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Overview of data analysis and reporting tools in the context of the SIGMA project

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Abstract

The SIGMA project aims at supporting the development and implementation of technical features with the goal of reducing the burden for the MSs to submit *ad hoc* animal disease and population data to EFSA.

This document reports the work that has been conducted as part of the objective 4 of Work Package 7 (WP7) of the Sigma σ project, focusing on the actions taken to gather detailed information on the tools for data analysis and reporting of disease outbreaks/surveillance activities, adopted or available among the EU Member States.

The technical feasibility of the integration of some of the inventoried tools into EFSA's dashboard is assessed, as well as the main features which make them suitable for their implementation as interactive web-tools designed to produce graphs, diagrams, tables or full reports to fulfil the EU legislation.

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Key words: SIGMA, tools, analysis, reporting, software, application

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1. Introduction

1.1. Background and Terms of Reference as provided by the requestor

This contract was awarded by EFSA to the **SIGMA Consortium**:

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Appointed as the leader of the group by the members of the group that submitted the joint tender and

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Partner 5:

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Contract title: Technical support to improve and automatize data collection and reporting on animal disease outbreaks and surveillance (SIGMA)

Contract number: OC/EFSA/ALPHA/2018/01

The SIGMA project originates from a critical assessment of the current practices to collect and submit data on animal populations and diseases among the European Member States (EU MSs). Among the main goals of the SIGMA project are the reduction of the resource burden on both MSs and EFSA related to data collection-analysis-transmission and the increasing of data quality and comparability, thus shortening the time to retrieve and analyze up-to-date information. The current workflow for collection and transmission of animal health data builds primarily on an e-mail exchange of Excel sheets or .xml files between EFSA and the data providers of the EU MSs. Apart from being tedious and time-consuming, the entire chain of data acquisition, processing and transfer

lacks routines for validation and consistency checking, and is, therefore, more prone to mistakes and inaccuracies.

In the SIGMA project, EFSA together with the partners of the SIGMA Consortium and the EU MSs worked with the purpose of addressing such technical issues, improving the current animal health data flows within each EU MSs' country, while reducing manual input for submission and reporting of data to EFSA and EU.

1.2. Interpretation of the Terms of Reference

For pursuing such accomplishments in a cost-effective manner there is a need for providing the EU MSs with tools to enhance data transmission and production of automatically draft reports on animal health and surveillance. Providing the MS with such a set of tools will enhance both the sharing of the analysis of data in a standardized way in a protected environment thus reducing the burden for analysing and reshaping data for reporting purposes. Furthermore, the connection of such tools for data processing to the EFSA Data Warehouse would ensure a higher degree of data integrity and confidentiality enabling harmonized analysis and reporting by national and European risk assessment bodies. There is a broad range of available software tools developed by European and international institutions, developed primarily for internal use to assist the process of analysing and reporting epidemiological data. However, there is a lack of knowledge about the solution adopted by each EU MSs and the state-of-the-art of these tools.

This document aims at reporting on the work that has been conducted as part of the Objective 4 of Work Package 7 (WP7) of the Sigma σ project. Specifically, the objective 4 aimed at providing an overview of tools for analysis and reporting of epidemiological data available among the partner of the Sigma Consortium and the EU MSs. The Objective 4 had two distinct but interconnected goals:

- to make an inventory of the data analysis and reporting tools in use amongst the EU MSs (within and outside the SIGMA Consortium);
- to analyze the technical feasibility for the integration of some of the inventoried data analysis and reporting tools into the EFSA dashboard.

In accordance with the project tender, three main deliverables were produced:

1. A list of all accessible and useful tools that have been identified;
2. A set of technical cards of tools considered to be of potential interest for inclusion into the EFSA dashboard
3. A technical proposal on how to integrate some of the identified tools into the EFSA dashboard

The deliverables 1 and 2 are provided into two Microsoft Excel spreadsheets while the deliverable 3 with the technical proposal will consist of a report in .pdf format. The three deliverables are published on the SIGMA Sharepoint website and available at these link

2. Methodologies

SVA WP7 obj.4 leader with the support of the other member of the SIGMA Consortium, worked to produce a list of tools for data analysis and reporting of disease outbreaks and surveillance activities with the aim of making them available to the MSs

The operative framework adopted for pursuing the expected results consisted of two main parts: an Initial Screening and a Full evaluation.

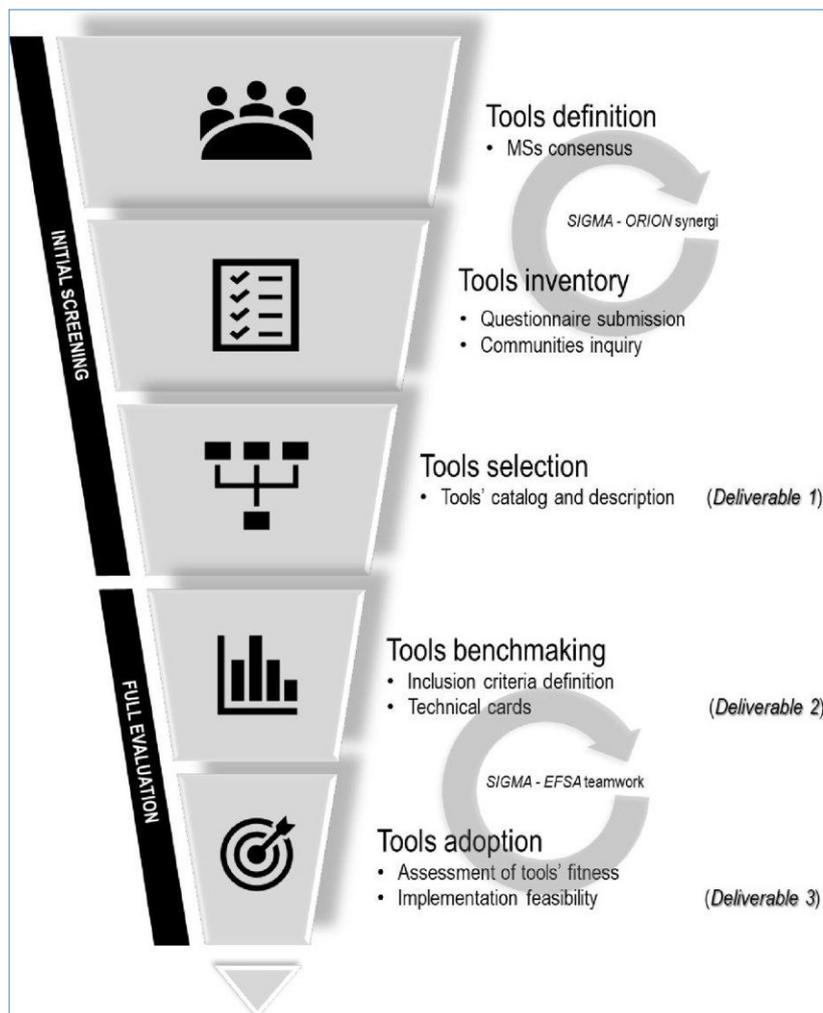


Figure 1: project outline

In the Initial Screening we focused on setting the foundation of our work, providing the definition of tool, the methods for collecting the information about the existing tools and the criteria for selecting potential candidates for the inclusion into the EFSA Dashboard. In the FE we moved the focus on the implementation stage. The tools collected in the previous step were benchmarked, assessing their fitness towards the implementation into the EFSA Dashboard.

2.1. Initial screening: definition, search strategy and tool information

The work has been focused on the collection of information to prepare an inventory of tools for analysis and reporting of epidemiological data.

