[ \text{Inf}_{\text{Total}} = \begin{cases} \sum_{i=1}^{\text{IG}_{\text{Season}}} \text{R}_{\text{eff}} \\ \sum_{i=1}^{\text{IG}_{\text{Det}}} \text{R}_{\text{eff}} \times \left( 1 + \sum_{i=1}^{\text{IG}_{\text{Det}}} \text{R}_{\text{CM}} \right) & \text{if } \text{IG}_{\text{Det}} < \text{IG}_{\text{Season}} \end{cases} \]

The likelihood of persistence (Pers) is based on the probability of overwintering for the most plausible overwintering route. Epidemic size (ES) is subsequently calculated as the expected total number of infected animals (or herds) over four vector seasons.

\[ \text{ES} = \begin{cases} 4 \times \text{Inf}_{\text{Total}} & \text{if } \text{Pers} \geq 0.8 \\ \left( 1 + \text{Pers} + \text{Pers}^2 + \text{Pers}^3 \right) \times \text{Inf}_{\text{Total}} & \text{if } \text{Pers} < 0.8 \end{cases} \]

The impact of disease (Impact) is based on questions related to economic impact, socio-ethical impact, and environmental impact. Only results for the economic impact are used to obtain the overall risk estimate, which is calculated as the product of the rate of introduction and the economic impact. At first, all inputs for the economic impact were based on monetary values for average epidemics. MINTRISK is currently under construction to directly connect the economic impact calculations to the epidemic size calculations.

### 3.3.2.2. RRAT

For each disease evaluated with RRAT, a risk score is calculated considering the number of units relevant for this pathway (i.e. animals or products) from each area of origin entering the Netherlands (N\text{PW}), the probability that a unit is infected or contaminated (P\text{PW}), the probability that infected units will not be detected or eliminated before exportation (1-P\text{det}) and the probability that entry will result in a first infection of native animals (P\text{inf}). The probability that pathway units are infected or contaminated is
based on the estimated disease prevalence in areas of origin and the rating of susceptibility of the pathway (e.g. reservoir host or incidental host, high-risk product or low-risk product). To estimate disease prevalence in areas of origin, data from OIE are used to either directly calculate disease prevalence or to derive a proxy value for disease prevalence based on the disease status of the area of origin. The probability of detecting or eliminating pathway units before exportation was estimated considering import restrictions defined in EU legislation. The probability of first infection was estimated considering the probability of disease transmission given the expected destination of the pathway. The overall risk score in RRAT is either calculated as the expected annual number of incursions ($R_n$) or the probability of at least one incursion per year ($R_p$):

\[
R_n = N_{PW} \times P_{PW} \times (1 - P_{det}) \times P_{inf}
\]

or:

\[
R_p = 1 - (1 - P_{PW} \times (1 - P_{det}) \times P_{inf})^{NPW}
\]

It should, however, be kept in mind that the calculated risk scores are semi-quantitative scores rather than quantitative estimates of the risk, because some input probability values are based on risk classes and not absolute values.

### 3.3.2.3. IDM

In IDM, risk scores are derived by considering disease outbreaks in areas of origin, trade volumes from areas of origin to the UK, an estimate of the disease risk of each pathway, and mitigation effects due to legislation in place. The tool also contains some pathways that cannot be expressed in trade volumes, such as migratory birds and vectors. Risk scores for individual pathways are calculated by multiplying the risk scores for the areas of origin and the pathways with the trade volumes, after which the risk score for mitigation is subtracted. The final risk score is calculated by summing the scores for all individual pathways and is given by:

\[
\text{Risk score} = \sum_{n} [(\text{area of origin risk} \times \text{pathway risk} \times \text{trade volume}) - \text{mitigation}] \text{ for } n \text{ pathways}
\]

Input variables in IDM are semi-quantitatively scored using information on trade volumes from Comtrade (UN, 2019) and TRACES (EU, 2019b), information on disease outbreaks from WAHIS (OIE, 2019) and ADNS (EU, 2019a), and information on disease characteristics (transmission pathways) from OIE and literature. Areas of origin are grouped. Risk scores for pathways are variable and sometimes seasonal. For vectors, wild birds, and transport seasonal variation is taken into account by manually rescaling the risk scores.

### 3.3.2.4. NORA

NORA consists of 63 questions about introduction pathways and 23 statements to define consequences, all of which have to be answered by the risk assessor. A total of nine entry pathways are considered in NORA. Questions are divided into profile questions to evaluate the relevance of pathways for a specific disease, and probability questions to evaluate the frequency of pathways. The risk assessor can also answer questions with “I don’t know” to account for uncertainty/ignorance and then the value applied in the calculations is in-between the values that would be used in case the question was answered with yes or no. Probability scores for the pathways are calculated by multiplying the results for the profile questions with the results for the probability questions. The contribution of pathways to the risk score is based on a predefined weighting of the pathways based on expert opinion. There are three weighting “patterns” of the pathways. The choice of the weighting is dependent on the transmission of the disease,
i.e. viral diseases that can be transmitted via animal products, viral diseases with an airborne transmission and viral diseases transmitted via by both animal products and an airborne route. However, the weights will be different for each disease. The risk score for the combined probability of entry and exposure ($P$) is then calculated as:

$$P = \sum_{i=1}^{9} W_i P_i / \text{Max}$$

where $P_i$ is the probability for pathway $i$, $W_i$ the weight for pathway $i$, and $\text{Max}$ the value that one would get if all pathways got maximum probability scores. NORA also provides an estimate of the consequences of introduction of disease based on the Finnish situation. To this end, risk scores for animal production and the industry are summed with scores related to the type of disease, the probability of losing the disease-free status, consequences due to human infections if the disease is zoonotic, and consequences related to the public opinion on the disease (fear). Again, an overall risk score is calculated by dividing the obtained score by the maximum score possible. The overall risk is then calculated as the product of the combined risk score for probability of entry and exposure and the risk score for consequences. Predefined tables are used to convert the numbers of the risk scores into qualitative output.

### 3.3.3. Qualitative risk assessment tools

#### 3.3.3.1. SVARRA

SVARRA is a purely qualitative tool and hence no explicit numeric calculations are performed. The risk assessor is asked to answer questions regarding the probability of entry and exposure for several pathways, i.e. live animal imports (legal and illegal), import of genetic material (legal and illegal), import of animal products (legal and illegal), indirect transmission routes (vehicles, persons, feed & bedding), vectors, and wild animals. Exposure is assessed for high biosecurity herds, low biosecurity herds, fenced wildlife (i.e. wildlife reared for meat production), and wildlife. Qualitative probability estimates have been defined using the terminology of OIE and EFSA (EFSA, 2006; OIE, 2010). Furthermore, the risk assessor is asked to document the considerations and the underlying data that led to the choice of a certain probability, as well as to report on his/her level of uncertainty using a table giving definitions of low, medium, and high uncertainty. To combine the estimated probabilities of entry and exposure per pathway, a risk matrix is used.

### 3.4. Comparison of the generic risk assessment tools

The seven generic RA tools were compared considering objectives, input data required, algorithms used, and presentation of results. Tables 4, 5 and 6 present an overview of the seven tools focusing on objectives, inputs, and outputs, respectively. A more detailed description of similarities and differences in algorithms and input data used is given in the following paragraphs.

All tools were designed with the aim to provide risk assessment outputs more rapidly than a disease-specific (bespoke) risk assessment can if it were to be developed from scratch (Table 4), although the time required to perform a generic risk assessment varies between hours to days (see resources required in Table 5). For all tools, the assessment will be less rapid if the disease has not been evaluated before with the tool as prevalence and all other disease parameters will need to be estimated. An overview of diseases for which the tools have been applied so far is given in Table 5. Incorporating a new disease will in general take a few days up to a week. RRAT and IDM have the data required to perform the risk assessment readily available in the tool for a multitude of diseases. SPARE and COMPARE have only been parameterised for a few diseases, although the data available on disease prevalence worldwide in these tools can theoretically be used to assess the risk of any OIE-listed disease. MINTRISK, NORA, and SVARRA come without underlying databases and inputs have to be provided by the risk assessor. Adding
a new pathway in the quantitative tools was deemed to be a much more time consuming task compared to changing country or disease.

All tools except MINTRISK have predefined pathways built in. MINTRISK asks the risk assessor to define relevant pathways either related to vertebrate host animals and their products, vectors, or humans. The other tools greatly vary with respect to the number of pathways that have been included. All of them assess the incursion risk from trade in live animals and products of animal origin. Most tools also address trade in germplasm, spread by arthropod vectors, wildlife dispersion including migratory birds, and human travel. The incursion risk from laboratory material is only addressed by IDM, whereas airborne spread is only considered by NORA.

Most tools can be used to rank diseases, pathways, or target regions, although not all of them were designed for this purpose. Figure 2 provides a comparison across the generic RA tools considered within this project for their ability to prioritise across diseases, pathways and regions. None of the tools can currently compare across all three attributes. Due to its qualitative nature, SVARRA is less suitable for prioritization, although ranking of pathways is feasible and can be a useful output. None of the tools was designed to evaluate preventive measures or control measures and the tools cannot be used for this purpose. All tools can be easily updated to allow for a change in disease status or movement of animals, although SPARE, COMPARE and MINTRISK were not designed for routine updates.

NORA and SVARRA were specifically developed to be used in response to disease events, e.g. a new outbreak of an epizootic disease in Europe. These tools aim to rapidly assess the incursion risk of such a new disease for the target region and consider the specific situation at that time taking into account, e.g., trade patterns in the preceding high-risk period (i.e. the period from first infection until first detection). All other tools assess a continuous incursion risk based on annual data for trade patterns and disease outbreaks. These tools will signal an increase in the risk of incursion for a specific disease over time rather than assessing the increased risk resulting from a specific disease event.

The expertise required to run and update each of the tools depends on the software in which the tool was built and the availability of data in the tool. If the disease and pathway are already included in the tool, results from SPARE and RRAT can be generated without the need for disease expertise. MINTRISK, IDM, NORA, and SVARRA, on the other hand, can only be used by disease experts but do not require any computing skills for day-to-day use. COMPARE is the most complex tool requiring both disease expertise and computing skills to run the model. To update the tools, in general both disease expertise and computing skills are needed. In addition, IDM and NORA also require expert knowledge to weight the input parameters when updating the tool with new diseases.
Figure 2: Ability of the seven generic RA tools to prioritise across regions, pathways and diseases.

A general overview of the tools is presented in Figure 3, indicating the potential steps in assessing disease incursion risk and to what extent each of the different tools includes those steps (Table 6). The tools have been colour-coded to indicate whether they provide quantitative, semi-quantitative or qualitative results. As shown, MINTRISK is most complete in assessing all steps, although the probability of first infection in this tool is addressed as part of the probability of establishment. SPARE only assesses the probability of entry, not considering the infection risk of native animals. The output of SPARE is, however, used to feed other models that do address the subsequent steps of the incursion risk. IDM and NORA have a special position in this figure in the sense that they perform a consequence assessment without going through all steps evaluating transmission of the disease. Both tools assess the probability of entry and exposure, after which IDM considers potential epidemiological consequences by assessing the $R_0$ value, whereas NORA combines the results for the probability of first infection with the expected economic consequences of a resulting outbreak. Although still under development, it is planned for COMPARE to also consider the probability of spread (epidemiological consequences).
Only a few of the RA tools have embedded uncertainty and/or variability in their risk assessment. COMPARE is the only tool addressing variability in calculating the incursion risk using stochastic calculations, including primarily the variability in prevalence within exported animals/products but also variability within disease parameters. MINTRISK and SVARRA are the only tools that explicitly ask the risk assessor for his/her uncertainty in estimating the input parameter values, and only MINTRISK uses stochastic simulation to address this uncertainty. NORA also acknowledges that risk assessors cannot be expected to know everything and offers the “I don't know” option in answering the questions. This uncertainty is reported in the results of the tool by counting the number of questions that were given this answer. Despite the fact that uncertainty is not embedded in the other RA tools, most of them offer the opportunity to consider uncertainty via scenario analysis. So, in effect, running the tool with alternative estimates for parameters deemed to be uncertain in order to ascertain the impact on the outputs of the risk assessment.
Table 4: Comparison of generic RA tools with respect to objectives.

<table>
<thead>
<tr>
<th>Risk assessment tool</th>
<th>Rapid risk assessment(a)</th>
<th>Data available in tool</th>
<th>Prioritisation</th>
<th>Scope of RA</th>
<th>Updates over time</th>
<th>Aimed for regular updates</th>
<th>Updates triggered by horizon scanning</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Scope of RA</td>
<td>Time scale</td>
<td>Easy to update for early warning purposes</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Prioritisation</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Disease(s)</td>
<td>Region(s)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Pathways</td>
<td>Target region</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Time scale</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SPARE</td>
<td>Yes</td>
<td>No</td>
<td>No, but possible(1)</td>
<td>Yes(4) EU member states</td>
<td>Annual</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>COMPARE</td>
<td>Yes</td>
<td>No</td>
<td>No, but possible(1)</td>
<td>Yes(4) Anywhere</td>
<td>Annual</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>MINTRISK</td>
<td>Yes</td>
<td>Yes</td>
<td>No(1)</td>
<td>Yes(4) Anywhere</td>
<td>Annual</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>RRAT</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes(1)</td>
<td>Yes(4) The Netherlands</td>
<td>Annual</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>IDM</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes(1)</td>
<td>No</td>
<td>United Kingdom</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>NORA</td>
<td>Yes</td>
<td>No</td>
<td>Yes(1)</td>
<td>Yes(4) Finland</td>
<td>Annual</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>SVARRA</td>
<td>Yes</td>
<td>No</td>
<td>No, but possible(1)</td>
<td>No</td>
<td>Anywhere (first version developed for Sweden)</td>
<td>Yes</td>
<td>Yes</td>
</tr>
</tbody>
</table>

(a) Tool designed with the aim to provide risk assessment outputs more rapidly than a disease-specific (bespoke) risk assessment developed from scratch
(b) Yes: contains information on many (listed) diseases; risk assessment can be performed immediately. No: tool only filled out for a subset of diseases; real rapid risk assessment only feasible in case the disease was previously assessed with the tool
(c) Prioritization of pathways is possible when evaluating the risk estimate for the rate of introduction
(d) Prioritization of target regions; areas of origin can also be ranked with this tool, this was, however, not a primary objective
(e) Prioritization of areas of origin
(f) Possible: This can be achieved by the tool but was not the original objective
Table 5: Comparison of generic RA tools with respect to input. Appendix B provides more detail on the data inputs for each tool.