Before starting the activities of data collection (i.e. the tools inventory) the Consortium made a collective effort for addressing some critical aspects related to the definition of tool and the strategy to adopt for searching and then selecting the identified tools. Each step is described in detail in the next paragraphs.

2.1.1. Definition of “tool”

The definition of 'tool' is sometimes problematic, because it is often prone to subjectivity and open to interpretation. Hence, the first step in our investigation was to propose a definition of tool that could suits the aims of our survey. As this was an exploratory stage, we agreed with the partners of the Consortium and the ORION project to propose an initial broad inclusive definition, rather than developing strict inclusion and/or exclusion criteria already from the beginning. For instance, although the focus of our work was on freely available tools, while making the survey we deliberately decided to not include any distinctions between open source or proprietary software in the questionnaire, letting the respondents to list all the tools having a significant impact in their daily data reporting and analysis workflow. In our vision the definition should have been broad enough to get an overview of which tools are today in use among the MS, but at the same time to collect information about which kind of task are the MS more involved in when it comes with analysing and reporting data.

These considerations lead us to the following definition of "tool":

"every piece of software (both stand-alone or module, package, template, extension, script from third-party software) developed or adopted by EU MSs with the purpose of analysing and/or reporting epidemiological data".

This definition was finally adopted in our survey and gather the information in our initial screening. Search Strategy for tools inventory

A systematic search and selection process were undertaken in order to identify which software and tools for reporting and/or analysing epidemiological data were currently adopted by MSs (and their external networks). The information was collected from 2 main sources:

- A survey made among the SIGMA Consortium members and the EU MSs;
- An inquiry among relevant software communities and repositories.

Each member within the Consortium was asked to provide a comprehensive inventory of the data analysis and reporting tools that could fit the provided definition of tool. To this purpose, an on-line survey was designed to gather detailed information on possible data analysis and reporting tools available, including those which were developed or are being developed as part of previous or ongoing EU or EFSA-financed projects (i.e. RISKSUR). The survey was conducted between October and December 2018. A web-based questionnaire was designed with the aid of an online survey and feedback software powered by Questback® (QuestBack GmbH, Berlin, Germany). The questionnaire divided in three sections was composed of several questions with an average time to complete of about 30 minutes. Each section was intended to collect information about the context in which the tools were developed and to broad the overview to those that could potentially be of EFSA's interest. In addition, some tailored questions were included in order to delineate the general availability of tools for data analysis and reporting among the MS, as well as collect insights from experts' opinion and their needs in relation to epidemiological tools. The questionnaire was made available to all the member of the Sigma Consortium between October 2018 and December 2019. After this piloting stage, where only the members of the Consortium were involved, the survey was extended to all the MS between December 2018 and January 2019. In this task and to reach the broadest audience possible, EFSA's network was exploited. The link to the survey was sent to all the national CPs already involved in a previous survey. Besides the list of tools, the results of the questionnaire provided important insights to delineate technical platforms and solutions adopted by each MS for the analysis and reporting of epidemiological data as well as collect expert's opinion about the needs of tailored tools for performing specific tasks. A brief analysis of the information collected in the survey was made by summarizing data in simple graphs (see Analysis of the survey).

The second source of information was an inquiry on the same topic made into relevant international communities. We selected the software repository GitHub and the open research platform Zenodo. GitHub is a code hosting platform for collaboration and version control that brings together the world's largest community of software developers. Zenodo is an open-access platform developed

under the European OpenAIRE program and maintained by CERN enabling researchers to share and preserve research output in any size, format and from, included software.

Using the tags associated to each software repository, we queried Github website using specific keywords related to the subjects of our inquiry. A typical query consisted of an URL plus the identified keyword (e.g. "<https://github.com/topics/>" + "keyword"). Likewise, the platform Zenodo was queried by using the same set of keywords adopted in the previous search.

Apart from the survey, information on tools available amongst Consortium members and EU MSs was collected exploiting synergies and networks created within previous and ongoing projects. In detail, a collaborative synergy was established with the ORION project since it was identified a partial overlap of the goals in two of the projects' Work Packages (WP) SIGMA WP7 (obj. 4) and ORION WP2-epi. Both WPs, in fact, had the aim of making an inventory of tools. While in ORION the focus was more towards the inventory of tools for surveillance data analysis, SIGMA aimed at providing an overview of tools for data analysis and reporting of epidemiological data in a broader sense. Although deadlines, main focus and method for data collection showed to be significantly different, the evidence of overlapping goals between the two projects led to the conclusion about sharing the output of the two inventories i.e. the list of the collected tools.

Data collected from all the sources were organized into MS Excel® spreadsheets (Microsoft Corporation).

2.2. Detailed information for tools (Deliverable 1)

The initial set of information collected for each tool was filtered and standardized in order to retain and synthesize only that information relevant for the purpose of the SIGMA project. Hence, the final list of tools was provided with the following information

- Tool name: The name provided by the participants in the survey or the name found in the repository
- Developer: The developer(s) of the application
- Development context: The framework in which the tool was developed (e.g. project development, personal initiative, etc.)
- Primary Purpose: the primary purpose in view of the SIGMA project aims. (i.e. DA = Data Analysis, RE = Reporting, DA-RE = both)
- Availability: The availability of the tool (i.e. FA = Freely Available, P = Proprietary, RS = Restricted). RS refers to the need of a membership or a proprietary software for using the tool.
- Software type: SA = Stand Alone, TP = Third Party, SaaS = Software as a Service
- Maintainer: if known the name of the maintainer of the tool
- Contacts: The contact of the maintainer(s) or the responsible(s) for the development of the tool as reported in the survey or in the repository. If the source of information is the web-survey, the contacts refer to the person(s) who listed the tool in the survey

The final list of tools inventoried during the Initial Screening (IS) is published jointly to this report (Appendix A).

2.3. Full Evaluation: inclusion criteria and technical cards

Once the inventory was concluded each software underwent a synthetic evaluation to assess its suitability for the inclusion in our list of potential candidates.

Inclusion criteria

After removing those tools that were collected more than once in the initial search and all the tools out of or beyond the scope of our survey (e.g. datasets, repositories created for teaching purposes, reports) the remaining ones underwent a systematic application of a set of inclusion criteria.

The following inclusion criteria were applied:

- tools developed or adopted for reporting and/or analysing epidemiological data;
- tools which are freely available or developed on top of freely available software;
- tools without any restrictions or limiting factor to their usage (e.g. copyright);
- tools with a link or access available to visually and practically explore them.

2.3.1. Technical cards of tools considered for inclusion in the EFSA dashboard (Deliverable 2)

The technical cards were designed to provide detailed specifications and features useful for the technical characterization of the tools identified in the previous step and facilitate the benchmarking and the consequent assessment of the tools' fitness in respect to their implementation into the EFSA IT infrastructure. The technical card consists of three main part:

- A brief description of the tool reporting about the main aim of the tool;
- A list of technical specifications which provide the main tool characteristics;
- A list of features of interest.