<table>
<thead>
<tr>
<th>Risk assessment tool</th>
<th>Input into tool</th>
<th>Diseases to which tool has been applied so far</th>
<th>Global databases used</th>
<th>Type of model input</th>
<th>Resources required</th>
<th>Time to answer a risk question (no updates required) (f)</th>
<th>Time for updating tool with new disease (g)</th>
<th>Time for updating tool to answer a risk question for a new country</th>
</tr>
</thead>
<tbody>
<tr>
<td>SPARE</td>
<td>Live animals (incl. companions) (legal only); POAO; illegal POAO; windborne vector spread; human travel; wild animal dispersion</td>
<td>CSF, rabies, BT</td>
<td>WAHIS (OIE), Eurostat, TRACES</td>
<td>Quantitative</td>
<td>R Computing</td>
<td>Disease, computing</td>
<td>&lt; 10 minutes</td>
<td>&lt; 1 day</td>
</tr>
<tr>
<td>COMPARE</td>
<td>Live animal (legal only); wild animal dispersion; windborne vector spread; human travel; bird migration; products of all origin (legal only)</td>
<td>LSD, ASF (AI and Zika will be added)</td>
<td>WAHIS (OIE), TRACES, Eurostat, FAOstat, GPW (SEDAC)</td>
<td>Quantitative</td>
<td>R</td>
<td>Disease, computing</td>
<td>Disease, computing</td>
<td>&lt; 10 minutes</td>
</tr>
<tr>
<td>MINTRISK</td>
<td>User defined (vector-borne and non-vector-borne)</td>
<td>AHS, Babesia, CCHF, EHD, RVF, Tularemia, West Nile (d)</td>
<td>Quantitative values and ranges (for those qualitative answering categories are Visual Studio with C# for the algorithms)</td>
<td>Disease</td>
<td>Disease, computing</td>
<td>&lt; 1 minute</td>
<td>&lt; 1 hour</td>
<td>1 day – 1 week</td>
</tr>
</tbody>
</table>
### Generic risk assessment tools

<table>
<thead>
<tr>
<th>Risk assessment tool</th>
<th>Input into tool</th>
<th>Diseases to which tool has been applied so far⁽⁾</th>
<th>Global databases used⁽⁾</th>
<th>Type of model input</th>
<th>Resources required</th>
<th>Time to run the tool (for pre-populated diseases)</th>
<th>Time to answer a risk question (no updates required)⁽⁾</th>
<th>Time for updating tool with new disease⁽⁾</th>
<th>Time for updating tool with new pathway</th>
<th>Time for updating tool to answer a risk question for a new country</th>
</tr>
</thead>
<tbody>
<tr>
<td>RRAT</td>
<td>Pathways in tool</td>
<td>Live animals (incl. horses, companions, Balai⁽⁾) (legal only); POAO⁽⁾ (legal only); germplasm</td>
<td>ASF, AHS, CSF, FMD, EIA, bTB, BT, AD, PPR, LSD (AI will be added)</td>
<td>TRACES, Eurostat, WAHIS (OIE), ADNS, FAOstat</td>
<td>Qualitative and quantitative (qualitative input categorized into semi-quantitative risk scores)</td>
<td>R and SQLite Computing Disease, computing</td>
<td>&lt; 1 hour</td>
<td>&lt; 1 hour</td>
<td>1 day – 1 week</td>
<td>1 – 2 months</td>
</tr>
<tr>
<td>IDM</td>
<td>Diseases to which tool has been applied so far⁽⁾</td>
<td>Many exotic notifiable diseases</td>
<td>TRACES, Comtrade, WAHIS (OIE), ADNS</td>
<td>Qualitative and quantitative (both categorized into semi-quantitative risk scores)</td>
<td>Excel Disease Disease, expert knowledge</td>
<td>&lt; 1 minute</td>
<td>&lt; 10 minutes</td>
<td>&lt; 1 day</td>
<td>&lt; 1 day</td>
<td>&lt; 1 day</td>
</tr>
<tr>
<td>NORA</td>
<td>Any</td>
<td>ASF, LSD, CWD, FMD, BT</td>
<td>Excel Disease Disease, expert knowledge</td>
<td>&lt; 1 minute</td>
<td>1 day</td>
<td>1 day – 1 week</td>
<td>1 day – 1 month</td>
<td>1 month</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
## Generic risk assessment tools

<table>
<thead>
<tr>
<th>Risk assessment tool</th>
<th>Input into tool</th>
<th>Diseases to which tool has been applied so far</th>
<th>Global databases used</th>
<th>Type of model input</th>
<th>Resources required</th>
</tr>
</thead>
<tbody>
<tr>
<td>SVARRA</td>
<td>Live animals; germplasm; POAO; indirect routes (transport, people, feed &amp; bedding); vectors; wild animals, AI, ASF, BT, PPR, LSD</td>
<td>TRACES</td>
<td>Qualitative and quantitative</td>
<td>Word, Excel (including some calculations to set the uncertainty level of the risk estimate)</td>
<td>Disease</td>
</tr>
</tbody>
</table>

(a) Balai animals are exotic animals for which regulations are given in Council Directive 92/65/EEC
(b) POAO = products of animal origin
(c) AD = Aujeszky’s disease; AHS = African horse sickness; AI = avian influenza; ASF = African swine fever; BT = bluetongue; bTB = bovine tuberculosis; CCHF = Crimean Congo haemorrhagic fever; CSF = classical swine fever; CWD = chronic wasting disease; EHD = epizootic haemorrhagic disease; EIA = equine infectious anaemia; FMD = foot and mouth disease; LSD = lumpy skin disease; PPR = peste des petits ruminants; RVF = Rift Valley fever
(d) An adapted version of MINTRISK was used by EFSA to evaluate the risk of 36 vector-borne diseases (EFSA AHAW Panel, 2017)
(f) Assuming that it is one of the risk questions that can be answered by that tool
(g) Assuming that certain data exist and are readily available for that disease
### Table 6: Comparison of generic RA tools with respect to output.

<table>
<thead>
<tr>
<th>Risk assessment tool</th>
<th>RA steps</th>
<th>Are risk scores for different steps combined?</th>
<th>Output from tool</th>
<th>Presentation of main output</th>
<th>Variability</th>
<th>Uncertainty</th>
<th>Number of diseases evaluated at a time</th>
</tr>
</thead>
<tbody>
<tr>
<td>SPARE</td>
<td>Entry</td>
<td>N/A</td>
<td>Quantitative + ranking (semi-quantitative)</td>
<td>Relative ranking of EU member states for incursion risk of diseases and contribution of pathways; risk maps on country level (EU)</td>
<td>No (via scenario analyses)</td>
<td>No (via scenario analyses)</td>
<td>1</td>
</tr>
<tr>
<td>COMPARE</td>
<td>Entry; First infection; Consequence (epidemiological)</td>
<td>Combined, multiplication of probability of first infection with probability of spread</td>
<td>Quantitative</td>
<td>Risk maps for incursion risk of diseases with colour coding used to identify hotspots, including variability (higher resolution than SPARE)</td>
<td>Yes</td>
<td>No (via scenario analysis)</td>
<td>1</td>
</tr>
<tr>
<td>MINTRISK</td>
<td>Entry; Establishment; Consequence (epidemiological: spread and persistence, economic, socio-ethical, environmental)</td>
<td>Combined, multiplication of introduction probability with impact; however, 2D presentation of probability versus impact preferred</td>
<td>Semi-quantitative risk scores (ranging between 0 and 1) translated into qualitative risk categories</td>
<td>Qualitative risk score and colour coding; semi-quantitative risk score and uncertainty interval; risk profile diagrams plotting probability of introduction vs consequences; comparison of diseases</td>
<td>No</td>
<td>Yes</td>
<td>&gt;1</td>
</tr>
<tr>
<td>RRAT</td>
<td>Entry; First infection</td>
<td>Combined, multiplication of probability of entry with probability of first infection</td>
<td>Semi-quantitative risk scores</td>
<td>Ranking of pathways, countries and diseases using tables and graphs; semi-quantitative risk scores translated into qualitative risk levels</td>
<td>No</td>
<td>No</td>
<td>&gt;1</td>
</tr>
<tr>
<td>IDM</td>
<td>Entry; Exposure (epidemiological); Consequence (epidemiological)</td>
<td>Visualised (colour coding and graphical presentation)</td>
<td>Semi-quantitative ranking of diseases; qualitative description of risk for a single disease</td>
<td>Graphical ranking of all diseases based on their individual semi-quantitative risk scores; qualitative risk score for individual diseases including brief explanation</td>
<td>No</td>
<td>No (but includes &quot;Disclaimer&quot;)</td>
<td>&gt;1</td>
</tr>
<tr>
<td>NORA</td>
<td>Entry; Exposure; First infection; Consequence (economic)</td>
<td>Combined, multiplication of estimate for probability of entry and exposure and estimate for economic consequences</td>
<td>Semi-quantitative</td>
<td>Qualitative risk score for a single disease, separately for probability of incursion and consequences, including short description</td>
<td>No</td>
<td>No (but includes &quot;I don’t know&quot;- answers)</td>
<td>1</td>
</tr>
<tr>
<td>SVARRA</td>
<td>Entry; Exposure</td>
<td>Combined, use of risk matrix to combine probability of entry and probability of exposure</td>
<td>Qualitative description of risk for a single disease</td>
<td>Qualitative risk score including uncertainty; 3-pages report for a single event triggering RA</td>
<td>No</td>
<td>Yes</td>
<td>1</td>
</tr>
</tbody>
</table>

(a) IDM considers probability that pathogen enters first farm by weighting the different pathways (e.g. products get less weight than live animals). Results of IDM feed into D2R2 model (Gibbens et al., 2016) which evaluates additional steps.
(b) NORA estimates the economic consequences only; however, these might be based on an implicit assessment of the epidemiological consequences of introduction of the disease (e.g. number of animals/farms infected).

(c) Exposure of animal to infection, i.e. e.g. the probability that wild boar are exposed to a contaminated meat product that was present on a farm or in woods (e.g. due to inappropriate disposal).

However, probability of subsequent infection not included.

(d) This relates only to the output of the tool and not how the output is presented which relates more to risk communication and is considered in the next column.

(e) These qualitative risk scores feed into the D2R2 model (Gibbens et al., 2016).

(f) All tools that do not explicitly address uncertainty in their output results but consider uncertainty associated with model parameters or for situations (conditional statements) via scenario analysis.

(g) MINTRISK is parameterised for one disease at a time. However, output results within one assessment are given for all diseases simultaneously.
3.4.1. Input data

All of the generic tools use large quantities of data to parameterize their risk assessments, and in general they draw from the same data sources. The main difference between the generic tools related to input data arises due to the differences in the level of complexity in their algorithms and in their outputs (e.g. in terms of time and space), thus requiring more detailed data input. This complexity varies both in terms of which pathways are included and how to model those pathways. For example, only NORA and SVARRA include the (sub-)pathways of fomites in feed and bedding, and thus only these two need input data for this. As another example, both COMPARE and RRAT calculate the probability of first infection but, due to differences in the algorithms, COMPARE requires a larger number of parameters to be parameterised in order to calculate transmission via $R_0$.

Another significant difference across the generic tools regarding input data is the use of national statistics. Only those RA tools which were built primarily for a single country (RRAT, IDM, NORA, SVARRA) are able to utilise national statistics or national databases. These are often more reliable than global databases and provide more detailed information. In comparison, SPARE, COMPARE and MINTRISK (depending on the risk question), are not able to use national statistics, except in rare circumstances and with strong assumptions that all the other countries will be similar to the one with the data. However, the reliance on global databases often occurs alongside a desire to use freely-available data, thus these generic tools are more easily adapted and updated by new users.

There is a similarity across all generic tools with regard to the data used for trade and prevalence in the area of origin. With the latter, all tools use the OIE as the primary source although some may enhance this with other sources, especially when used for disease alerts rather than estimating prevalence during ongoing disease situations. For legal trade of live animals and products of animal origin, all the tools draw from the same global databases of TRACES (EU, 2019b), Comext (Eurostat, 2019a) and Comtrade (UN, 2019). However, there are discrepancies between these trade databases and problems regarding accessibility, which means that there is no preferred database. TRACES provides the most information for all pathways, but also has the most problems regarding accessibility. Similarly, the disease-related parameters often use the same data sources across the generic tools, with published literature being the preferred source. The other main source, when there is no available relevant published literature, is expert opinion.

The input data used for the exposure to susceptible species is subject to the widest variation across the generic tools and this arises primarily due to differences in how the tools choose to model this. COMPARE, the only quantitative tool to require this (as SPARE only assesses probability of entry), uses population abundance maps at a fine scale or regional data on average farm size, depending on the risk question, to model exactly how many susceptible animals could be in contact with the infected agent. Across the semi-quantitative and qualitative tools that consider contact with susceptible animals, there is still great variation in which data sources they use. NORA and SVARRA use the population abundance maps or national farm registries indirectly, while others use published literature, expert opinion and national databases, if available. In contrast, RRAT and IDM do not consider the abundance or exact locations of susceptible animals at risk but focus more generally on whether contact/infection could occur.

3.4.2. Algorithms

The generic tools have different levels of detail and different levels of complexity with respect to the algorithms used. Despite these differences, all tools use the basic principles of the Binomial model to estimate the probability of entry. The quantitative tools and most of the semi-quantitative tools calculate the rate of entry by multiplying pathway numbers ($M$) with probabilities of infection ($\rho$) based on prevalence levels. In some tools, prevalence levels are adjusted to take into account the probability of survival of the pathogen depending on mitigation measures and/or travelling time. IDM and NORA, however, use a semi-quantitative approach in estimating the probability of entry. IDM adds the semi-
quantitative scores for individual pathways and subtracts a semi-quantitative score for mitigation actions in place. NORA does not take into account prevalence, because values are usually not known at the time of an emergent disease situation, prevalence levels are usually very low at the start of a new outbreak, and because their estimate can be highly biased. Otherwise, the assumptions used in NORA are the same as for the other tools and the pathways numbers are scaled by weights that are disease and country specific.

SPARE only assesses the probability of entry without evaluating whether these will result in exposure or infection of native livestock populations. All other tools consider the probability of exposure (IDM, SVARRA), first infection (COMPARE, RRAT, NORA), or establishment (MINTRISK) and multiply this probability with the probability of entry to arrive at a combined risk estimate for the first steps of the risk assessment, although COMPARE does this stochastically rather than using the mean of the Binomial. Since estimates in SVARRA are purely qualitative, a risk matrix is used to combine the probability of entry with the probability of exposure (given entry) to arrive at an overall probability score. However, it is recognised that taking a matrix approach will still have underlying assumptions on how qualitative probabilities can be combined. Only four tools (COMPARE, MINTRISK, IDM and NORA) proceed into assessing the epidemiological and/or the economic consequences of disease incursion.

COMPARE, MINTRISK and IDM use the basic reproductive number $R_0$ to evaluate transmission of the disease once introduced. The basic reproductive number is usually defined as the average number of secondary infections caused by one typical infectious individual in a completely susceptible population during its entire infectious period (Keeling and Rohani, 2008). Infection will spread if $R_0 > 1$, resulting in either minor (i.e. small) or major (i.e. large) outbreaks, whereas infection will gradually fade out if $R_0 < 1$ with only minor outbreaks possible. Whereas COMPARE and MINTRISK use the $R_0$ value to calculate first infection and expected disease spread, IDM only uses the estimated $R_0$ value to indicate potential epidemic spread if a disease would enter the target region. The formula used to estimate $R_0$ depends on the main mode of disease transmission, e.g. the equations for $R_0$ for direct contact and vector-borne transmission will differ. As MINTRISK was especially developed to assess incursion risks of vector-borne diseases, only one $R_0$ formula was used. COMPARE, on the other hand, allows for different calculations of the $R_0$ value. This makes COMPARE very flexible, but also more complex to adapt to new diseases. Whereas COMPARE and MINTRISK both utilize $R_0$ by including it within mathematical equations, IDM only visualizes the estimate of the $R_0$ value by colour coding the risk scores for the combined probability of entry and exposure across all diseases in the tool in a graphical presentation.

Economic consequences are only assessed by MINTRISK and NORA. In the first version of MINTRISK, economic consequences were assessed using monetary values for direct and indirect economic losses related to infected animals and, if zoonotic, infected humans. However, these were not automatically connected to the estimated epidemic size. Currently, these calculations are under revision to link better with the epidemiological consequences. NORA also estimates the economic consequences separately from the epidemiological consequences, since epidemiological consequences are not considered in this tool. In NORA, a semi-quantitative risk score is obtained for the economic consequences by scoring the animal sectors that might be affected, the disease’s classification in national legislation, and possible multiplier effects. Both MINTRISK and NORA also take the more socio-ethical consequences into account, such as menace of the disease and animal welfare. Both tools use multiplication to combine results of probabilities and consequences, but prefer the two-dimensional presentation of the output of their tools.

### 3.4.3. Classification of tools

Based on the comparison of tools above with respect to objectives, algorithms, input and output, we tried to further classify the tools and to indicate their usefulness for different risk questions, e.g. considering the primary objective of the risk assessment, the timescale at which the risk assessment has to be completed, the disease and technical expertise available, etc. For this purpose, we formulated...
six questions that can be used to decide which generic RA tool best suits the need of the risk assessor. Not all questions might be relevant for each risk question. Depending on the risk assessor’s needs, one or more generic RA tools might classify as being useful to address the risk question. However, it can happen that none of the tools is perfectly fit for purpose. In that case, the risk assessor should evaluate which selection criteria are most important and make his/her choice for one of the tools based on these criteria and available resources (expertise, time).

1. What is the rationale for the risk assessment?
   a. Response to a disease event (NORA, SVARRA)
   b. Continuous assessment of incursion risk over a particular time period (SPARE, COMPARE, MINTRISK, RRAT, IDM)
   c. Horizon scanning (SPARE, COMPARE, RRAT, IDM)

2. Is there a need to prioritize diseases and/or pathways and/or target regions (for surveillance)?
   a. No (all RA tools)
   b. Yes, pathways (COMPARE, RRAT, NORA, SVARRA)
   c. Yes, diseases (MINTRISK, RRAT, IDM)
   d. Yes, target regions (SPARE, COMPARE, MINTRISK)

3. Which risk assessment steps are needed to obtain the required output?
   a. Entry (all tools)
   b. Exposure (IDM, SVARRA)
   c. First infection (COMPARE, RRAT, NORA)
   d. Establishment (MINTRISK)
   e. Epidemiological consequence (COMPARE, MINTRISK, IDM)
   f. Economic consequence (MINTRISK, NORA)

4. Is a qualitative or quantitative risk assessment preferred?
   a. Qualitative (SVARRA)
   b. Semi-quantitative (MINTRISK, RRAT, IDM, NORA)
   c. Quantitative (COMPARE, SPARE)

5. Which expertise is available to perform the risk assessment?
   a. Disease expertise only (MINTRISK, IDM, NORA, SVARRA)
   b. Computing expertise only (SPARE, RRAT)
   c. Both (all RA tools)

6. What time period is available to perform the risk assessment (in case a new disease or country has to be evaluated)?
   a. < 3 days (IDM, SVARRA)
   b. < 1 week (MINTRISK, RRAT)
   c. > 1 week (SPARE, COMPARE, NORA)

3.4.4. Summarizing overview

- All generic tools evaluated in this grant were designed with the aim to allow for a risk assessment to be conducted more rapidly than with a bespoke, disease-specific, risk model. However, for all tools the assessment will be less rapid if the disease has not been evaluated before with the tool due to the estimation of prevalence and other disease-related parameters.

- Prioritization is feasible with all tools, especially because of their generic character (allows for comparison between assessment results). Some tools were primarily designed for prioritization purposes and automatically provide ranking results. Other tools were primarily designed to ensure consistency over risk assessments, which allows for prioritization. However, these tools need manual ranking of results.
All tools can signal an increase in disease incursion risk if run over multiple time periods. However, some tools (NORA, SVARRA) were primarily developed to respond to disease events and are therefore better prepared to answer specific questions arising from outbreak situations.

Although most tools return semi-quantitative or qualitative results, they mostly need quantitative inputs. In the semi-quantitative tools, qualitative information or quantitative data are sometimes inserted as semi-quantitative risk scores.

Some tools (RRAT, IDM) contain all data required to perform the risk assessment, whereas other tools only provide the algorithms for the calculations. The latter tools require more time in day-to-day use, but are in general more flexible to adjust to new diseases. Tools with data embedded within them require regular updating.

All tools use input data on disease prevalence in the areas of origin, movements from the areas of origin to the target regions such as international trade, exposure to susceptible species, and disease-related parameters. The tools use similar global databases for disease prevalence and movements, although these are inputted directly or indirectly depending on the parameter and the tool. Data on disease-related parameters are mainly sourced from scientific literature and expert opinion. Data on exposure to susceptible species, if used, varies most among the tools. The main differences between the tools in terms of data input does not arise due to preferences for certain sources of data, but rather due to the algorithms in the tools, the pathways included and the chosen end-points.

All tools use the Binomial model to evaluate the probability of entry and the basic reproductive number $R_0$ to assess epidemiological consequences, if included in the tool. However, the level of detail included in the algorithms varies widely among the tools. Also different output parameters of the Binomial model are used to describe the incursion risk, e.g. the expected number of entries versus the probability of at least one entry.

For day-to-day use of most tools, either expertise on diseases or computing is required. This is closely related to the level in which data are included in the tools. The ease in which other users can apply the tool varies greatly.

Inclusion of variability and uncertainty is not always addressed due to the necessary compromise when considering multiple diseases and pathways resulting in a lower level of detail for each pathway. Some tools, however, address variability by performing regular updates. The results of several assessments will then indicate variability of risk over time. Other tools have variability/uncertainty embedded within the risk assessment (e.g. COMPARE, MINTRISK and SVARRA).

The resolution of the evaluated generic tools results in their unsuitability to evaluate intervention strategies such as preventive measures and control measures. This is not a primary goal of any of the tools.
3.5. Cross-validation of the generic risk assessment tools: the ASF case study

As described in Section 2.1 in order to cross-validate the generic RA tools, they were all applied to a case study on ASF. Three scenarios were considered by each of the tools, inputting standardised data, where available (Section 2.2.1), but otherwise parameterised in their normal way. This exercise did not assess the accuracy of each tool as the “true” risks are not known but instead cross-compares the results of the tools. However, as previously concluded, the tools did not have comparable outputs, which made the comparison of the absolute results impossible. For example, COMPARE, RRAT and NORA all considered first infection as an endpoint, but still the output parameter to evaluate this probability differed. Table 7 provides a summary of the endpoints of each tool for the ASF case study and the output parameters used. As a consequence, the cross-validation focused on the comparison of the relative risks as estimated by each tool.

IRTA developed a tailor-made quantitative risk assessment for the ASF case study. Although not a generic tool, the results are included here for comparative purposes. Two pathways were investigated in this risk assessment: legal trade in live animals and migrating wild boar. A summary of the IRTA approach taken is given in Appendix A.

Table 1 of Appendix C provides the results for each of the three scenarios for each of the RA tools. These are the absolute results, which were then used to determine the relative risks for each scenario and country (the Netherlands or Finland) across the individual pathways.

Table 7: Summary of the outputs of the RA tools for the ASF case study.

<table>
<thead>
<tr>
<th>RA tool</th>
<th>Output type</th>
<th>Endpoint</th>
<th>Output parameter</th>
</tr>
</thead>
<tbody>
<tr>
<td>SPARE</td>
<td>Quantitative</td>
<td>Entry</td>
<td>Number per year</td>
</tr>
<tr>
<td>COMPARE</td>
<td>Quantitative</td>
<td>First infection</td>
<td>Annual probability</td>
</tr>
<tr>
<td>MINTRISK</td>
<td>Semi-quantitative</td>
<td>Establishment</td>
<td>Annual rate, translated into risk score between 0 and 1</td>
</tr>
<tr>
<td>RRAT</td>
<td>Semi-quantitative</td>
<td>First infection</td>
<td>Probability-based risk score between 0 and 1</td>
</tr>
<tr>
<td>IDM</td>
<td>Semi-quantitative</td>
<td>Exposure</td>
<td>Risk score, translated into qualitative risk category</td>
</tr>
<tr>
<td>NORA</td>
<td>Semi-quantitative</td>
<td>First infection</td>
<td>Risk score, translated into qualitative risk category</td>
</tr>
<tr>
<td>SVARRA</td>
<td>Qualitative</td>
<td>Exposure</td>
<td>Qualitative probability category</td>
</tr>
<tr>
<td>IRTA</td>
<td>Quantitative</td>
<td>First infection (legal trade)</td>
<td>Annual probability</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Entry (wild boar)</td>
<td>Annual probability</td>
</tr>
</tbody>
</table>

(a) A tailor-made quantitative risk assessment for the ASF case study

3.5.1. Comparison of relative risks

As indicated in Section 2.1, three outputs of the ASF case study were compared across the tools, the results of which are described below.

3.5.1.1. Relative risk across the pathways by country and scenario

Most of the RA tools are able to compare the relative importance of the risk pathways considered within the tool (Table 8), although not all were designed for this purpose. To allow for a comparison between the RA tools, this analysis was done only for the three most commonly investigated pathways: live animals, animal products and wild boar. The red cells in the table indicate which pathway contributed the greatest risk; the grey cells indicate that the pathway was not incorporated within the tool. It was not possible to compare pathways for IDM as they are not scored consistently (the aim of the tool is to compare diseases, not pathways). Likewise, due to the different outputs for SPARE for the live animal pathway (number of infected animals) and animal products (kg of contaminated product) it was not possible to compare pathways for this tool either. The results show that most of the tools are unanimous.
in their identification of the main risk pathway in the baseline scenario (S1). For example, for the baseline scenario in the Netherlands (S1) and for all three scenarios in Finland, all of the tools that considered animal products identified that this was the pathway with the highest risk. Of the tools that did not consider animal products, IRTA estimated live animal trade to have the highest risk for both countries under all scenarios, whereas MINTRISK concluded that the pathway with the highest incursion risk was wild boar for both countries under all scenarios.

For S2 and S3 in the Netherlands, the animal products route was still predicted to have the highest risk in the quantitative tools (SPARE and COMPARE). However, NORA indicated a change in risks, such that live animal trade became the highest incursion risk. In SVARRA, the risks in S2 and S3 were assessed to be equally high for all pathways.

Some of the tools included more pathways than the three investigated here (Table 3). When taking into account these additional pathways, only in NORA the pathway ranking top for Finland was changed from trade in animal products to human travel for all three scenarios (Appendix C). In NORA, the human travel pathway includes the risk of ASF incursion via animal products carried for own consumption.

3.5.1.2. Relative risk for the Netherlands compared to Finland in the baseline scenario

For each of the generic tools, for each pathway investigated, the risk for the Netherlands was compared to Finland. The results are given in Figure 4 for the baseline (S1) scenario. For each figure, any bar that is above the value of 1 indicates that the risk was higher for the Netherlands than Finland, and any bar that is below the value of 1 indicates that the risk was higher for Finland than the Netherlands.

From Figure 4A it can be seen that, for each of the tools applied, the risk assessment predicted a higher risk for the Netherlands compared to Finland for the live animal trade pathway. In particular SPARE, COMPARE, RRAT and NORA predicted a much higher risk (i.e. over 100,000 times higher). The large differences in risk relate to the extremely low or even negligible incursion risk via live animals in Finland rather than a high risk for the Netherlands. This is because, in Finland, only 300 pigs were imported in 2017, in comparison to 1.95 million to the Netherlands (Eurostat, 2019a).

Only six of the tools evaluated the pathway for animal products (MINTRISK and IRTA did not). For NORA, RRAT and COMPARE, this risk was estimated to be higher for the Netherlands compared to Finland. For IDM and SVARRA the risks were equivalent between the two countries. SPARE uniquely predicted that the risks would be lower for the Netherlands compared to Finland. This tool is the only one that has entry (and not first infection or exposure) as an endpoint and as a consequence its results are difficult to compare to the other tools. The relatively high risk for Finland calculated by SPARE is most likely explained by the large amount of pork and pork products imported by Finland from Estonia.

Finally, for wild boar, the risks were predicted to be similar for the Netherlands and Finland from the RA tools COMPARE, NORA and IRTA, all being very low or negligible. SPARE, MINTRISK, IDM and SVARRA predicted a reversed risk for this pathway, i.e. Finland having a higher risk than the Netherlands. Results for the wild boar pathway are explained by the proximity parameters used in those models to estimate the wild boar risk with reported ASF cases in wild boar (Russia) being much closer to Finland than the Netherlands. The predicted risk of SPARE for the Netherlands was much lower than for Finland, which might again be explained from the fact that SPARE has the probability of entry as an endpoint. RRAT did not evaluate the wild boar pathway. For this pathway, there was a lot of uncertainty, especially in the estimated risk for Finland (relating to the data on the presence of wild boar in Russia near to the border with Finland and also the ASF situation near the border to Russia).
Table 8: Pathways contributing most to the ASF incursion risk for each country and scenario (indicated in red). The grey cells indicate that this pathway was not considered within the tool. The blank cells indicate that the pathway was considered but was not the pathway with the highest risk of ASF incursion.

<table>
<thead>
<tr>
<th>RA Tool(a)</th>
<th>Scenario(b)</th>
<th>The Netherlands</th>
<th>Finland</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Live Animals</td>
<td>Animal Products</td>
</tr>
<tr>
<td>COMPARE</td>
<td>S1</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S2</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>MINTRISK</td>
<td>S1</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S2</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RRAT</td>
<td>S1</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S2</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>NORA(c)</td>
<td>S1</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S2</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SVARRA(d)</td>
<td>S1</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S2</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IRTA</td>
<td>S1</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S2</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>S3</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

(a) It was not possible to compare pathways in SPARE and IDM
(b) S1: the ASF disease situation as of December 2017 (baseline); S2: hypothetical ASF cases in wild boar in Germany in December 2017; S3: hypothetical ASF cases in wild boar and domestic pigs in Germany in December 2017
(c) In NORA, the pathway passengers has the highest risk for Finland in all three scenarios
(d) Equal contribution of several pathways in one scenario

3.5.1.3. Relative risk for the hypothetical scenarios compared to the baseline scenario

The presence of ASF in Germany in wild boar (S2) and both wild boar and domestic pigs (S3) resulted in an equal or increased risk to both the Netherlands and Finland from all of the RA tools for the pathways live animals, animal products and wild boar. Figure 5 presents these results.

The relative risks are relatively small (but >1) for both NL and Finland for most of the tools for the live animal trade pathway (Figure 5A). The only exceptions are the results for MINTRISK (NL, S3:S1) and NORA (NL, S2:S1 and S3:S1), the latter of which had a relatively large increase. For animal products, the relative risks did not widely differ between the tools. However, for wild boar trade there is more variability between the tools. The quantitative tools SPARE, COMPARE and IRTA all estimated a much higher risk of disease entry into the Netherlands, if ASF was detected in Germany, compared to the baseline (S1) scenario. Viewing the differences for the Netherlands, when comparing the risk due to presence of ASF in domestic pigs and wild boar in Germany (S3) to the risk due to presence of ASF in wild boar only (S2), all of the tools except SVARRA indicate an increased risk due to live animal trade (reflecting the presence of the disease in the domestic pig population in Germany and the relatively large trade volumes from Germany to the Netherlands). However, the relative risks remain the same for Finland with the exception of SPARE and IDM, which indicate an increased risk via livestock trade. For the animal products pathway for the Netherlands, the risks all increase slightly with the exception of IDM, NORA and SVARRA for which they remain the same. In Finland, there is virtually no change (or none at all) for any of the tools. The presence of ASF in a domestic pig herd in Germany (S3) did not increase the risks to the Netherlands and Finland via the wild boar pathway compared to the presence of ASF in wild boar only (S2).
Figure 4: Relative risk of introducing ASF into the Netherlands compared to Finland in the baseline scenario (S1) by (A) trade in live animals, (B) trade in animal products, and (C) movement of wild boar. A relative risk above 1 (bold line) denotes the Netherlands has a higher risk than Finland, while a relative risk below 1 denotes Finland has a higher risk. If the relative risk equals 1, i.e. the risk of the Netherlands is equal to the risk of Finland, no bar is visible in the graph. <NA> indicates that a pathway was not available for a particular tool. Please note the different scales used on the y-axes.
Figure 5: Relative risk of the hypothetical scenarios (S2 and S3) to the baseline (S1) for introducing ASF into the Netherlands and Finland by (A) trade in live animals, (B) trade in animal products, and (C) movement of wild boar. A relative risk above 1 (bold line) denotes that S2 or S3 has a higher risk than S1. If the relative risk equals 1, i.e. the risk of S2 or S3 is equal to the risk of S1, no bar is visible in the graph. <NA> indicates that a pathway was not available for a particular tool. Please note the different scales used on the y-axes.

3.5.2. Uncertainty in results for the ASF case study
Only some of the generic tools explicitly include uncertainty (MINTRISK, SVARRA) or variability (COMPARE). In SVARRA, uncertainty is expressed for the risk estimate of each individual pathway and for the overall probability estimate.

In general, model results for the pathway trade in live pigs were more certain than model results for the pathway trade of animal products. The uncertainty in results for the wild boar pathway was highly dependent on the distance from infected wild boar to Finland and the Netherlands. With infected wild boar in Germany being relatively close to the Dutch border in scenarios 2 and 3, uncertainty in the model results for the Netherlands increased. Sporadically wild boar may migrate long distances, although this is less likely for ASF-infected boar. Uncertainty on the real number of wild boar being infected, when e.g. 10 cases are reported, was considered to be higher than uncertainty in migrating distances, especially for highly infected countries that do not report many cases in wild boar. In such cases, the spatial distribution of ASF cases in wild boar is also highly uncertain and therewith the distance from outbreaks to neighbouring countries. Furthermore, illegal or semi-legal (i.e. movement under Balai regulations, but animals sourced from unregistered premises or land) wild boar transportations could not be included in the tools but might contribute to the ASF incursion risk. Hence, the estimate of the incursion risk due to presence of infected wild boar in close proximity to the countries at risk was highly uncertain except for the Netherlands in the base scenario (2017 situation).