TOOL NAME		ASF spatio-temporal model
DESCRIPTION		
Description of the tool	R script for the calculation of the K-function on a set of ASF spatio-temporal data	
TOOL SPECIFICATIONS		
Data Input Requirements (data format)	dataset	
Data Input Format	.csv	
Data Outputs Generated	report	
Data Outputs format	.pdf	
Operating System (OS)	Unix/Linux, Mac OS, Windows	
Programming Language	R	
Framework	R Package & R shiny app	
Interface	CLI, GUI	
Natural Language	English	
Development Status	PS	
Current stable release (as of December 1, 2018)	0.2	
Last Updated (year)	2016	
License	CC BY 4.0	
Required IT Skills	Familiarity with R	
Website or Repository	https://zenodo.org/record/198181#_XF_2tPZFzmQ	
TOOL FEATURES		
1.	Calculation of epidemiological relevant indicators	•
2.	Data aggregation according to temporal/spatial dimensions	•
3.	Spatial representation of the data (e.g. maps or Web-GIS, contact networks)	
4.	Disease notification	
5.	Active/Passive/Syndromic surveillance	
6.	Risk factor analysis	
7.	Identification and analysis of clusters	
8.	Visualisation of control measures (e.g. zoning, vaccination status)	
9.	Temporal or spatial analysis of outbreaks	
10.	Integration of outcomes from other projects (e.g. ENETWILD, GISAI, Vectornet, WAHIS,	
10.	Scenarios/Simulations	

Figure 2: example of technical card (for illustration purposes)

All the candidate tools identified in the previous step were short listed and provided with a technical card. An example of technical card is provided in the Figure 2.

The list of technical cards is published jointly to this report (Appendix B).

2.4. Full evaluation: analysis of the technical feasibility for integration in the EFSA dashboard

A preliminary investigation was made to test the suitability of the software collected during the inventory to be appropriate candidates for integration into the EFSA dashboard. The analysis included a high-level investigation of software features and capabilities as well as a characterization of the potential barriers to the adoption of such tools.

We proposed a generic stage-based methodology for selection of any software package considered a suitable candidate which consisted of the following step:

1. by applying a set of exclusion criteria, we eliminated those tools which did not have the requirements for being implemented into EFSA's existing IT architecture (e.g. hardware, operating system and database management software or network);
2. we made an empirical assessment of some metrics and an overall ranking of them to evaluate the fitness of the tools retained after the previous step;
3. we finally assessed the possibility of implementation for the first quintile as well as provided a brief evaluation of the main and constraints to the implementation of the other candidates.

Each point is discussed with more detail in the next paragraphs.

2.5. Exclusion criteria

All the tools collected in the initial screening were subject to a systematic application of some exclusion criteria in order to eliminate those tools not meeting the minimum requirements appropriate for their integration into the EFSA dashboard. The following exclusion criteria were applied:

- i) tools with no possibility to visually and practically explore them;
- ii) tools lacking or without transparent information on licensing;
- iii) tools without freely available source code or version control repository;
- iv) For what concerns the tools inventoried through the survey: general purpose tools not specifically designed to work with epidemiological data (e.g. ArcGIS, Qgis, SAS, Matlab);
- v) For what concerns the tools hosted on the investigated repositories (i.e. Github, Zenodo): tools with over four years since the last update made by the authors or the contributors of the software/repository.

The remaining tools underwent to a full evaluation where the suitability of each tool to be included into the EFSA Dashboard was assessed.

2.6. Tools fitness

A set of metrics was identified with the aim of assessing the fitness of each tool in respect to their implementation into the EFSA Dashboard. Eight qualitative parameters defining performance, utility and usability were applied to each tool and assessed against 2 or 3 levels of detail assigning from the top to the bottom a rating of 10, 5 or 1 (Table 1)

For each tool the overall assessment was performed with a descriptive numerical analysis consisting of generation of sum of ratings.

Table 1: . Parameters considered in the FE process and the assessment 3 Point Scale adopted for assessing the tools fitness

Parameter	Level	Rating
Documentation	Tools' features and specifications are well documented	10
	Tools' features and specifications are partially documented	5
	Tools' features and specifications are no documented	1
Portability	The tool is accessible from 3 or more OS	10
	The tool is accessible from 2 OS	5
	The tool is accessible from 1 OS	1
Extensibility	Yes	10
	No	5
Transparency	The source code of the tool is of public domain (e.g. 10 Github)	10
	The source code can be made available upon request	5
	The source code is not available	1
Popularity	The tool is used by more than 3 institution	10
	The tool is used by more than 1 institution	5
	The tool is not used but available to all the institutions	1
Scalability	The tool can be scaled	10
	The tool can not be scaled	5
Usability	Graphical user interface (GUI) and command line	10
	Graphical user interface (GUI)	5
	Command line	1
Sustainability	The tool has a open license (MIT, GPL3)	10
	The tool has a semi-open license (GPL2)	5
	The tool has a commercial license or no info	1

Those tools showing highest fitness (1st quartile) in terms of highest score were analyzed to provide a list of pros and cons in respect to their adoption into the EFSA Dashboard.

3. Results

3.1. Inventoried tools

Twenty-five persons from 16 EU MSs (Italy, Austria, Germany, Portugal, Spain, Latvia, Czech Republic, Ireland, Estonia, Bulgaria, Sweden, Denmark, Belgium, Switzerland, Greece, Cyprus) answered the survey for a total of 99 collected tools.

For what concerns the inquiry among relevant communities, four main keywords have been investigated for a total of 444 checked repositories. The list of keywords and the total number of inventoried software/repositories is shown in Table 2.

Table 2: Keywords and number of repositories investigated.

	Github Software/Repository (n.)	Zenodo Software/Repository (n.)
Keyword		
epidemiology	129	49
epidemic(s)	33	15
infectious-diseases	25	65
disease-surveillance	6	122

All the repositories were investigated and only those tools relevant and in line with the aim of our inquiry (i.e. tools for analysis and reporting of epidemiological data) were retained for a total of 67 collected tools. After the screening phase and the application of the inclusion criteria a total of 144 tools collected from both sources were retained and provided with detailed information (Figure xx).

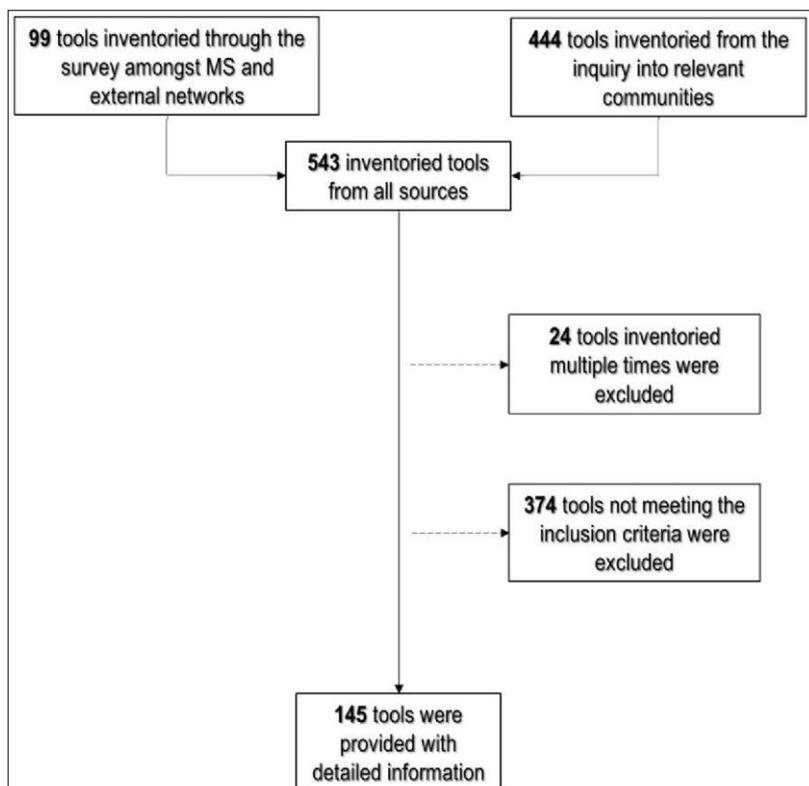


Figure 3: Flowchart with the result of the search and selection process

3.2. Analysis of the survey

It was found from the answers provided by the SIGMA Consortium Members and the EU MSs that Excel (72%) stood out as the most popular among the tools routinely used by the 25 respondents (Figure 4), followed by “Web-based software/tools” (60%), “GIS applications/extensions” (48%) and the category “Other” (44%).

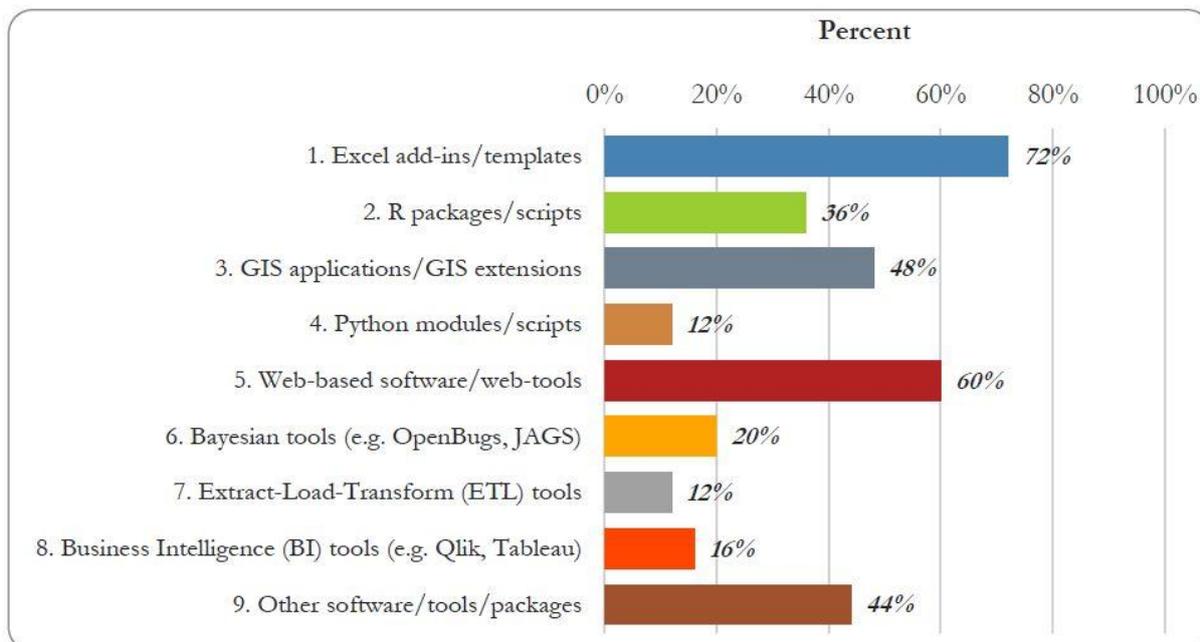


Figure 4: Percentage of respondents (n=25) for each group of tools.

The greatest part of the respondents (56%) declared to use regular Excel sheets, while 50% declared to use Excel plug-ins/templates developed in house or from third party sources (Figure 5).

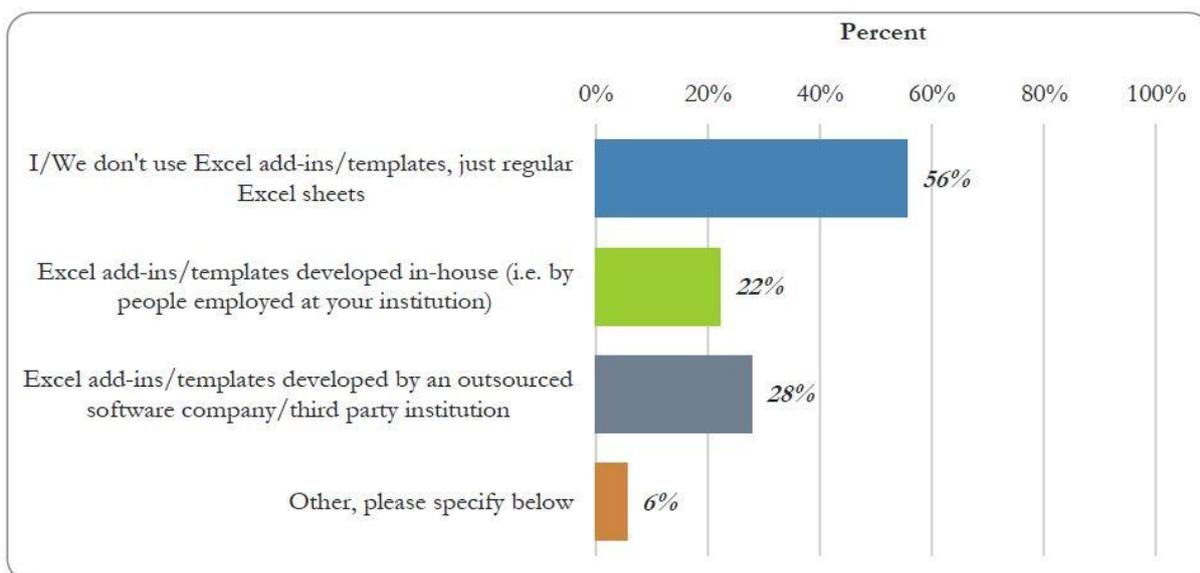


Figure 5: Percentage of respondents (n=18) for each Excel tools development alternative.

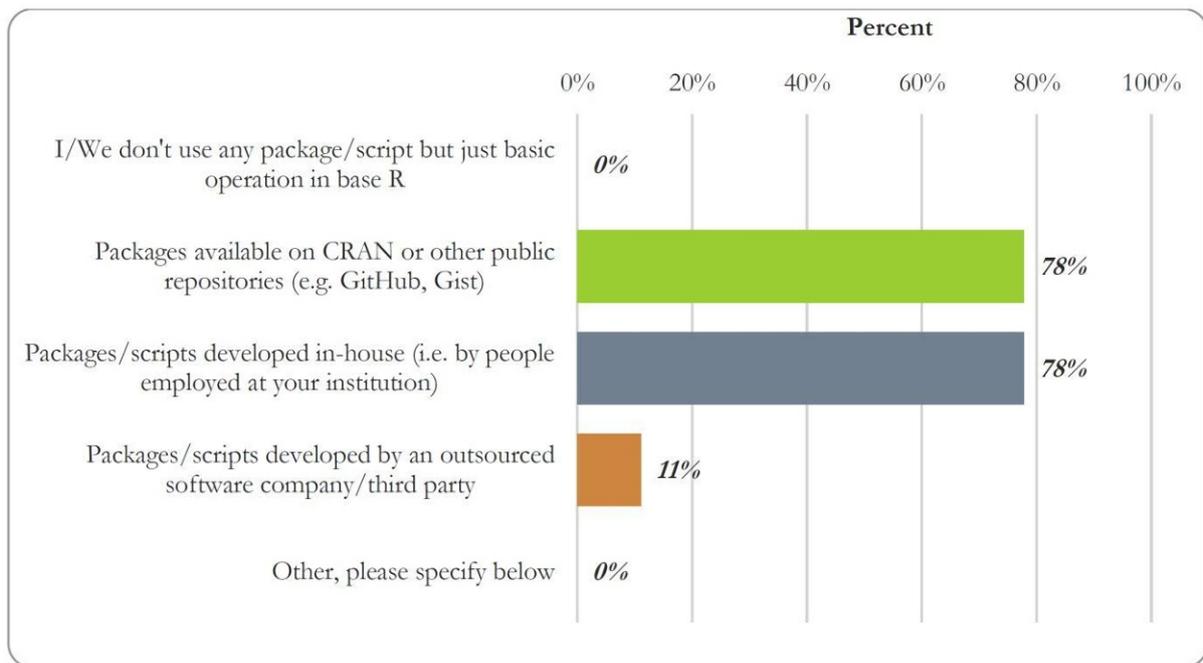


Figure 6: Percentage of respondents (n=9) for each R packages/scripts development alternative

R packages/scripts were the more mentioned (36%) among the freely available tools, although the results showed a concentration of usage and expertise in some of the respondent Institutions (e.g. SVA, FLI) and profiles (e.g. Epidemiologists, Statisticians). Almost all the R tools mentioned by the respondents are available at CRAN (the official R repository) or other public repositories or packages developed in-house (Figure 6).