Generally, generic RA tools have lower resolution with respect to uncertainty and variability, compared to tailor-made models. The tailor-made IRTA model did include both uncertainty and variability for the pathways trade in live pigs and wild boar. The most important question, when addressing uncertainty, is whether the uncertainty would impact the risk management decisions based on the results of the risk assessments.

3.5.3. Limitations in comparing the results from the generic risk assessment tools

A full comparison of the absolute results of the different generic RA tools for the case study was not possible for several reasons: (a) objectives of the tools differed (Table 4); (b) the tools gave different output values ranging from qualitative probability levels, semi-quantitative risk scores to quantitative numbers (Table 6); (c) the tools provided different endpoints for their risk estimates (see Figure 3 and Table 6); (d) the pathways considered differed between the tools (Table 3 and Table 5). Further, differences in results between the tools might have resulted from different approaches used to transform global databases into input values. Each of these factors is discussed below.

3.5.3.1. Objectives of the tools

The generic RA tools were developed for different purposes with the main objectives of the tools ranging from rapid response to a new emergency to horizon scanning and prioritization of diseases, pathways or regions. SVARRA, a purely qualitative tool, and NORA, a semi-quantitative tool were both developed for preparedness purposes. SVARRA, for example, is used to evaluate the risk due to a changing situation with respect to disease presence or incidence. Most semi-quantitative tools (MINTRISK, RRAT, IDM) and the quantitative tools (SPARE, COMPARE) are used for horizon scanning and prioritization purposes rather than for immediate response to a changing situation. These tools are used to identify differences or changes in disease incursion risks and their results can be a reason to perform a more detailed risk assessment for a specific disease, region, or situation.

3.5.3.2. Output values

While quantitative results can in theory be translated into qualitative probability levels, qualitative results cannot be translated into quantitative numbers. However, comparison based on qualitative probability levels is not unambiguous either, as it is difficult to define and use transparent and objective risk levels to compare the results of the different tools. In SVARRA, EFSA terminology is used to define qualitative risk levels (EFSA, 2006). Other definitions of qualitative risk levels exist, some of them using quantitative
values to describe the qualitative levels. These are, however, not consistently used and scaling of quantitative values varies from linear scales to log scales. The EFSA terminology or other definitions of risk levels could be used to compare the results of the different tools for the ASF case study. However, even when using pre-defined risk levels, comparison of results of the different tools is not straightforward, since quantitative results or semi-quantitative risk scores first have to be translated into these qualitative categories. Even for the quantitative tools, comparison of the results is not possible as the outputs are different, e.g. SPARE outputs the numbers of infected/contaminated entries per year and COMPARE the annual probability of first infection. Likewise, some of the tools focus on the annual probability and others only on the high risk period.

3.5.3.3. Endpoints for risk estimates

To compare the results of the generic tools for the ASF case study, only the probabilities of entry, exposure, first infection and establishment were considered (Table 7). Consequences were not included, since not all tools do evaluate consequences. The different steps of the risk pathway included in the results of the generic tools also hampered comparison.

Not all tools were explicit in whether they evaluated the exposure risk to wild boar or to domestic pigs when assessing the probability of first infection. $R_0$ values do differ for wild boar populations and domestic pigs, where for domestic pigs values will also be different for within-herd transmission and between-herd transmission. In MINTRISK, it was not possible to take into account different values for $R_0$. The only tool that explicitly separated the wild boar and domestic pig population, when calculating the probability of first infection, is COMPARE. In COMPARE, transmission parameters are used for transmission from wild boar to wild boar, from wild boar to domestic pigs, and from domestic pigs to domestic pigs.

3.5.3.4. Risk pathways

The number of pathways evaluated differed among the tools. The total number of pathways considered was highest in NORA and SVARRA (Table 3). All tools evaluated legal trade in live animals. Importation of meat and meat products were evaluated by all tools but MINTRISK. Furthermore, IDM only accounted for products of animal origin illegally imported from third countries (based on a single score considering the potential for the disease to be introduced through illegal imports from different regions in the world). In contrast to all other tools, pathways in MINTRISK are user-defined. The choice for pathways is thus to some extent subjective. For the ASF case study, for example, it was decided by the risk assessor not to include import of meat and meat products as no data were available to distinguish between products derived from domestic animals and wild boar. Also the tailor-made model by IRTA did not evaluate this pathway. Wild boar was included in all tools but RRAT, although the way in which the wild boar pathway was evaluated differed between the tools. Some tools explicitly modelled wild boar ecology and/or wild boar movements (COMPARE, IRTA), whereas others only evaluated geographical proximity (SPARE, IDM, NORA, SVARRA).

3.5.3.5. Global databases

All of the RA tools considered the disease status of the areas of origin on the country level, except for MINTRISK and IDM where individual countries were clustered into larger geographic regions. All tools were fed with data on ASF outbreaks and cases reported to WAHIS (OIE, 2019). Prevalence estimates for areas of origin, however, varied between the tools, especially for non-infected countries. IDM, NORA, and SVARRA did not consider the potential risk of ASF-free countries, whereas the other tools did. The quantitative models SPARE and COMPARE, the semi-quantitative tool RRAT, and the tailor-made IRTA model estimated a probability of disease presence despite current absence based on (fixed) algorithms. In MINTRISK the incursion risk by ASF-free countries bordering ASF-infected countries was taken into account. Some tools (SPARE, COMPARE, SVARRA) explicitly accounted for underreporting, whereas others did not (RRAT, NORA, IDM, IRTA). In MINTRISK, correction for underreporting is possible in the assumptions made by the risk assessor. It is, however, not explicitly addressed in the questions.
Furthermore, SVARRA can account for infected regions within a country, whereas most other tools cannot.

Prevalence estimates in SPARE, COMPAR, RRAT, and IRTA are based on a one-year period. The default period when filling out MINTRISK and NORA is also a one-year period. In SVARRA, a user-defined time window can be used to account for, e.g., the high-risk period (period from introduction of the disease into a region until its detection). For the ASF case study, a 3-month period before the new outbreaks was considered in SVARRA (i.e. October till December 2017). IDM uses a risk score for disease presence rather than a prevalence estimate, distinguishing between presence of disease in wildlife only, sporadic cases in domestic animals, and widespread presence of disease in commercial farms. This risk score can be updated ad hoc. Hence, when new cases are reported, the score can be adjusted immediately. For SVARRA, it was concluded that results for a time period shorter than one year will be different only if a seasonal trend is observed in e.g. trade or disease outbreaks. Although changes in trade resulting from newly reported disease outbreaks might also affect the risk estimate differently for different time windows, it was assumed that this did not affect the comparability of results in the present case study. In the scenarios investigated, all hypothetical ASF outbreaks in Germany were assumed to be reported on 30 December 2017 and could therefore not affect trade patterns during the evaluated year.

In general, the qualitative tool SVARRA and the semi-quantitative tools NORA and IDM are better equipped to take into account short-term changes, such as a disease emerging in a new region, than the semi-quantitative tools MINTRISK and RRAT and the quantitative models SPARE, COMPAR and IRTA. Furthermore, the qualitative tool SVARRA can also more easily consider pathways for which quantification is difficult, such as human-mediated spread. Since risk assessments with SVARRA are performed on an ad hoc basis considering the current disease situation, their results are only valid for a limited period of time. As soon as the disease situation would change, an update of SVARRA’s risk assessment is required. Changes in the disease situation of course also require an update of the other RA tools. However, most of these tools use an annual time scale in performing the risk assessment and results will therefore be less dynamic.

All tools used data from Comext (Eurostat, 2019a) to assess the volumes of livestock and animal products traded. Despite the tools using the same database, choices made on which animal product codes to consider in the risk assessment for ASF differed among the tools, e.g. resulting in a different ranking of areas of origin contributing most to the incursion risk. Furthermore, it was concluded that data on trade in live pigs in Comext are not equal to data in TRACES. Especially for Finland, this might have led to deviations in the risk. Also data on trade in porcine germplasm could not be derived from Comext, because a general customs code was used for germplasm from all animal species except bovine semen.

### 3.5.4. Validation of the generic risk assessment tools

There is no golden standard with which to validate the generic RA tools. Therefore, due to the reasons mentioned above the outcomes of all tools for the case study were compared with a focus on the ranking of relative risks (by country and scenario) rather than the estimation of absolute values (Section 3.5.2). In addition the pathways within individual RA tools were compared against each other where possible.

Comparing the results of the generic RA tools for the ASF case study indicated that the tools agreed to a large extent on the trends of the estimated risks. It was therefore concluded that the cross-validation contributed to the credibility of the results. Furthermore, the assessment of the ASF incursion risk with several tools provided an indication of the overall uncertainty of the risk estimates.

Using the tools for a prolonged period might create an opportunity for external validation using field data. Some of the generic tools have been up and running for at least five years now. IDM was first released in 2011 and has intensively been used in the UK by Defra and the Scottish Government’s Centre of Expertise on Animal Disease Outbreaks (EPIC) to prioritise their risk levels for incursion of disease at different times of the year. SVARRA was first used in 2013 and has been used for several rapid risk
assessments including bluetongue, avian influenza, lumpy skin disease, and ASF. Furthermore, tools like SPARE and RRAT could potentially be validated by running the tools with a long range of historical data. However, one of the difficulties in validating models evaluating the incursion risk of exotic diseases, is that the adverse events being modelled have a low probability of occurrence. Hence, one would need a very long period to be able to validate those models with field data, which is furthermore hampered by the fact that the risk is not static over time due to e.g. changes in trade patterns and disease occurrences and risk management which is put in place as a result of the tool highlighting an increased incursion risk.

It should be noted that understanding and explaining the risk is often more important than the absolute value or level of the risk predicted. Risk communication is very important, when using results from the different tools. This applies to all of the RA tools.

3.5.5. Ease of applying the generic risk assessment tools to the ASF case study

An important attribute of a generic RA tool is the ease in which it can be applied to a new disease situation, both in terms of tool flexibility but also resources required. The ASF case study gave the opportunity for this attribute to be investigated. Unfortunately, the comparison was not straightforward due to some of the tools (e.g. SPARE, COMPARE, RRAT) already having been parameterised for ASF (or a similar disease), some required new pathways to be incorporated, or the parameterisation was only specific to the country the tool was originally developed for (e.g. NORA). Some of the tools were still under development at the time of the case study, so it was not a true reflection of the time required to run the case study (e.g. COMPARE, RRAT). Many of the tools found the collection of data from a country that was not their own to be the biggest difficulty. This was especially challenging for the qualitative tool (SVARRA) and the semi-quantitative tools that did not have an underlying database (MINTRISK and NORA).

MINTRISK was developed by WBVR. To assess its ease of use by risk assessors unfamiliar with the tool, DTU used MINTRISK to evaluate the baseline scenario (2017 situation) of the ASF case study (results not shown). A key conclusion from this exercise was that it is important to have a thorough explanation of the tool so that the questions that form the model inputs can be correctly answered. The need for the analyst to identify the number and type of pathways to be considered in the risk assessment resulted in a difference in pathways considered for the case study. WBVR only included two pathways, viz. trade in live animals and wild boar movements, whereas DTU considered trade in live animals, trade in pork and pork products, farm workers from other countries, and returning trucks. The number of pathways used for the final risk estimate in MINTRISK is, however, limited to three. Preferably, these are the three pathways that have the highest risk score for the rate of introduction. The choice on which pathways to include in the final risk estimate is, however, made by the risk assessor.

3.6. G-RAID Symposium

Results from the G-RAID project were disseminated at a one-day symposium in May 2019. Plenary lectures during the morning session provided an overview of generic RA tools, illustrated the need for harmonised data, presented the results from the ASF case study, and informed the audience on EFSA's efforts on harmonisation of risk assessment. In the afternoon, the seven generic RA tools of G-RAID were informally presented by poster presentations and demos. Furthermore, three interactive workshops were held to discuss (1) the choice for qualitative, semi-quantitative or quantitative modelling approaches, (2) data needs for generic risk assessment and options for harmonization, and (3) communication of risk assessment results to risk managers. Each workshop was held two times, giving the participants the opportunity to participate in two workshops. Information on the symposium is
The symposium was attended by 17 people, including both risk managers and risk assessors, from 10 different European countries (Figure 6). A bias was observed towards countries from North Western Europe, which could either be related to budget and logistics (the symposium was in Amsterdam, the Netherlands), the network of the consortium members (5 out of 6 being from North Western Europe), or a geographical bias with most expertise on veterinary risk assessment being concentrated in this part of Europe. The symposium was on average evaluated very positively with average scores for the lectures, posters/demos and workshops varying from 3.9 to 4.6 on a scale of 1-5 (Appendix D).

![Figure 6: Resident countries of participants (n=17) that attended the G-RAID symposium.](image)

## 3.6.1. Workshops

### 3.6.1.1. Modelling approaches

**Title:** Qualitative, semi-quantitative and quantitative approaches for risk assessment: which method in which situation?

**Objective:** To obtain the participants’ opinions on preferred approaches for risk assessment and the reasons underlying these preferences.

**Approach:** First, a brief introduction was given on qualitative, quantitative and semi-quantitative risk assessment methods and the differences between those. Then, the participants received different risk questions with some background information, including information on available data and resources and the timeframe to complete the risk assessment. Participants discussed in small groups on the preferred risk assessment method for each risk question, after which conclusions reached were discussed with all participants.

### 3.6.1.2. Data needs

**Title:** Data needs for generic risk assessment and options for harmonization

**Objective:** To discuss issues around the collection and use of data on disease incidence, volumes of different trade products and human travel. To identify limitations in using data and to find solutions to overcome these limitations.
**Approach:** Three 15-minute discussions were planned on specific areas related to data needs:

- Why do the participants need data and what for?
- What barriers have they encountered in getting these data?
- What suggestions do they have to overcome the barriers?

The participants were guided to consider five sub-criteria in their discussions; 1) Accessibility, e.g. does the data exist? Is access limited? 2) Availability, e.g. can data be easily extracted? 3) Completeness, e.g. are all the data you need included? 4) Consistency, e.g. are data presented in a similar format to those in other datasets? 5) Quality, are the data fit for purpose.

### 3.6.1.3. Risk communication

**Title:** Communication of risk assessment results to risk managers

**Objective:** To share and gather experience, information and comments from the participants (both risk assessors and risk managers) on the communication of results from risk assessments.

**Approach:** As an introduction, a short presentation about the risk analysis process was given. Participants were given questions to discuss good and bad communication of risk assessment results. As a basis for the discussion, the participants were given one of the scenarios from the G-RAID case study (Scenario 3) and the results from two of the tools (COMPARE and SVARRA) presented in one sentence. Questions discussed were:

- What is your experience as assessors or managers concerning communication to formulate the risk question in risk assessment assignments?
- As a risk assessor, would the risk question given here be clear to you? Would there be anything that you would like to have clarified?
- Are the two examples of communication of risk assessment results useful for you as a risk manager? Is something missing? Would you need more information on certain aspects?
- What are key factors for good communication of risk management strategies between managers and target groups? List at least five key factors.

### 3.6.2. Main conclusions from the symposium

- The major advantage of generic RA tools is the speed with which they can produce results (dependent on information on diseases/pathways in the tool). Generic tools are suited for horizon scanning and prioritisation of diseases. Results of generic tools might warrant further assessment of specific diseases including a higher level of detail for which bespoke models are preferred.
- It is preferable for generic risk assessments to include a consequence assessment in order to provide an accurate representation of the incursion risk. However, not all generic RA tools of G-RAID have included consequences in their risk assessment.
- There is no generic RA tool that outperforms all others. The generic RA tools of G-RAID were mostly developed independently by different groups and for different purposes. The choice for a tool will depend on the specific risk question (Need for spatial resolution? Need for consequence assessment?) and the resources and time available.
- There is not a single preferred modelling approach for risk assessment. Both qualitative, semi-quantitative and quantitative assessments can provide useful results. The choice for a specific approach is not only influenced by factors such as data availability, timeframe and human resources available, but also by personal bias/preference of the risk assessor. It is therefore advised to not have the decision on the approach taken by a single risk assessor.
• Semi-quantitative risk assessment needs to be defined more precisely. Although its use is discouraged by OIE (OIE, 2010), results of e.g. IDM are considered very useful by risk managers. Semi-quantitative risk assessment is not merely the translation of qualitative risk categories into numbers, but rather is a powerful parameterization of model parameters fit for purpose. The generic RA tools of G-RAID include four semi-quantitative tools. Most of these tools use algorithms to combine purely quantitative data with semi-quantitative risk scores that are based on either quantitative or qualitative input.