Less popular is the use of “Python modules/scripts” (12%) However, all the respondents declared to use Python modules/scripts developed in-house showing the presence of some expertise in their Institutions (Figure not showed).

The use of GIS applications/extensions is limited to those provided by the software house (e.g. ESRI) or the community (e.g. QGIS). One third of the respondents declared to use “GIS applications, extensions or plug-ins developed by an outsourced software company or third-party institution” (Figure 7). From the list of tools provided emerged clearly how several Countries has implemented ad-hoc web-GIS solutions or server-client frameworks to query and display spatial data (e.g. ECOSEA). The use of Bayesian tools is limited to the 20% of the respondents and relies mostly on “Web-based software/web-tools freely available on the web”. However, the answers showed that the in some cases the Bayesian tools are used through R where the binding to most known framework have been implemented (e.g. JAGS - Rjags...)

The same cannot be said for “Extract-Load-Transform (ETL)” tools and “Business Intelligence (BI) tools used respectively by 12% and 16% of the respondents. In this case also, the use of such tools relies heavily on “software developed by outsourced software companies or third-party institutions”. Only 20% of the 25 respondents answered to have knowledge or use existing freely available tools (e.g. EFSA RiBESS+, AusVet Epitools) and only 12% declared to use these free tools for analyzing and reporting epidemiological data (Figure not showed).

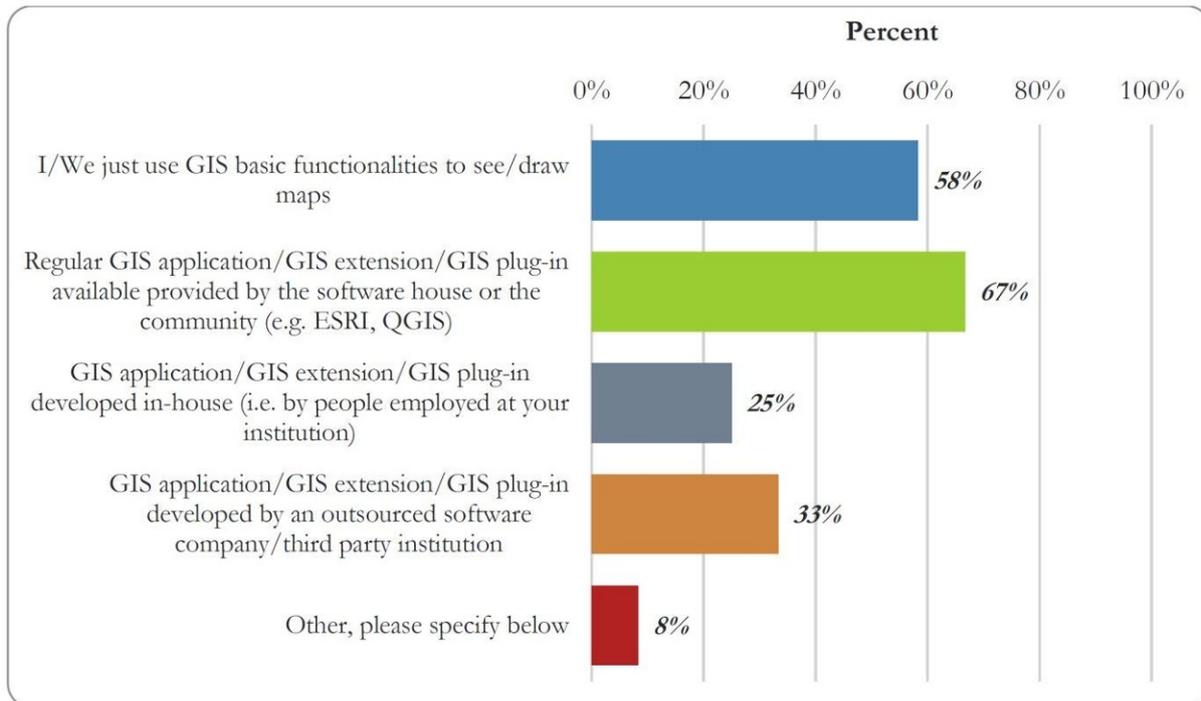


Figure 7: Percentage of respondents (n=12) for each GIS application/extensions development alternative

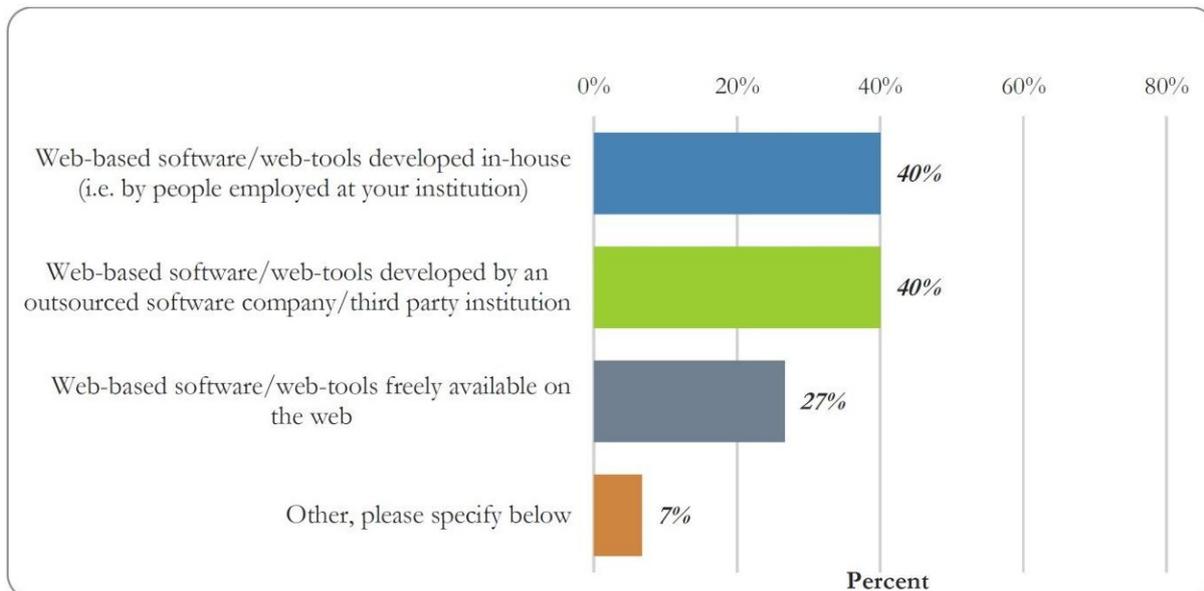


Figure 8: Percentage of respondents (n=15) for each web-based software/web-tools development alternative

Twenty-three respondents answered the question about the benefits of having web tools for analyzing and reporting epidemiological data provided by EFSA (Figure 9). According to the 65% of the respondents, tools for Spatial representation of the data (maps or web-GIS) and Integration of outcomes from other projects (e.g. ENETWILD, GISAID, Vectornet, WAHIS, EMPRES-i) would be the

most desirable. However, in general all the options mentioned in the question were mentioned at least by one-third of the respondents.