• All modelling approaches need data. The required level of detail in data increases from qualitative to semi-quantitative to quantitative approaches.

• For any risk assessment there is a need for continual dialogue between risk assessor and risk manager throughout the risk assessment process, i.e. not to focus only on communication of results.

• The message to the risk manager should include information on assumptions, limitations and uncertainties of the risk assessment. The detail of information that needs to be provided is context-dependent. In general, communication of results should be concise, but contain the essentials for a good understanding of the results.

• Accessibility and availability of global databases are of main concern to risk assessors, as well as consistency in data across different databases. Furthermore, metadata are considered essential for a correct interpretation and use of data from such databases.

• There is unlikely to be a “One Data” solution that will be adhered to by all data providers and that will serve all risk assessment needs, so risk assessors will need to continue working on analytical methods to deal with these issues.

• Negative results, e.g. from experimental or surveillance studies, can provide useful information for risk assessment studies. Negative results are, however, often not available due to publication bias favouring studies with positive results. Encouraging the submission of short communications on studies with negative results could contribute to the accessibility of such data. Also, an online repository where such negative results could be easily uploaded and maintained might be useful, but researchers would need encouragement to upload their results. Furthermore, issues around copyright and data protection would need to be considered.

• An international risk assessment community or platform to share and discuss data accessibility, availability and quality would be of benefit to future risk assessments as it will reduce time needed to resource data and improve quality of the data.

• There is an obvious need for data that are not available from global databases, such as disease-related parameters or parameters related to animal husbandry or ecology. These input parameters contribute a lot to the overall uncertainty in risk assessment results. A repository with such data could be part of the international risk assessment platform.

3.7. Impact of G-RAID

The impact of G-RAID was evaluated using three criteria: (1) the exchange of experience and expertise among the partner institutes, (2) the further development and validation of the generic RA tools, and (3) the dissemination of results to inform and educate a wider audience on generic risk modelling. Achievements for each of the three criteria are listed below.

A key achievement of G-RAID is the establishment of a strong network on generic risk assessment for animal disease incursions. The project not only contributed to the exchange of information between the partner institutes, but also to capacity building. G-RAID has contributed to the ability of the consortium members to provide a quick and effective response to questions of national and international
The present document has been produced and adopted by the bodies identified above as author(s). In accordance with Article 36 of Regulation (EC) No 178/2002, this task has been carried out exclusively by the author(s) in the context of a grant agreement between the European Food Safety Authority and the author(s). The present document is published complying with the transparency principle to which the Authority is subject. It cannot be considered as an output adopted by the Authority. The European Food Safety Authority reserves its rights, view and position as regards the issues addressed and the conclusions reached in the present document, without prejudice to the rights of the author(s).
- Oral presentation at APHA Modelling Symposium, 7 Feb 2019, London, UK
- Oral presentation at EFSA’s Advisory Forum meeting, 4 April 2019, Bucharest, Romania (by videoconference)
- Two posters presented at the SVEPM Annual Meeting, 27-29 March 2019, Utrecht, the Netherlands
- Poster presented at the EPIZONE Annual Meeting, 26-28 Aug 2019, Berlin, Germany
- Poster submitted to the Finnish Annual Veterinary Congress, 11-13 Dec 2019, Helsinki, Finland
- G-RAID Symposium, 15 May 2019, Amsterdam, The Netherlands
  - 17 participants from 10 different countries; mix of risk assessors and risk managers
- Paper submitted to Frontiers in Veterinary Science
  - Title: Validation of generic RA tools for animal disease incursion based on a case study for African swine fever
4. Conclusions

In this study, seven generic RA tools developed in four different European countries were compared and contrasted with respect to objectives, algorithms, input data, and output. All seven tools were designed to assess the incursion risk for multiple diseases and pathways and with the aim to provide risk assessment outputs more rapidly than a disease-specific risk assessment can if it were to be developed from scratch. Specific objectives of the tools varied from immediate response to new disease events to prioritization of diseases and horizon scanning, resulting in different approaches to evaluate the incursion risk of infectious animal diseases and different outputs.

The type of generic RA tool selected for use will depend on the risk question that needs to be addressed and the available resources. Issues to consider include the rationale for the risk assessment, the needs for prioritization, the required output, and the expertise and time available to perform the risk assessment (Section 3.4.3). NORA and SVARRA were specifically developed to be used in response to disease events, e.g. a new outbreak of an epizootic disease in Europe. These tools aim to rapidly assess the incursion risk of such a new disease for the target region and consider the specific situation at that time. All other tools assess a continuous incursion risk based on annual data for trade patterns and disease outbreaks. These tools will signal an increase in the risk of incursion for a specific disease over time rather than assessing the increased risk resulting from a specific disease event. Most tools can be used to rank diseases, pathways, or target regions. None of the tools can, however, compare across all three attributes. COMPARE, MINTRISK and RRAT are most suited for prioritization purposes, allowing for a ranking across two attributes (Figure 2).

The seven generic RA tools differ widely with respect to the number of diseases and pathways that have been assessed so far. For most tools, including additional diseases or pathways requires both disease expertise and modelling skills. In general, the more simple tools are more flexible to address new diseases or pathways. However, some of the complex tools have been built such that they contain information on the worldwide occurrence of all OIE-listed diseases, also allowing quite some flexibility to quickly perform the risk assessment for a disease not evaluated before.

All seven generic RA tools are primarily based on the OIE import risk assessment framework (OIE, 2010). However, the RA tools differ widely with respect to the steps they address to assess the disease incursion risk. MINTRISK is the most complete tool considering both the probability of entry and establishment, and epidemiological and economic consequences. SPARE on the contrary only considers the probability of entry. The need to include each of those steps will depend on the risk question addressed. It should, however, be noted that a comparison of the incursion risk across the different pathways is not possible if the RA tool only evaluates the probability of entry into the target region, as for some pathways entry of the pathogen will not always result in exposure of native animals. A fair comparison of the incursion risk over diseases is possible only if an impact assessment is included.

Based on the output provided by the generic RA tools, they were classified as quantitative (SPARE, COMPARE), semi-quantitative (MINTRISK, RRAT, IDM, NORA) or qualitative (SVARRA). The qualitative tool can quickly provide the information that risk managers need to act upon a new disease event without implying a level of precision that may not exist. Furthermore, this tool can consider pathways that are difficult to quantify such as human-mediated spread. Use of the qualitative tool requires knowledge on both the disease assessed and the livestock production sectors involved. The qualitative tools can quickly assess the risk for multiple diseases or regions without a need for expert judgement. These tools are in-depth risk assessment models that are resource-intensive with respect to input data and technical expertise. However, the outputs reflect this effort, e.g. COMPARE has the capacity to evaluate the risk of incursion at differing spatial resolution from 1km² to EU member state level. The semi-quantitative tools were mainly designed for prioritisation purposes and need in general less detailed data than the quantitative tools. All four semi-quantitative tools use algorithms to convert qualitative or quantitative input data into semi-quantitative or qualitative scores for the disease incursion risks. Although semi-quantitative risk assessments are not recommended by OIE, because they might give a misleading impression of objectivity and precision and might lead to inconsistent outcomes (OIE,
2010), most of the semi-quantitative tools in this study have been used to inform risk managers and were valued positively. Unambiguous definition of qualitative scores for both input data and output of the risk assessment is a prerequisite for both semi-quantitative and qualitative RA tools.

The availability of different generic RA tools provides the risk assessor with a repository of tools of which one can be chosen that is fit for purpose with respect to the objective of the risk assessment, the required outputs and level of detail, the time scale at which the risk assessment has to be completed, and the disease and technical expertise available (Section 3.4.3). Furthermore, the variety of generic RA tools of G-RAID enables the risk assessor to answer a risk question with more than one tool, the results of which might contribute to an increased insight in the risk and uncertainties involved.

4.1. Algorithms and input data

All seven generic RA tools use the basic principles of the Binomial model to assess the probability of disease incursion, combining information on pathway numbers with probabilities of infection based on prevalence levels. Although lack of data might hamper the estimation of infection probabilities and volumes moved for some pathways, such as vector dispersal and fomites, the Binomial approach can still be used though semi-quantitatively as illustrated by IDM. Although all based on the Binomial model, calculations in the tools differ with respect to the level of detail included and the output parameter calculated (e.g. the expected number of entries versus the probability of at least one entry).

Only three tools (COMPARE, MINTRISK and IDM) evaluate the epidemiological consequences of disease incursion. They do so by estimating the basic reproductive number $R_0$. Two tools (MINTRISK and NORA) also take economic and socio-ethical consequences into account, such as menace of the disease and animal welfare. Both tools use multiplication to combine results of probabilities and consequences, but prefer the two-dimensional presentation of the output of their tools.

All seven tools use a large quantity of data to inform their generic risk assessments including global databases, national statistics, published literature and expert opinion. The majority of the data required for the risk assessments can be broken down into four categories: 1) prevalence in area of origin; 2) movement from one area to another; 3) exposure to susceptible species; and 4) disease-related parameters. Prevalence is primarily based on data from WAHIS (OIE, 2019), although EMPRES-i (FAO, 2019a), ADNS (EU, 2019a), and official reports of the European Commission are also used across the tools. Movement of animals, products and other pathways are predominantly derived from global databases, such as TRACES (EU, 2019b), Comext (Eurostat, 2019a) or Comtrade (UN, 2019). For exposure to susceptible animals, more variation is observed between the seven tools due to contrasting choices made to model contact between susceptible animals and infected animals/products. Also for disease-related parameters, the tools differ in whether or how they incorporate these; however, all of them primarily use published literature and expert opinion to find relevant parameter values. Harmonization of these data across the tools appeared to be difficult due to different levels of detail in the calculations. Nevertheless, a need was felt to have a repository with data on disease parameters and other parameters commonly used in risk assessment that relate to disease transmission or exposure rates.

It can thus be concluded that the seven RA tools use similar input data and basic algorithms, but that further detailing of both was dependent on the objective of the tool, the pathways included, the chosen end-point, and access to global databases. Standardization of input data and algorithms across the tools was deemed not feasible. Nevertheless, the development of individual tools benefitted from the inventory of databases and input data, as most tools need similar raw input data, which now no longer had to be resourced for each tool separately. Furthermore, it was concluded that generic RA tools would benefit from standardization of names and codes of e.g. diseases, countries, animals and products across databases as well as uniform grouping of e.g. countries and product codes derived from such databases. An international risk assessment community or platform could contribute to such standardization.
4.2. Cross-validation

To explore the opportunities for cross-validation, all seven tools were used to assess the incursion risk of African swine fever (ASF) to the Netherlands and Finland for the 2017 situation and for two hypothetical scenarios in which ASF cases were reported in wild boar and/or domestic pigs in Germany. In addition, a tailor-made risk assessment was developed for this case study (IRTA). All tools were parameterized using the same global databases for disease occurrence (WAHIS; OIE, 2019) and trade in live animals and animal products (Comext; Eurostat, 2019a) to ensure that, as far as possible, variation in results would result from model uncertainty rather than parameter uncertainty.

Comparison of the absolute results of the different generic RA tools was not possible for several reasons, including their differing objectives, endpoints, risk estimates, output types and the different subsets of risk pathways considered. However, comparing relative risks of countries (Netherlands and Finland) and scenarios (baseline and two hypothetical ones) it was possible to cross-validate the tools across the different pathways.

In general, the tools agreed on the ranking of the target countries for the pathways evaluated, although the magnitude of relative risks calculated differed widely. For the 2017 situation (baseline), all tools evaluated the risk to the Netherlands to be higher than Finland for the live animal trade pathway, the risk to Finland the same or higher as the Netherlands for the wild boar pathway, while the tools were inconclusive on the animal products pathway. When comparing the hypothetical scenarios to the baseline all of the risk assessments indicated an increased risk to the Netherlands due to presence of ASF in wild boar and/or domestic pigs in Germany, whereas most tools agreed that the risk to Finland would stay at the same level or increase slightly. Investigating the risk pathways, comparisons could only be made for five of the seven tools, as the risk estimates for individual pathways in SPARE and IDM were given in different units and at a different scale, respectively. Of the remaining tools, most agreed that the animal product pathway (when considered) constituted the highest risk to both countries in the baseline scenario.

The ultimate aim of generic RA tools is to provide risk-based evidence to support risk managers in making informed decisions to mitigate the incursion risk of infectious animal diseases. The case study illustrated that conclusions on the ASF risk were similar across the generic RA tools, despite differences observed in calculated risks. Hence, it was concluded that the cross-validation contributed to the credibility of their results. In addition, the cross-validation of the generic RA tools based on the ASF case study contributed to a further understanding of the tools and as such to the internal validation of the tools.

4.3. Symposium

Results from G-RAID were disseminated at a one-day symposium in May 2019. At this symposium three important topics were discussed with the participants, i.e. (1) the choice for qualitative, semi-quantitative or quantitative modelling approaches, (2) data needs for generic risk assessment and options for harmonization, and (3) communication of risk assessment results to risk managers. The most important conclusions from the symposium were:

- The major advantage of generic RA tools is the speed with which they can produce results.
- Generic RA tools should preferably also include a consequence assessment.
- There is no uniform definition of semi-quantitative risk assessment. Its added value over qualitative risk assessments depends on the exact approach being used.
- The message to the risk manager should not merely convey the results of the risk assessment, but include information on assumptions, limitations and uncertainties of the risk assessment.
- There is a need for dialogue between risk assessor and risk manager throughout the risk assessment process.
• An international risk assessment community or platform to share and discuss data accessibility, availability and quality would be of benefit to future risk assessments.

• There is an obvious need for data that are not available from global databases, such as disease-related parameters or parameters related to animal husbandry or ecology.

• Publication of negative results, e.g. from experimental or surveillance studies, should be encouraged as these can provide useful information for risk assessment studies.

• There is unlikely to be a “One Data” solution that will be adhered to by all data providers and that will serve all risk assessment needs.
5. Recommendations

In this section, recommendations are given that would benefit the (future) development and validation of generic RA tools.

- Ideally, a generic RA tool should assess both the probability and consequences of disease incursions. Only then is a fair prioritization of diseases possible. Prioritization of pathways is feasible if at least the probability of exposure of native animals is considered in the risk assessment.

- Considering the algorithms, the Binomial approach is recommended to estimate the probability of entry of disease into a target region and the basic reproductive number is recommended for the evaluation of epidemiological consequences.

- Accessibility and availability of global databases are essential to parameterize generic RA tools. Risk assessment studies would benefit from a code of good practice for database curators to ensure easy access to such data, options for download in different formats, consistency of names and codes used across different databases, and inclusion of metadata explaining the data. It should, however, be realized that there is unlikely to be a “One Data” solution that will be adhered to by all data providers and that will serve all risk assessment needs.

- An international risk assessment community or platform to share and discuss data accessibility, availability and quality would be of benefit to future risk assessments as it will reduce time needed to source data and improve quality of the data. Such an international risk assessment community is preferably to be established by an international body in order to achieve sustainability, respectability and to reach as wide a community as possible.

- There is an obvious need for data that are not available from global databases, such as disease-related parameters or parameters related to animal husbandry or ecology. These data can often be hard to find by risk assessors, for example they may be part of a wider publication that would not be picked up using specific search terms relevant to that parameter. These input parameters contribute a lot to the overall uncertainty in risk assessment results. A repository with such data could be part of an international risk assessment platform.

- Negative results, e.g. from experimental or surveillance studies, can provide useful information for risk assessment studies. Such results are, however, often not available due to publication bias. An online repository where negative results could be easily uploaded and maintained would be useful.

- Cross-validation of generic RA tools by applying them all to a single risk question is an important step in the validation of such tools. Even if absolute results cannot directly be compared, because of different endpoints, output types and output parameters, a comparison of relative results is usually possible to evaluate if the tools would set the same priorities across diseases, pathways and regions. Furthermore, the comparison of results can indicate inconsistencies between the models that need to be investigated. This contributes to the internal validation of the tools, i.e. checking if model behaviour is as expected.

- Assessment of the risk by more than one generic risk assessment tool contributes to the credibility of the results obtained if all indicate similar priorities across regions, pathways, and/or diseases. Furthermore, the comparison of results of several tools provides an indication of the overall uncertainty of the risk estimate.

- There should be an ongoing dialogue between the risk assessor and risk manager as part of the full risk assessment process. Risk communication should not only involve results of the risk assessment, but also formulation of the risk question, defining the scope of the risk assessment and choosing a proper approach. When communicating results to the risk manager, also
There is no uniform definition of semi-quantitative risk assessment. In theory, it could be any risk assessment that is not purely qualitative or purely quantitative. All semi-quantitative generic RA tools in G-RAID transformed qualitative and/or quantitative input data into semi-quantitative risk scores. However, the approaches used varied widely. The credibility of semi-quantitative risk assessment would benefit from guidelines for good practices in semi-quantitative risk assessment.
References

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Glossary

**Area of origin:** Region or country where infection is present and from where the infectious agent might spread to the target region

**Basic reproductive number \( (R_0) \):** The average number of secondary infections caused by one typical infectious individual in a completely susceptible population during its entire infectious period

**Cross-validation:** Validation of model results by comparing them with results of other models that addressed the same question

**Epidemiological consequences:** Expected spread of the infectious agent in the target region in the native (susceptible) population or from the target region to new areas, considering e.g. the basic reproductive number \( R_0 \), epidemic size and geographic area affected

**Economic consequences:** Expected monetary losses resulting from an outbreak with the infectious agent in the target region due to e.g. morbidity and mortality, production losses, control measures and trade restrictions

**Incursion risk:** Generic term to indicate any metric to estimate the risk of an infectious agent entering the target region, varying from the probability of entry only to a full risk assessment including epidemiological and economic consequences

**Pathway:** A route along which the infectious agent can travel from the area of origin to the target region, e.g. trade in live animals or products of animal origin, vector dispersion, or human travel

**Probability of entry:** Probability that an infectious agent enters the target region

**Probability of establishment:** Probability that the infectious agent will start spreading in the target region given its entry into the target region and a first infection of a native host animal

**Probability of exposure:** Probability that a susceptible native host comes into contact with the infectious agent given its entry in the target region

**Probability of first infection:** Probability that contact with the infectious agent results in infection of a first native host in the target region (= index case) given its entry into the target region and exposure of the host animal

**Qualitative risk assessment:** An assessment where the outputs on the likelihood of the outcome or the magnitude of the consequences are expressed in qualitative terms such as high, medium, low or negligible (OIE, 2010)

**Quantitative risk assessment:** An assessment where the outputs of the risk assessment are expressed numerically (OIE, 2010)

**Semi-quantitative risk assessment:** An assessment where numbers are assigned to qualitative estimates, in the form of probability ranges, weights or scores, and combined by addition, multiplication or other mathematical operations (OIE, 2010)

**Target region:** The region or country for which the risk assessment is performed

**Uncertainty:** The lack of precise knowledge of the input values which is due to measurement error or to lack of knowledge of the steps required, and the pathways from hazard to risk, when building the scenario being assessed (OIE, 2010)

**Variability:** A real-world complexity in which the value of the input is not the same for each case due to natural diversity in a given population (OIE, 2010)
Appendix A – Further description of the generic risk assessment tools

SPARE: Development of SPatial risk assessment framework for Assessing exotic disease incuRsion through Europe

- To develop an overarching model to make rapid use of available metadata to identify pathways of potential risk for classes of disease transmission (e.g. vector-borne).
- Objectives: To provide valuable information for risk assessors in the first instances of a disease outbreak where typically information on imports and routes of entry and potential for spread is undertaken on a case-by-case basis. It will also allow for an objective and systematic evaluation to inform risk-based animal health and zoonotic surveillance activities.
- Pathways: Legal trade in livestock and pets, legal and illegal trade in products of animal origin, human travel by aircraft, vector dispersion, wild animal dispersion.
- Diseases: The case studies in the original project were classical swine fever (CSF), classical rabies and bluetongue.
- Main elements: The main routes of transmission considered are; Live animals, trade of meat products, wild animal dispersion, windborne spread of vectors, people movement and pets.
- Main inputs:
  - Country level pathogen prevalence/numbers (OIE, WAHIS annual/weekly reports)
  - Volumes of trade between countries (Comext, Eurostat)
  - Human travel data (Eurostat)
  - Pet movement data (TRACES)
  - Livestock density maps (FAO)
  - Wild animal prevalence/density/habitat suitability maps (from wider SPARE project or published literature)
- Main algorithms:
  - Algorithms to obtain and format input data from the internet
  - Distributions for expected number of cases per country
  - Spatial algorithms to assess expected dispersion of vectors/wild animals
  - Expected number and/or probability of introduction into EU member states for each route/pathogen/country combination e.g. expected number of live animals infected with CSF imported to Spain from Brazil, probability of at least one mosquito infected with bluetongue entering Italy from Tunisia.
- Outputs:
  - Relative risk scores to rank diseases and/or areas of origin.
  - User friendly visualization interface, to present outputs in the form of maps.
  - Results from various stages of the model (e.g. distributions for expected number of cases, expected number and/or probability of introduction into EU member states) can be used as inputs for a subsequent exposure assessment.
- Main author: Robin Simons, APHA, United Kingdom.
- Software: R.
- Available at: https://spare-europe.shinyapps.io/app_spare_v2/ (SPARE interface to explore pre-run results).

COMPARE: COllaborative Management Platform for detection and Analyses of (Re-)emerging and foodborne outbreaks in Europe

- Framework and R code that allows calculation of risk of infection for any disease from any area to any other area at any spatial scale, depending on data availability.
• Objectives: To identify hotspots for infection to target surveillance; to allow comparisons across diseases and pathways.
• Pathways: Legal trade of live animals, legal trade of food products, wild animal movement, vector dispersion, human travel, bird migration.
• Diseases: The completed case studies are lumpy skin disease, African swine fever and Zika. A case study for avian influenza is also planned.
• Main elements: Risk of infection at different spatial scales; risk of spreading to new areas.
• Main input: Prevalence data (derived from SPARE or calculated using EMPRES-i data), trade data (Comext and TRACES), abundance/presence of wild animals, number of farms and animals in area of interest, disease-related parameters.
• Main algorithms: Calculation of probability of first infection and spread based on modelling, quantitative input and stochastic simulations to produce a distribution of risk. Different models included for different pathways, with the main pathways being trade of livestock and products, vector-borne, wild animal introduction, migratory birds and human travel.
• Output: Color-coded maps at different spatial scales showing the risk of infection and spread in different areas, with separate maps showing variability.
• Main author: Rachel Taylor, APHA, United Kingdom.
• Software: R.
• More information: Taylor et al., 2018; Taylor et al., 2019a; Taylor et al., 2019b; Taylor et al., 2019c.

MINTRISK: Method for INTEGRATED RISK assessment of vector-borne diseases

• Web-based calculation tool for quick and more in-depth risk assessments of vector-borne diseases.
• Objectives: To ensure completeness and consistency in risk assessment of vector-borne diseases; for comparison and prioritization.
• Pathways: User-defined.
• Diseases: Vector-borne diseases, user-defined.
• Main elements: Probability of entry, transmission, and establishment, extent of spread, likelihood of persistence, impact.
• Main input: Answering of questions that have qualitative answer categories with a quantitative explanation.
• Main algorithms: Sampling from triangular distributions on a linear scale between 0 and 1; the sampling range is based on the selected answer category and indicated uncertainty; the sampled risk scores are log-transformed into quantitative values that are consistent with the quantitative explanation of the answer category chosen; input values are combined using mathematical algorithms that are based on the principles of risk assessment and mathematical modelling in epidemiology; output values are back-transformed into a risk score, where the relevant output levels are scaled between 0 and 1.
• Output: Risk scores between 0 and 1 translated into qualitative risk scores for each step in the tool and for the overall risk estimate; two additional summarizing risk scores are provided: rate of introduction and epidemic size; use of a two-dimensional risk profile diagram indicating the overall probability of introduction versus the epidemic size or the impact of disease.
• Main author: Aline de Koeijer, WBVR, The Netherlands.
• Software: Visual Studio with C# for algorithms.
• Available at: https://www.wecr.wur.nl/mintrisk/
• More information: De Vos et al., 2012; De Vos et al., 2016; EFSA AHAW Panel, 2017; EFSA 2017.

RRAT: Rapid Risk Assessment Tool
Relational database that can be queried to answer risk questions related to the introduction of exotic animal diseases.

Objectives: To prioritize diseases for risk management and early warning; to identify high risk trade flows.

Pathways: Legal trade in live animals, germplasm and products of animal origin.

Diseases: The tool has been parameterized to estimate the risk for ten diseases, viz. African swine fever, bluetongue, equine infectious anaemia, lumpy skin disease, peste des petits ruminants, bovine tuberculosis, pseudorabies, classical swine fever, foot and mouth disease, and African horse sickness. Avian influenza will be included in a later stage.

Main elements: Probability of entry, probability of establishment.

Main input: Tables on worldwide distribution of diseases (WAHIS), on trade in animals and animal products and other pathways (TRACES, Comext Eurostat), and on infectivity of pathways such as susceptibility of animal species, disease parameters, and contamination of animal products (information derived from literature).

Main algorithms: Calculation of probability of introduction and establishment of diseases into the Netherlands; while pathway numbers are based on quantitative data, probabilities of infection and establishment are based on semi-quantitative values derived from risk categories.

Output: Relative risk scores to rank diseases, pathways and/or areas of origin.

Main author: Clazien de Vos, WBVR, The Netherlands

Software: R and SQLite.

Release and upgrades: First version to be finished in 2019.

More information: De Vos et al., 2018.

IDM: International Disease Monitoring tool for risk of incursion

A semi-quantitative rapid risk assessment tool for incursion of disease through trade routes and other high risk pathways.

Objectives: To provide an evidence base for the most high priority exotic notifiable diseases and the risk of incursion for the UK. The tool compares different pathways (trade of live animals, products and germplasm, vectors, wildlife and transport) for different diseases to give a comparative risk score and help policy makers decide on areas for concern.

Pathways: Trade in live animals including horses, pets, and the Balai animals, trade in products of animal origin (POAO), transportation, and migratory birds.

Diseases: The tool includes a large number of mostly exotic notifiable diseases, but can do any new or emerging disease.

Main elements: Excel workbook with interlinked spreadsheets giving scores for the level of trade from and the presence of disease in different geographic regions (not individual countries) for different diseases. Mitigation is based on whether regulations or disease control measures are in place at the area of origin. A final additive risk score for each pathway is then compared between all the diseases, graphically.

Main input: Disease presence in wildlife or domestic livestock (either as sporadic domestic outbreaks in small non-commercial farms or widespread in commercial farms); trade volume as a score of 0 to 3 for geographic regions and for different risk products (live animals, germplasm, products of animal origin); option for including transport (fomites), vectors and exotic animal trade; a “degree of separation” score is used to account for whether there are overlapping wild bird migration routes and the same proximity score is used for wildlife movements in the ASF case study.

Main algorithms: Risk scores are calculated by multiplying the scores for the pathways and trade volume, adding the risk score for additional pathways (migratory birds) and by subtracting the risk score for mitigation.

Output: Table and graph comparing the diseases.

Main author: Helen Roberts, APHA, United Kingdom.

Software: Excel.
- Release and upgrades: First release: 2011. Regular updates as requests were made to include new diseases. Updated seasonally or if a large jump in disease distribution is seen. New version in 2013 to account for wild bird migration routes.
NORA: NOpea RiskArviointityökalu (rapid risk assessment tool)

- NORA was developed for situations where there is a change in the disease status of easily transmissible animal diseases in neighbouring countries or in countries with significant interactions with Finland.
- Objectives: The goal was to develop a tool that is quick to use and will provide consistent results in order to support risk management decisions.
- Pathways: Trade in live animals, germplasm and products of animal origin, vector dispersion, wild animal dispersion, airborne spread, feed and bedding, and fomites and transport means related to human travel.
- Diseases: NORA has been parameterized for African swine fever, lumpy skin disease, chronic wasting disease, foot and mouth disease, and bluetongue.
- Main elements: importance/relevance of different introduction routes, probability score of entry and establishment (in other words introduction), impact.
- Main input: Answering of questions that have qualitative answer categories with a quantitative explanation.
- Main algorithms: Combination of values within a route are calculated by applying the basic probability calculation rules of serial (multiplying) and parallel (summing) processes. There are no Monte Carlo simulations in the estimation.
- Output: The potentiality of nine different introduction routes, their relative importance and the overall incursion risk on a semi-quantitative scale. If the impact score is assessed, there is a possibility to also estimate combined risk that is relative to FMD impact of Finnish RA.
- Main author: Tapani Lyytikäinen, Ruokavirasto, Finland.
- Software: Excel.

SVARRA: Rapid risk assessment tool for introduction of exotic disease to the Swedish animal population

- Qualitative risk assessment tool to assess the probability of introduction of exotic diseases into the Swedish animal population.
- Objectives: To ensure systematic, structured, transparent and well documented qualitative rapid risk assessments.
- Pathways: Live animals, germplasm (semen, ova, embryos), indirect transmission (vehicles, persons including clothes and equipment, feed and bedding), animal products, vectors and wild animals.
- Diseases: Designed to be used for any disease. SVARRA has so far been used for risk assessments on avian influenza, African swine fever, lumpy skin disease, peste des petits ruminants, and bluetongue.
- Main elements: Probability of entry, probability of exposure. SVARRA consists of three parts: instructions, a template to be filled out by the risk assessor, and a summarizing report based on the template. Only the summarizing report is communicated to external parties. The template provides the documentation of the risk assessment.
- Main input: Answering of probability questions related to pre-established risk pathways with answers being based on import data, legal requirements in area of origin and Sweden, expert opinion on illegal trade, indirect transmission, and wildlife populations. Uncertainty is assessed for each probability question.
- Main algorithms: Risk matrix to combine the estimated probabilities of entry and exposure per pathway. Algorithm to derive the overall level of uncertainty from the uncertainties of the single pathways.
- Output: Probability of exposure of Swedish wild or domesticated animal populations expressed in qualitative terminology: negligible, very low, low, medium, high, very high. Uncertainty is
expressed using the terms low, medium, high. Both sets of terms are provided with an interpretation of each term. Result of the assessment is communicated in a 3-page report.

- **Main authors:** Cecilia Hultén and Kaisa Sörén, SVA, Sweden.
- **Software:** Word (2013 version); Excel (2018 version; developed by Arianna Comin).
- **Release and upgrades:** First (Swedish) version in Word in 2013; English version in Word in 2018; Excel version in 2018.
- **More information:** EFSA, 2017.

**IRTA: Risk assessment for introduction of ASF into the Netherlands and Finland via live animal movements and migratory wild boar**

- Quantitative risk assessment tool to assess the probability of introduction of ASF into the Netherlands and Finland
- **Objectives:** To develop a tailor-made risk assessment to address the scenarios posed by the case study.
- **Pathways:** legal trade in live animals; migrating wild boar
- **Diseases:** ASF only.
- **Main elements:**
  - The probability of ASF introduction by legal trade was evaluated using a scenario tree approach. Parameters considered were (1) the probability that domestic pigs in the areas (countries) of origin were infected, by modelling the annual probability of an epidemic of ASF in the areas of origin, and the probability of a pig being infected in the case of an epidemic (considering the expected number of infected farms during the high risk period, the expected within-herd prevalence at these farms, and the average census of pig herds in the areas of origin) (2) the probability that the infected animals would not be detected before export using information on the incubation period and course of disease, and (3) the numbers of pigs imported from the areas of origin based on Eurostat data. The probability of first infection was based on the percentage of pigs imported for life, assuming that this would always result in a first infection of local pigs.
  - The probability of ASF introduction by wild boar was evaluated by modelling active movements of wild boar using a modification of the Levy walk algorithm. The model contained information on the expected daily distance migrated by wild boar using a Pert distribution. The shape of the Pert distribution was set such that 90% of the samples would result in a daily distance travelled < 1000m. The model indicated that no infected wild boar could reach the Netherlands or Finland within a period of 365 days in the base scenario. In scenarios 2 and 3, a small probability was calculated that infected wild boar could reach the Netherlands. These results were, however, very sensitive to the shape parameter of the Pert distribution. This model only calculates the probability of entry, not exposure or first infection.