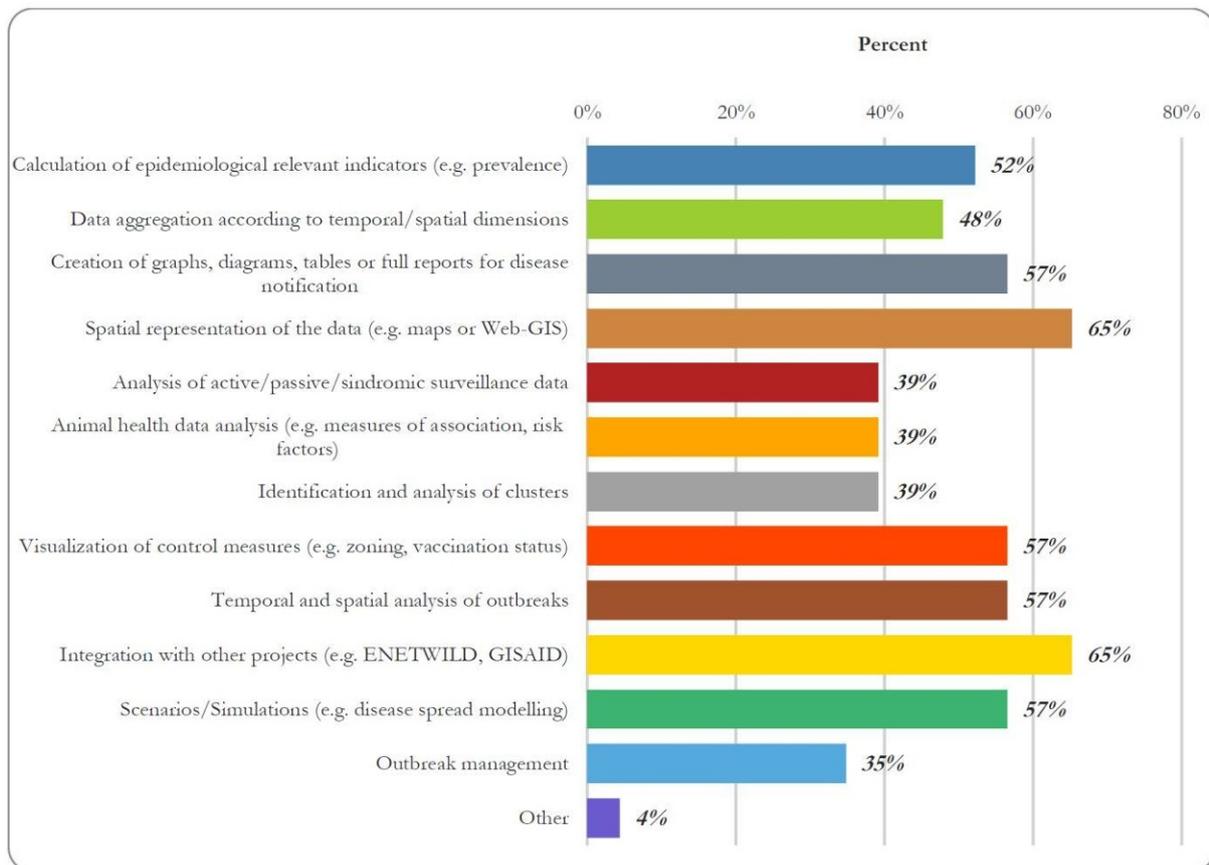


Figure 9: Percentage of respondents (n=23) for tools needs.

3.3. Analysis of the tool's fitness for the retained candidate tools

All the tools collected and described through the technical cads were assessed for their fitness according to the criteria described in the paragraph "Tools Fitness". The results of the assessment are reported in Appendix A. The characteristics of the first ten tools in terms of sum of scores was finally assessed for the implementation stage.

3.4. Proposal on how to integrate the tools into the EFSA dashboard (Deliverable 3)

In this paragraph we provide an overview about the possible integration of the tools identified in the previous step into the EFSA Dashboard.

As stated at the beginning of our work and in accordance to the project tender, we investigated preferably freely available tools because of the possibility to be deployed or embedded without putting extra efforts in recoding but only some efforts for managing the data in input and output. Since the results of the survey, the inquiry and in general of the tools' assessment showed that R is the most popular language/framework used by to build freely available tools, we focused our proposal mainly on the implementation of such tools.

However, some alternative options have been listed for those tools not implemented in R.

3.4.1. IT barriers to the tools' implementation

EFSA is currently in the process of migrating their server to a new platform, moving EFSA's Scientific Data Warehouse environment to the Cloud hosted in the Cancom data centers located in Germany. According to the information provided by EFSA, the new platform will add flexibility and scalability in the EFSA scientific computational environments and for what concern the installation and the maintenance of the hosted tools.

To the best of our knowledge, since the migration is not yet finalized, the implementation of freely available software will have no limitation due to the migration to this new platform. However, a possible barrier to the implementation of proprietary software is mainly due to the possible fee for plug-ins of licensed products (e.g. Matlab) that currently are not used at EFSA.

3.4.2. Implementation of the tools with higher fitness

In our analysis we divided the potential candidates into two groups reflecting the amount of estimated work for implementing the tools into the EFSA Dashboard. The identified groups and the tools are reported in Table 3.

Table 3: Keywords and number of repositories investigated.

	Group 1	Group 2
	distcrete	Siminf
	epiflows	DTU-DADS (FMD/ASF)
	incidence	EpiTools
	projections	EpiModels
	QMRA model	
	vimes	
PROS	Good level of utility and usability	Adaptable to a wide range of contexts
	Graphical user interface	More added features
	MIT/CC 4.0 License	GPL License
CONS	High degree of specificity	Programming experience

3.4.2.1. Group 1 "ready-to-use" tools.

Group 1 tools consists almost exclusively of "ready-to-use" tools. The tools in this group have in general less built-in functionality features, specifically addressed to fulfill specific task (e.g. outbreak management) and are generally associated to good levels of utility and usability due to the presence of a graphical user interface and/or good documentation.

In contrast, these tools show a high degree of specificity that makes them relatively inflexible, and less adaptable to a wide range of contexts. Another peculiarity is that these tools comes with a MIT

license. The MIT license permits reuse within proprietary software provided that all copies of the licensed software include a copy of the MIT License terms and the copyright notice.

The greatest part of the tools identified in this group were developed by the REpidemic Consortium (RECON), an international not-for-profit, non-governmental organization of experts in public health using the R software and other free, open-source resources for data science, modelling methodology, and software development”.

3.4.2.2. Group 2 “in need of extra efforts” tools

Group 2 tools consists of tools which need of some efforts to make available such tools for a broader audience a certain amount of work should be invested to design and develop a user-friendly graphical interface and for some of them (e.g. EpiModel) to meet specific requirements for epidemiological data analysis and reporting. Among the advantages there is the higher degree of configurability of these tools suitable for meeting specific requirements and fulfill the desired tasks.

On the other hand, these tools have a lower degree of usability, mainly due to a higher burden on the end user in terms of subject matter expertise, coding and systems configuration experience. In addition, these tools have more added features.

3.4.3. Methods for implementation

For what concern the investigated alternatives for implementing new R tools the following alternatives

can be mentioned.

1. Implementation in [shiny-efsa.openanalytics](#)
2. App on-premises and local deployment (see [RInno](#))
3. Electron + shiny ([link](#))

However, once the migration to the Cloud will be completed the installation of a Shiny Server could be evaluated by the technical bodies at EFSA.

For the tools not available as R packages the following alternative could be considered:

1. Implementation of an ad-hoc EFSA Dashboard ([dashboard](#))
2. Use of Microsoft Power BI or another BI software (Qlik, Tableau)
3. Creation of an API services

4. Caveat

The list of tools provided in this work is not exhaustive as other examples are known to exist and other tools could have been chosen as well. In addition, during our assessment the following aspects were not considered:

- speed. The efficiency of some tools could be affected by several computationally intensive processes. Even if deployed on dedicated services, the algorithm implemented in some freely available tools could show poor performances if not properly designed;
- robustness. All the freely available tools are prone to programming errors which in some cases could be particularly relevant. Both algorithms and code are seldomly “peer-reviewed” even if published on official repositories.

Abbreviations

SVA	Statens Veterinärmedicinska Anstalt
EU MSs	European Member States
IZSAM	Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale"
FLI	Friedrich-Loeffler-Institut
SVA	Swedish National Veterinary Institute
BFSA	Bulgarian Food Safety Agency
EMU	Institute of Veterinary Medicine and Animal Sciences, Estonian University of Life Sciences

Appendix A – Tools inventoried during the Initial Screening (Deliverable 1)

Appendix A can be found in the online version of this output ('Supporting information' section):
<https://doi.org/10.2903/sp.efsa.2019.1690>

Appendix B – Technical cards of tools considered for inclusion in the EFSA dashboard (Deliverable 2)

Appendix B can be found in the online version of this output ('Supporting information' section):
<https://doi.org/10.2903/sp.efsa.2019.1690>

Tool name	Developer	Development context
@RISK	PALISADE	Business
ai.fvst.dk	Miljø- og Fødevarestyrelsen	Internal
ai.fvst.dk	Miljø- og Fødevarestyrelsen	Internal
AI-DB	FLI	FLI initiative
ArcGIS	ESRI	Business
ASF spatio-temporal model	Biomathematics and Statistics Scotland	Research project
Atlas of infectious diseases	ECDC	Public
Australian Animal Disease Spread (AADIS)	NA	NA
AusVet EpiTools	Ausvet	Ausvet Pty Ltd initiative
BayesX	Nikolaus Umlauf et al.	NA
BDN_ETL_PL_SQL	IZSAM	Internal
BI Publisher	IZSAM	Business
Bioconductor	R Community	CRAN
Bluetongue model	University of Copenhagen	Research project
branchr	R Epidemics Consortium	RECON project
Brugs	Uwe Ligges	NA
CAPS2	IZSAM	internal
Crystal Ball	ORACLE	Business
CSF-WB-surveillance	FLI	EC's Seventh Framework
C-TSEMM	AHVLA	AHVLA mandate
CulBase	FLI	FLI initiative
Cytoscape	Cytoscape Project	Cytoscape Project
CZ State Veterinary Administration	CZ State Veterinary Administration	Internal/Outsourced
Datonix Query Objects	IZSAM	Business
dibbler	R Epidemics Consortium	RECON project
distcrete	R Epidemics Consortium	RECON project
DMD	IZSAM	internal
DTU-DADS-ASF	DTU	Research project
DTU-DADS-FMD	DTU	NA
earlyR	R Epidemics Consortium	RECON project
ECOSEA	IZSAM	IPA Adriatic
EMMa	ECDC	Public
Epi Info	CDC	NA
EpiCalc 2000	NA	NA
EpiCollect	Imperial College London	Research project
epicontacts	R Epidemics Consortium	RECON project
EpicontactTrace	SVA	Internal
EpiData Classic Software	The EpiData Assoc.	Friends Of EpiData
EpiData Manager	The EpiData Assoc.	Friends Of EpiData

EpiEstim	R-Epi	R-epi project
EpiExploreR	R Community	CRAN
epiflows	R Epidemics Consortium	RECON project
EpigearXL	WHO	WHO
epimaps	R Epidemics Consortium	RECON project
epimatch	R Epidemics Consortium	RECON project
EpiModel	Emory Univeristy	Research project
epinet	R-Epi	R-epi project
EpiTools	RISKSUR partners	RISKSUR project
EpiTrace	IZSAM	Internal
epitrix	R Epidemics Consortium	RECON project
Ersatz	WHO	WHO
EURL CSF / ASF DB	European Commission	EC mandate
flusight	Reich Lab	Public
FolkhälsöStudio	Folkhälsomyndigheten	Private
FRAGSTATS	K. McGarigal & D. Cushman	Research project
freedom	SVA	Internal
GeoDa	Luc Anselin	Luc Anselin initiative
Geonetwork	Open Source Geospatial Foundation	OSGEO project
Geoserver	Open Geospatial Consortium (OGC)	OGC initiative
gephi	IZSAM	Business
GISAID EpiFlu	FLI	FLI initiative
GISEntoTrap	IZSV	Internal
hlt	SVA	Internal
Hotline	HOTLINE partners	HOTLINE project
IEBTlabNET	IZSAM	internal
incidence	R Epidemics Consortium	RECON project
incidence	R-Epi	R-epi project
INLA	Håvard Rue	NA
IUVENE	IZSAM	internal
JAGS	Martyn Plummer	Martyn Plummer initiative
JUNDA - SSD2 XML	EFSA	Public project
Kartenexplorer	FLI	FLI initiative
kcde	The Reich Lab at UMass-Amherst	Research project
Kendrick	NA	Research project
lme4	AGES	CRAN
maptools	AGES	CRAN
mem	José Lozano initiative	José Lozano initiative
MetaXL	WHO	WHO
Microsoft Power BI	IZSAM	Business
Migratory Birds in Europe	FLI	FLI initiative

mill	SVA	Internal
Mintrisk	EFSA - WBVR	Research project
MIX 2.0	BiostatXL	Business
Multibugs	University of Cambridge	BUGS project
Mückenatlas	FLI	FLI initiative
New Flubird database	FLI	FLI initiative
NFB model	New Flubird Consortium	New Flubird project
NIMBLE	NIMBLE Develop.Team	NSF grants
OIEparser	Norbert Solymosi initiative	Research project
OpenBugs	University of Cambridge	BUGS project
OpenEpi	NA	NA
Oracle BI	IZSAM	Business
outbreaker	R-Epi	R-epi project
outbreaker2	R Epidemics Consortium	RECON project
OutbreakTools	R-Epi	R-epi project
projections	R Epidemics Consortium	RECON project
QGis	QGIS community	QGIS project
Qlik View	IZSAM	Business
R2WinBUGS	University of Cambridge	BUGS project
Rabies - Bulletin - Europe	WHO	WHO mandate
Rapid Miner	Rapid Miner team	Business
RASVE	NA	Internal
Rcmd	IZSAM	CRAN
Restriction zones for BT	IZSAM	internal
RIBESS+	EFSA mandate	EFSA mandate
rjags	Martyn Plummer	NA
RLadyBug	Michael Höhle	NA
rsatscan	R-Epi	R-epi project
Sampelator	EFSA	EFSA mandate
SAP BusinessObjects BI Platform	SAP	Business
SaTScan	Martin Kulldorff	Martin Kulldorff initiative
sf	AGES	CRAN
SIMAN	IZSAM	Business
SimInf	SVA	Internal
SpatialEpi	Smith College	Smith College
spBayes	Andrew Finley & Sudipto Banerjee	NA
Spread model for PPR	Eriot-Watt University	Research project
STAN	STAN Develop. Team	Research project