- **Main elements:** Risk of ASF spreading to the Netherlands and Finland.
- **Main input:** Prevalence data (derived OIE data), trade data (Comext), number of farms and animals in area of interest, disease-related parameters
- **Main algorithms:** Different quantitative models included for the 2 different pathways. Stochastic models for both pathways.
- **Output:** Annual probability of disease introduction into Finland and Netherlands via the movement of live animal. Analysis of probability of entry via wild boar displayed spatially.
- **Main author:** Sebastian Napp, IRTA, Spain.
- **Software:** @Risk for live animals model and R for wild boars model.
- **Release and upgrades:** First release: November 2018.
- **More information:** Napp, 2019.

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www.efsa.europa.eu/publications 70 EFSA Supporting publication 2019:EN-1743

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Appendix B – Comparison of input data for the generic risk assessment tools

Tables 1 – 4 summarise the data inputs for each of the generic RA tools.
Table 1: Summary of the input data used in the seven generic RA tools included in G-RAID: Movement from one area to another.

<table>
<thead>
<tr>
<th>Data Details</th>
<th>SPARE</th>
<th>COMPERE</th>
<th>MINTRISK(a)</th>
<th>RRAT</th>
<th>IDM</th>
<th>NORA</th>
<th>SVARRA</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Trade data for live animals</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Use?</strong></td>
<td>Use directly</td>
<td>Use directly</td>
<td>Use indirectly</td>
<td>Use directly</td>
<td>Use indirectly</td>
<td>Use indirectly</td>
<td>Use indirectly</td>
</tr>
<tr>
<td><strong>Use 1 source or many?</strong></td>
<td>1</td>
<td>1</td>
<td>&gt;1</td>
<td>1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
</tr>
<tr>
<td><strong>Usual Sources</strong></td>
<td>Comext, Traces</td>
<td>Comext, Traces</td>
<td>Comext, Traces, FAOstat, national statistics found</td>
<td>Comext, Traces</td>
<td>Traces</td>
<td>Traces</td>
<td>Traces, national statistics</td>
</tr>
<tr>
<td><strong>Able to change source data easily?</strong></td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td><strong>Illegal Trade, both POAO and live animals</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Use?</strong></td>
<td>Use directly</td>
<td>No</td>
<td>Use indirectly</td>
<td>Not yet</td>
<td>Use indirectly</td>
<td>Use indirectly</td>
<td>Use indirectly</td>
</tr>
<tr>
<td><strong>Use 1 source or many?</strong></td>
<td>&gt;1</td>
<td>0</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
</tr>
<tr>
<td><strong>Usual Sources</strong></td>
<td>Passenger and ferry statistics, literature</td>
<td>N/A</td>
<td>Passenger statistics; info on migrants, seasonal workers, custom seizures</td>
<td>Passenger statistics, customs/border inspection info, expert judgement</td>
<td>?</td>
<td>Travel statistics, border control, custom registries</td>
<td>Grey literature, published reports</td>
</tr>
<tr>
<td><strong>Able to change source data easily?</strong></td>
<td>Yes</td>
<td>N/A</td>
<td>Yes</td>
<td>Yes</td>
<td>?</td>
<td>Yes but data sources hard to find</td>
<td>Yes but data sources hard to find</td>
</tr>
<tr>
<td><strong>Movement of wild animals</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Use?</strong></td>
<td>Yes</td>
<td>Yes</td>
<td>Use indirectly</td>
<td>Not yet</td>
<td>Yes?</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td><strong>Use 1 source or many?</strong></td>
<td>1</td>
<td>1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
</tr>
<tr>
<td><strong>Usual Sources</strong></td>
<td>published abundance maps</td>
<td>published abundance maps</td>
<td>Published presence/abundance data; information on migration distances; published and grey literature; relevant</td>
<td>Published presence/abundance data; flight ways</td>
<td>?</td>
<td>Information of natural resources</td>
<td>Published and grey literature, relevant</td>
</tr>
</tbody>
</table>
### Generic risk assessment tools

<table>
<thead>
<tr>
<th>Able to change source data easily?</th>
<th>authorities and stakeholder organisations</th>
<th>centre, border control</th>
<th>authorities, stakeholder organisations</th>
</tr>
</thead>
<tbody>
<tr>
<td>No - unless maps are already published for species</td>
<td>Yes</td>
<td>Still uncertain</td>
<td>?</td>
</tr>
</tbody>
</table>

### Transport (leading to transfer of fomites etc.) both by vehicles and movement of farm labourers etc.

<table>
<thead>
<tr>
<th>Use?</th>
<th>Use 1 source or many?</th>
<th>Usual Sources</th>
<th>Able to change source data easily?</th>
</tr>
</thead>
<tbody>
<tr>
<td>No</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>No</td>
<td>N/A</td>
<td>Traces, information from the field</td>
<td>Yes</td>
</tr>
<tr>
<td>Use indirectly</td>
<td>&gt;1</td>
<td>Traces?</td>
<td>N/A</td>
</tr>
<tr>
<td>No</td>
<td>Yes</td>
<td>TRACES, information from the field</td>
<td>Yes</td>
</tr>
<tr>
<td>Yes</td>
<td>Yes</td>
<td>Traces, published reports, information from stakeholder organisations</td>
<td>Yes</td>
</tr>
</tbody>
</table>

### Movement of Vectors

<table>
<thead>
<tr>
<th>Use?</th>
<th>Use 1 source or many?</th>
<th>Usual Sources</th>
<th>Able to change source data easily?</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yes</td>
<td>Yes</td>
<td>Published and grey literature</td>
<td>Yes</td>
</tr>
<tr>
<td>Use indirectly</td>
<td>&gt;1</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>No</td>
<td>Yes</td>
<td>Grey literature, published reports</td>
<td>Yes</td>
</tr>
</tbody>
</table>

### Trade of POAO

| Use? | Use indirectly | Yes | Yes | Yes | Yes |

---

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## Generic risk assessment tools

<table>
<thead>
<tr>
<th>Use 1 source or many?</th>
<th>1</th>
<th>1</th>
<th>&gt;1</th>
<th>1</th>
<th>1?</th>
<th>&gt;1</th>
<th>&gt;1</th>
</tr>
</thead>
</table>

### Usual Sources
- Traces, Comext
- Comext, FAOstat, national statistics
- Comext
- Traces
- customs, border control, inspections
- national statistics

### Able to change source data easily?
- Yes
- Yes
- Yes
- Yes
- Yes
- Yes

### Movement of feed and bedding

<table>
<thead>
<tr>
<th>Use?</th>
<th>No</th>
<th>No</th>
<th>Use indirectly</th>
<th>No</th>
<th>Yes</th>
<th>Yes</th>
<th>Yes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Use 1 source or many?</td>
<td>No</td>
<td>No</td>
<td>&gt;1</td>
<td>No</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
</tr>
</tbody>
</table>

### Usual Sources
- N/A
- Comext, national statistics, grey literature
- N/A
- ?
- custom statistics
- national statistics

### Able to change source data easily?
- N/A
- Yes
- N/A
- Yes
- Yes
- Yes

### Trade of genetic material (semen, ova etc.)

<table>
<thead>
<tr>
<th>Use?</th>
<th>No</th>
<th>No</th>
<th>Use indirectly</th>
<th>Yes</th>
<th>Yes?</th>
<th>Yes</th>
<th>Yes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Use 1 source or many?</td>
<td>N/A</td>
<td>N/A</td>
<td>&gt;1</td>
<td>1</td>
<td>1</td>
<td>&gt;1</td>
<td>1</td>
</tr>
</tbody>
</table>

### Usual Sources
- Traces, Eurostat, national statistics
- Traces, Comext
- Traces
- Traces, customs
- Traces

### Able to change source data easily?
- N/A
- Yes
- N/A
- Yes
- Yes
- Yes

(a) MINTSRISK can do any pathway defined by the risk assessor and so data sources indicated here are only examples. All data are used indirectly, i.e. the risk assessor has to conclude him/herself what is the relevant number and insert that in the tool.
## Table 2: Summary of the input data used in the seven generic RA tools included in G-RAID: Prevalence in area of origin.

<table>
<thead>
<tr>
<th>Data</th>
<th>Generic Risk Assessment Tool</th>
</tr>
</thead>
<tbody>
<tr>
<td>Details</td>
<td>SPARE</td>
</tr>
<tr>
<td>Prevalence in areas of origin</td>
<td></td>
</tr>
<tr>
<td>Use?</td>
<td>Indirectly through a model</td>
</tr>
<tr>
<td>1 source or many? &gt;1</td>
<td>&gt;1</td>
</tr>
<tr>
<td>Usual Sources</td>
<td>OIE, EMPRES-i</td>
</tr>
<tr>
<td>Able to change source data easily?</td>
<td>No?</td>
</tr>
<tr>
<td>Mitigation measures in areas of origin</td>
<td></td>
</tr>
<tr>
<td>Use?</td>
<td>Yes (restriction of trade?)</td>
</tr>
<tr>
<td>1 source or many? &gt;1</td>
<td>&gt;1</td>
</tr>
<tr>
<td>Usual Sources</td>
<td>EU legislation?</td>
</tr>
<tr>
<td>Able to change source data easily?</td>
<td>Yes?</td>
</tr>
</tbody>
</table>

**Test Sensitivity for testing in export countries (also useful for import detection)**
### Generic risk assessment tools

<table>
<thead>
<tr>
<th>Use?</th>
<th>No?</th>
<th>Potentially use it to determine import detection</th>
<th>Yes, indirectly</th>
<th>Yes</th>
<th>?</th>
<th>Yes?</th>
<th>No</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 source or many?</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Usual Sources</td>
<td>N/A</td>
<td>published literature</td>
<td>Published literature, expert opinion</td>
<td>Factsheets, published literature, manufacturer’s data</td>
<td>?</td>
<td>?</td>
<td>N/A</td>
</tr>
<tr>
<td>Able to change source data easily?</td>
<td>N/A</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>N/A</td>
</tr>
</tbody>
</table>

### Probability that infection will survive during transport to the import country

<table>
<thead>
<tr>
<th>Use?</th>
<th>Yes indirectly</th>
<th>Only for food/feed route?</th>
<th>Yes, indirectly</th>
<th>No</th>
<th>?</th>
<th>Yes</th>
<th>Yes, indirectly</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 source or many?</td>
<td>&gt;1</td>
<td>N/A</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Usual Sources</td>
<td>distance (through google maps?), published literature, duration of clinical signs (literature)</td>
<td>published literature</td>
<td>Published literature, expert opinion, distances (e.g. google maps)</td>
<td>N/A</td>
<td>?</td>
<td>published literature</td>
<td>Published literature</td>
</tr>
<tr>
<td>Able to change source data easily?</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>N/A</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
</tbody>
</table>
Table 3: Summary of the input data used in the seven generic RA tools included in G-RAID: Exposure to susceptible species.

<table>
<thead>
<tr>
<th>Data Details</th>
<th>SPARE</th>
<th>COMPARE</th>
<th>MINTRISK</th>
<th>RRAT</th>
<th>IDM</th>
<th>NORA</th>
<th>SVARRA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Is it possible for pathogen to come into contact with susceptible animals?</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Use?</td>
<td>Not included</td>
<td>Yes - use data on farms/density of Sus animals</td>
<td>Yes, indirectly</td>
<td>Yes – based on expected destination of pathway</td>
<td>Assumed that live imports will reach a farm? Will about other pathways?</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>1 source or many?</td>
<td>N/A</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
</tr>
<tr>
<td>Usual Sources</td>
<td>N/A</td>
<td>Eurostat, FAO density maps, OIE, TRACES, SEDAC gridded pop of the world</td>
<td>Destination of pathway, expert opinion</td>
<td>TRACES, Comext, published literature, expert opinion</td>
<td>?</td>
<td>TRACES, Finnish animal movement registry, variable sources</td>
<td>Relevant authorities, expert opinions</td>
</tr>
<tr>
<td>Able to change source data easily?</td>
<td>N/A</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Import detection</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Use?</td>
<td>Not included</td>
<td>Yes</td>
<td>Yes, indirectly</td>
<td>Not included</td>
<td>?</td>
<td>Yes - import quarantine</td>
<td>Yes - farm biosecurity measures, disinfection of transport</td>
</tr>
<tr>
<td>1 source or many?</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
</tr>
<tr>
<td>Usual Sources</td>
<td>N/A</td>
<td>published literature, EU legislation, national legislation</td>
<td>Legislation, expert opinion</td>
<td>N/A</td>
<td>?</td>
<td>Registry of animal disease prevention association</td>
<td>Stakeholder biosecurity programs, expert opinion on compliance with biosecurity rules</td>
</tr>
</tbody>
</table>
## Generic risk assessment tools

### Able to change source data easily?

<table>
<thead>
<tr>
<th></th>
<th>N/A</th>
<th>Yes</th>
<th>Yes</th>
<th>N/A</th>
<th>Yes</th>
<th>Yes</th>
</tr>
</thead>
</table>

### Breakdown of susceptible animals into classes (not just species)

<table>
<thead>
<tr>
<th>Use?</th>
<th>Not included</th>
<th>Not included</th>
<th>Yes - include non-susceptible hosts causing dilution effect</th>
<th>Yes - include if reservoir host, spill over host, experimental host, dead-end host</th>
<th>No</th>
<th>No?</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

| 1 source or many?     | >1           | >1           |                                                          |                                                                                  | >1 |     |
| Usual Sources         | N/A          | N/A          | Published literature, expert opinion                    | Factsheets, published literature                                               | N/A| N/A |
|                       |              |              |                                                          |                                                                                  |    |     |
|                        |              |              |                                                          |                                                                                  |    | Relevant authorities, stakeholders |

### Location and abundance of susceptible animals

<table>
<thead>
<tr>
<th>Use?</th>
<th>Not included</th>
<th>Use directly</th>
<th>Yes - distribution of vectors (hosts only relative to vector)</th>
<th>No</th>
<th>No</th>
<th>Yes - abundance in expected area at risk</th>
<th>Use indirectly - volume and geographical distribution</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

| 1 source or many?     | >1           | >1           |                                                             | 1  | >1 |                                          |                                               |
| Usual Sources         | N/A          | FAO livestock density map for pigs, wild boar map          | Presence/abundance data, published literature, expert opinion | N/A| N/A| Animal farm registry                    | Relevant authorities, stakeholder organisations |
|                       |              |              |                                                             |    |    |                                          |                                               |

<table>
<thead>
<tr>
<th>Able to change source data easily?</th>
<th>N/A</th>
<th>Yes (if map is available)</th>
<th>Yes</th>
<th>N/A</th>
<th>N/A</th>
<th>Yes</th>
<th>Yes</th>
</tr>
</thead>
</table>

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### Table 4: Summary of the input data used in the seven generic RA tools included in G-RAID: Disease-related parameters.

<table>
<thead>
<tr>
<th>Data Details</th>
<th>SPARE</th>
<th>COMPARE</th>
<th>MINTRISK</th>
<th>RRAT</th>
<th>IDM</th>
<th>NORA</th>
<th>SVARRA</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Length of infectious period</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Use?</strong></td>
<td>Yes?</td>
<td>Use directly</td>
<td>Included indirectly</td>
<td>Use directly</td>
<td>Included with $R_0$ estimate but not calculated separately?</td>
<td>Included indirectly</td>
<td>Yes, indirectly</td>
</tr>
<tr>
<td><strong>1 source or many?</strong></td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
</tr>
<tr>
<td><strong>Usual Sources</strong></td>
<td>Published literature</td>
<td>Published literature</td>
<td>Published literature, expert opinion</td>
<td>Factsheets, published literature</td>
<td>Published literature</td>
<td>published literature</td>
<td>Published literature</td>
</tr>
<tr>
<td><strong>Able to change source data easily?</strong></td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
</tbody>
</table>

| **Length of latent period, length of clinical period, time till seroconversion** | | | | | | | |
| **Use?**                      | No            | May use length of latent period | Included indirectly | Yes, indirectly | No?            | No?            | Yes, indirectly (length of latent and clinical period) |
| **1 source or many?**         | N/A           | >1                | Published literature, expert opinion | >1              | Factsheets/ published literature | N/A             | N/A             | >1             |
| **Usual Sources**             | N/A           | Published literature | Published literature, expert opinion | N/A             | N/A            | N/A            | Published literature |
| **Able to change source data easily?** | N/A          | Yes               | Yes              | Yes             | N/A            | N/A            | Yes            |

| **Contact and transmission rates between animals (wild and domestic)** | | | | | | | |
| **Use?**                      | No            | Yes               | Yes (from vector to host and from host to vector) | Yes (as an estimated probability of contact between imported and native) | Included with $R_0$ estimate but not calculated separately? | No (only if contact is possible but not how much contact or if it will transmit?) | No (only contact is possible but not how much contact or if it will transmit?) |
### Contact with and transmission probabilities from infectious materials in the environment (including clothes/transport of farm labourers)

<table>
<thead>
<tr>
<th>Use?</th>
<th>1 source or many?</th>
<th>Usual Sources</th>
<th>Able to change source data easily?</th>
<th>Contact with and transmission probabilities from infectious materials in the environment (including clothes/transport of farm labourers)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Not included</td>
<td>&gt;1</td>
<td>N/A</td>
<td>Yes</td>
<td>Include transmission through wild boar carcasses&lt;br&gt;Yes (presuming this is chosen as a pathway) No Yes? No (same as above)? Yes - contact (include regulations on cleaning and disinfection, farm biosecurity)</td>
</tr>
<tr>
<td>Published literature</td>
<td>N/A</td>
<td>Published literature, expert opinion</td>
<td>Yes</td>
<td>Include transmission through wild boar carcasses&lt;br&gt;Yes (presuming this is chosen as a pathway) No Yes? No (same as above)? Yes - contact (include regulations on cleaning and disinfection, farm biosecurity)</td>
</tr>
<tr>
<td>Published literature, expert opinion</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
<td>Include transmission through wild boar carcasses&lt;br&gt;Yes (presuming this is chosen as a pathway) No Yes? No (same as above)? Yes - contact (include regulations on cleaning and disinfection, farm biosecurity)</td>
</tr>
<tr>
<td>Published literature, expert opinion</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
<td>Include transmission through wild boar carcasses&lt;br&gt;Yes (presuming this is chosen as a pathway) No Yes? No (same as above)? Yes - contact (include regulations on cleaning and disinfection, farm biosecurity)</td>
</tr>
<tr>
<td>Length of persistence in the environment/ bedding etc.</td>
<td>1 source or many?</td>
<td>Usual Sources</td>
<td>Able to change source data easily?</td>
<td>Length of persistence in the environment/ bedding etc.</td>
</tr>
<tr>
<td>Not included</td>
<td>&gt;1</td>
<td>N/A</td>
<td>Yes</td>
<td>Length of persistence in the environment/ bedding etc.</td>
</tr>
<tr>
<td>Yes - persistence in wild boar carcasses</td>
<td>Published literature</td>
<td>Published literature, expert opinion</td>
<td>Yes</td>
<td>Length of persistence in the environment/ bedding etc.</td>
</tr>
<tr>
<td>Included indirectly (presuming this is chosen as a pathway)</td>
<td>Published literature</td>
<td>Published literature, expert opinion</td>
<td>Yes</td>
<td>Length of persistence in the environment/ bedding etc.</td>
</tr>
<tr>
<td>No</td>
<td>Yes?</td>
<td>N/A</td>
<td>Yes</td>
<td>Length of persistence in the environment/ bedding etc.</td>
</tr>
<tr>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>N/A</td>
<td>Length of persistence in the environment/ bedding etc.</td>
</tr>
<tr>
<td>Yes</td>
<td>Yes?</td>
<td>N/A</td>
<td>N/A</td>
<td>Length of persistence in the environment/ bedding etc.</td>
</tr>
<tr>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Length of persistence in the environment/ bedding etc.</td>
</tr>
<tr>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Length of persistence in the environment/ bedding etc.</td>
</tr>
</tbody>
</table>
### Decay rate in POAO

<table>
<thead>
<tr>
<th>Use?</th>
<th>Use directly</th>
<th>Use directly</th>
<th>Included indirectly (presuming this is chosen as a pathway)</th>
<th>Yes</th>
<th>Yes?</th>
<th>Yes</th>
<th>Yes</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>1 source or many?</strong></td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>Yes</td>
<td>Yes?</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td><strong>Usual Sources</strong></td>
<td>Published literature</td>
<td>Published literature</td>
<td>Published literature, expert opinion</td>
<td>Factsheets/published literature</td>
<td>Published literature, expert opinion</td>
<td>published literature</td>
<td>Published literature, expert opinion</td>
</tr>
<tr>
<td><strong>Able to change source data easily?</strong></td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
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</table>

### Contact and transmission between POAO with domestic or wild animals

<table>
<thead>
<tr>
<th>Use?</th>
<th>Not included</th>
<th>Yes - but only domestic animals with POAO destined for animal swill</th>
<th>Yes (presuming this is chosen as a pathway)</th>
<th>Yes (only for domestic animals)</th>
<th>Yes?</th>
<th>No (includes if contact possible but not how much contact)?</th>
<th>Yes for contact (animal swill regulations, wild animal feeding regulations, garbage management)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>1 source or many?</strong></td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>Yes?</td>
<td>Yes</td>
<td>Yes?</td>
<td>Yes for contact (animal swill regulations, wild animal feeding regulations, garbage management)</td>
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<td><strong>Usual Sources</strong></td>
<td>N/A</td>
<td>published literature, relevant authorities for regulations and compliance</td>
<td>Published literature, expert opinion</td>
<td>Published literature, expert opinion</td>
<td>?</td>
<td>?</td>
<td>relevant authorities</td>
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<td>Yes</td>
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<td>?</td>
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### Contact and transmission rates with germplasm

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<th>Yes</th>
<th>Yes?</th>
<th>No (includes if contact possible but not how much contact)?</th>
<th>Yes - farm biosecurity measures and regulations</th>
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</thead>
<tbody>
<tr>
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<td>&gt;1</td>
<td>&gt;1</td>
<td>&gt;1</td>
<td>Yes</td>
<td>Yes?</td>
<td>Yes?</td>
<td>Yes - farm biosecurity measures and regulations</td>
</tr>
</tbody>
</table>

---

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<th>N/A</th>
<th>Published literature, expert opinion</th>
<th>Published literature, expert opinion</th>
<th>?</th>
<th>?</th>
<th>relevant authorities, stakeholder organisations</th>
</tr>
</thead>
<tbody>
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<td>Able to change source data easily?</td>
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<td>N/A</td>
<td>Yes</td>
<td>Yes</td>
<td>?</td>
<td>Yes</td>
<td>Yes</td>
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<tr>
<td>Clinical symptoms</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Use?</td>
<td>Not included</td>
<td>Not included</td>
<td>Yes, indirectly</td>
<td>Yes, indirectly</td>
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<td>Not included</td>
<td>Not Included</td>
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<tr>
<td>1 source or many?</td>
<td></td>
<td></td>
<td>&gt;1</td>
<td>&gt;1</td>
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<td>Factsheets/published literature</td>
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<td>Yes</td>
<td>N/A</td>
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</table>
Appendix C – Results of the generic risk assessment tools for the ASF case study
Table 1: Results of the seven generic RA tools and the bespoke model included in the ASF case study for each of the considered pathways.

<table>
<thead>
<tr>
<th></th>
<th>Results NLD</th>
<th></th>
<th></th>
<th>Results FIN</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>S1 (Baseline)</td>
<td>S2</td>
<td>S3</td>
<td>S1 (Baseline)</td>
<td>S2</td>
<td>S3</td>
</tr>
<tr>
<td><strong>SPARE (Entry; number of infected units per year)</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Live animals</td>
<td>0.118</td>
<td>0.125</td>
<td>0.142</td>
<td>1.00×10⁻⁹</td>
<td>1.00×10⁻⁹</td>
<td>1.24×10⁻⁹</td>
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<tr>
<td>Products of animal origin (kg)</td>
<td>38.95</td>
<td>47.97</td>
<td>72.61</td>
<td>90.04</td>
<td>90.33</td>
<td>91.1215</td>
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<tr>
<td>Wild boar</td>
<td>1.85×10⁻⁵</td>
<td>0.166</td>
<td>0.166</td>
<td>3.63×10⁻²</td>
<td>3.63×10⁻²</td>
<td>3.63×10⁻²</td>
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<tr>
<td>Illegal trade (products of animal origin) (kg)</td>
<td>1.49</td>
<td>1.49</td>
<td>1.49</td>
<td>2.69×10⁻²</td>
<td>2.69×10⁻²</td>
<td>2.69×10⁻²</td>
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<tr>
<td><strong>COMPARE (First infection; annual probability of at least one event)</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Live animals</td>
<td>2.44×10⁻²</td>
<td>2.50×10⁻²</td>
<td>2.98×10⁻²</td>
<td>Negligible</td>
<td>Negligible</td>
<td>Negligible</td>
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<tr>
<td>Products of animal origin</td>
<td>5.73×10⁻²</td>
<td>7.48×10⁻²</td>
<td>0.121</td>
<td>2.23×10⁻²</td>
<td>2.24×10⁻²</td>
<td>2.26×10⁻²</td>
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<tr>
<td>Wild boar</td>
<td>Negligible</td>
<td>2.00×10⁻⁵</td>
<td>2.00×10⁻⁵</td>
<td>Negligible</td>
<td>Negligible</td>
<td>Negligible</td>
</tr>
<tr>
<td><strong>MINTRISK (Establishment; annual rate)</strong></td>
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<td></td>
<td></td>
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<tr>
<td>Live animals</td>
<td>4.38×10⁻⁴</td>
<td>1.28×10⁻³</td>
<td>3.44×10⁻³</td>
<td>9.19×10⁻⁸</td>
<td>9.19×10⁻⁸</td>
<td>9.19×10⁻⁸</td>
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<tr>
<td>Wild boar</td>
<td>8.91×10⁻⁴</td>
<td>2.82×10⁻²</td>
<td>2.82×10⁻²</td>
<td>2.82×10⁻³</td>
<td>2.82×10⁻³</td>
<td>2.82×10⁻³</td>
</tr>
<tr>
<td><strong>RRAT (First infection; probability-based risk score)</strong></td>
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<td></td>
<td></td>
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<tr>
<td>Live animals</td>
<td>9.07×10⁻³</td>
<td>9.10×10⁻³</td>
<td>1.11×10⁻²</td>
<td>7.45×10⁻¹⁰</td>
<td>7.45×10⁻¹⁰</td>
<td>7.45×10⁻¹⁰</td>
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<tr>
<td>Products of animal origin</td>
<td>0.223</td>
<td>0.223</td>
<td>0.266</td>
<td>2.19×10⁻²</td>
<td>2.20×10⁻²</td>
<td>2.45×10⁻²</td>
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<tr>
<td>Germplasm(a)</td>
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<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
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<tr>
<td><strong>IDM (Exposure; risk score)</strong></td>
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<tr>
<td>Live animals</td>
<td>7.5</td>
<td>13</td>
<td>18</td>
<td>2.5</td>
<td>5.5</td>
<td>8.5</td>
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<tr>
<td>Products of animal origin(b)</td>
<td>12</td>
<td>12</td>
<td>12</td>
<td>12</td>
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<tr>
<td>Wild boar</td>
<td>0.5</td>
<td>2.8</td>
<td>2.8</td>
<td>3.9</td>
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<tr>
<td>Other pathways including transport</td>
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<td>7</td>
<td>7</td>
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### Results NLD

<table>
<thead>
<tr>
<th>NORA (First infection; risk score)</th>
<th>S1 (Baseline)</th>
<th>S2</th>
<th>S3</th>
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<tbody>
<tr>
<td>Live animals</td>
<td>1.50×10⁻³</td>
<td>4.54×10⁻²</td>
<td>4.84×10⁻²</td>
</tr>
<tr>
<td>Products of animal origin(b)</td>
<td>1.52×10⁻²</td>
<td>2.02×10⁻²</td>
<td>2.02×10⁻²</td>
</tr>
<tr>
<td>Wild boar</td>
<td>1.50×10⁻⁵</td>
<td>1.50×10⁻⁵</td>
<td>1.50×10⁻⁵</td>
</tr>
<tr>
<td>Germplasm</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Transport (animal transport vehicles)</td>
<td>1.00×10⁻⁴</td>
<td>1.00×10⁻⁴</td>
<td>1.00×10⁻³</td>
</tr>
<tr>
<td>Goods and traffic other than animals or animal products</td>
<td>5.00×10⁻⁵</td>
<td>5.00×10⁻⁵</td>
<td>5.00×10⁻³</td>
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<tr>
<td>Feed and bedding</td>
<td>5.00×10⁻⁴</td>
<td>5.00×10⁻⁴</td>
<td>5.00×10⁻⁴</td>
</tr>
<tr>
<td>Human travel(b)</td>
<td>2.64×10⁻³</td>
<td>2.64×10⁻³</td>
<td>5.00×10⁻³</td>
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### Results FIN

<table>
<thead>
<tr>
<th>SVARRA (Exposure; qualitative probability level)</th>
<th>S1 (Baseline)</th>
<th>S2</th>
<th>S3</th>
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</thead>
<tbody>
<tr>
<td>Live animals</td>
<td>Very low</td>
<td>Very low</td>
<td>Very low</td>
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<tr>
<td>Products of animal origin(b)</td>
<td>Very low</td>
<td>Very low</td>
<td>Very low</td>
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<tr>
<td>Wild boar</td>
<td>Negligible</td>
<td>Very low</td>
<td>Neg-Very low</td>
</tr>
<tr>
<td>Germplasm</td>
<td>Negligible</td>
<td>Negligible</td>
<td>Negligible</td>
</tr>
<tr>
<td>Indirect (transport, human travel, feed and bedding)</td>
<td>Very low</td>
<td>Very low</td>
<td>Very low</td>
</tr>
</tbody>
</table>

### IRTA (First infection; annual probability of at least one event)

| Live animals | 0.14 | 0.14 | 0.2 | 1.70×10⁻⁵ | 1.70×10⁻⁵ | 1.70×10⁻⁵ |
| Wild boar (Entry only) | 0 | 0.0016 | 0.0016 | 0 | 0 | 0 |

(a) Volume of trade in pig semen could not reliably estimated from Eurostat (2019).
(b) Including illegal trade of animal products

References

## Appendix D – Evaluation of the G-RAID symposium

Table 1: Participants’ rating of the presentations and workshops(a) of the G-RAID symposium (average, minimum and maximum scores). Participants were asked to rate the presentations on a scale of 1 – 5 (1=very poor; 2=poor; 3=neutral; 4=good; 5=very good).

<table>
<thead>
<tr>
<th>Symposium part</th>
<th>Average score (min-max)</th>
<th>Number of respondents</th>
</tr>
</thead>
<tbody>
<tr>
<td>Presentations in the morning session</td>
<td>4.6 (4-5)</td>
<td>11</td>
</tr>
<tr>
<td>Presentation of generic RA tools by posters and demos</td>
<td>4.4 (3-5)</td>
<td>10</td>
</tr>
<tr>
<td>Workshop on modelling approaches</td>
<td>4.5 (2-5)</td>
<td>10</td>
</tr>
<tr>
<td>Workshop on data needs</td>
<td>3.9 (2-5)</td>
<td>9</td>
</tr>
<tr>
<td>Workshop on communication of results</td>
<td>4.0 (3-5)</td>
<td>4</td>
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</tbody>
</table>

(a) Participants had the possibility to attend two workshops