STATA	StataCorp	Business
STEM	Eclipse Foundation	Eclipse project
STOC-free data	STOC-free project	STOC-free project
surveillance	R-Epi	R-epi project
SurvTools	RISKSUR partners	RISKSUR project
Svemap	SVA	Internal
Svamp	SVA	Internal
SVASSS (see vetsyn)	SVA	Internal
TemporalNetworkAccessibility	FLI	Research project
TreePar	R-Epi	R-epi project
TreeSim	R-Epi	R-epi project
TSA	EFSA BIOHAZ	EFSA mandate
TSIS	FLI	FLI initiative
TSN-KVP	reRe	FRG mandate
Web survey	IZSAM	Internal
VESLA	NA	NA
VetEpiGIS-Tool	IZSV	IZSV mandate
VetIS	Bulgarian Food Safety Agency	Internal
vetsyn	R-Epi	R-epi project
WHONet Software	WHO Collab. Centre	NA
vildsvin.fvst.dk	DTU	Internal
vimes	R Epidemics Consortium	RECON project
WinBUGS	University of Cambridge	BUGS project
WINPEPI	Joseph H Abramson	J. H. Abramson initiative
Wolfram Mathematica	Wolfram	Business
XLSTAT	IZSAM	Business
Navicat	PremiumSoft	Business

Primary Purpose	Availability	Software type	Maintainer
DA-RE	P	TP	PALISADE
DA-RE	P	SA	Miljø- og Fødevarerstyrelsen
DA-RE	P	SA	Miljø- og Fødevarerstyrelsen
RE	RS	SA	FLI
DA-RE	P	SA	Esri
DA	FA	TP	Innocent, Giles, & J. McKendrick, Iain.
RE	P	SA	ECDC GIS Team
NA	NA	NA	NA
DA	FA	SA	Evan Sergeant
DA-RE	FA	TP	Nikolaus Umlauf
DA-RE	P	SA	IZSAM
DA-RE	P	SA	ORACLE
DA-RE	FA	TP	Bioconductor development team
DA	FA	TP	Denwood, Matthew
DA	FA	TP	Pierre Nouvellet
DA-RE	FA	TP	Uwe Ligges
RE	RS	SA	IZSAM
DA-RE	P	TP	ORACLE
DA	FA	TP	FLI
DA	FA	TP	AHVLA
RE	RS	SA	FLI
DA-RE	FA	SA	Cytoscape development team
DA-RE	P	SA	Marie Bleierova
DA-RE	P	SA	Datonix
DA	FA	TP	Thibaut Jombart
DA	FA	TP	Rich Fitzjohn
DA	P	SA	IZSAM
RE	FA	TP	T. Halasa
RE	FA	TP	T. Halasa
DA	FA	TP	Thibaut Jombart
RE	FA	SA	IZSAM
RE	P	SA	ECDC GIS Team
DA	FA	SA	Not specified
DA	FA	SA	Not maintained
RE	FA	SA	David Aanensen
DA	FA	TP	VP Nagraj
DA-RE	FA	TP	Stefan Widgren
DA-RE	FA	SA	Friends Of EpiData
DA-RE	FA	SA	Friends Of EpiData

DA	FA	TP	Anne Cori et al.
DA-RE	FA	TP	NA
DA	FA	TP	Pawel Piatkowski
DA	FA	TP	WHO
DA	FA	TP	Thibaut Jombart
DA	FA	TP	Hackout Team
DA-RE	FA	TP	Jenness SM, Goodreau SM and Morris M.
DA	FA	TP	Chris Groendyke
DA-RE	FA	SA	Fernanda Dórea
DA-RE	FA	SA	IZSAM
DA	FA	TP	Thibaut Jombart
DA	FA	TP	WHO
RE	RS	SA	CSF / ASF WB-DB Support Team
RE	FA	TP	Tushar A, Reich NG, Ray EL
DA-RE	P	SaaS	www.statisticsstudio.com
DA	FA	TP, SA	K. McGarigal
DA	FA	TP	Thomas Rosendal
DA	FA	SA	Luc Anselin et al.
RE	FA	SA	GeoCat bv
RE	FA	SA	Open Geospatial Consortium (OGC)
DA	P	SA	
RE	RS	SA	Federal Republic of Germany
DA	FA	TP	Matteo Mazzucato
RE	FA	TP	Thomas Rosendal
DA	FA	TP	NA
RE	FA	SA	IZSAM
DA	FA	TP	Thibaut Jombart et al.
DA	FA	TP	Thibaut Jombart et al.
DA-RE	FA	TP	Håvard Rue
RE	FA	SA	IZSAM
DA	FA	SA	Martyn Plummer
RE	P	SA	EFSA
DA	FA	SA	Bundesforschungsinstitut für Tiergesundheit
DA-RE	FA	TP	The Reich Lab at UMass-Amherst
NA	NA	NA	Serge Stinckwich, Bui Thi Mai Anh
RE	FA	TP	NA
RE	FA	TP	NA
DA-RE	FA	TP	José Lozano
DA	FA	TP	WHO
DA-RE	P	SA	Microsoft
RE	RS	SA	FLI

RE	FA	TP	Thomas Rosendal
RE	RS	SA	Wageningen BioVeterinary Research (WBVR)
DA-RE	P	TP	Leon Bax
DA	FA	SA	Andrew Thomas
RE	RS	SA	FLI
RE	RS	SA	FLI
DA	FA	TP	New Flubird Consortium
DA	FA	TP	Perry de Valpine et al.
DA-RE	FA	TP	Norbert Solymosi
DA	FA	SA	Andrew Thomas
DA	FA	SA	Not maintained
DA-RE	P	SA	ORACLE
DA	FA	TP	Thibaut Jombart
DA	FA	TP	Finlay Campbell
DA	FA	TP	Hackout Team
DA	FA	TP	Thibaut Jombart
DA-RE	FA	SA	qgis community
DA-RE	P	SA	Qlik
DA	FA	TP	Uwe Ligges
RE	RS	SA	WHO
DA-RE	P	SA	Rapid Miner team
DA-RE	P	SA	NA
DA-RE	FA	TP	John Fox
DA-RE	FA	TP	NA
DA-RE	FA	SA	Open Analytics NV
DA-RE	FA	TP	Martyn Plummer
DA-RE	FA	TP	Michael Höhle
DA	FA	TP	Ken Kleinman
DA-RE	FA	SA	Open Analytics NV
DA-RE	P	SA	NA
DA	FA	SA, TP	Martin Kuldorff
RE	FA	TP	NA
DA	P	SA	NA
DA	FA	TP	Stefan Widgren
DA	FA	TP	Albert Y. Kim
DA-RE	FA	TP	Andrew Finley
DA-RE	FA	TP	Adrakey Hola, Gibson Gavin
DA	FA	SA	Bob Carpenter et al.

DA	P	SA	William Gould
DA	FA	SA	Eclipse Members
DA	FA	TP	STOC-free Consortium
DA	FA	TP	Sebastian Meyer
DA-RE	RS	TP	Fernanda Dórea
RE	FA	TP	Thomas Rosendal
DA-RE	FA	TP	Thomas Rosendal
DA-RE	FA	TP	Fernanda Dórea
DA	FA	TP	Hartmut Lentz
DA	FA	TP	Tanja Stadlet
DA	FA	TP	Tanja Stadlet
DA-RE	FA	SA	EFSA BIOHAZ Panel
RE	RS	SA	FLI
DA-RE	FA	SA	Federal Republic of Germany
DA-RE	FA	SA	IZSAM
NA	NA	NA	NA
DA-RE	FA	TP	Nicola Ferré
DA-RE	P	SA	Alexandra Miteva, Vasil Shulev (maintainer)
DA	FA	TP	Fernanda Dórea
DA-RE	FA	SA	WHO
RE	RS	SA	Sten Mortensen
DA	FA	TP	Thibaut Jombart
DA	FA	SA	Andrew Thomas
DA	FA	SA	Not maintained
DA-RE	P	SA	Wolfram
DA-RE	P	SA	Datonix
DA-RE	P	SA	PremiumSoft

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NA	Open repositories
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epitools@ausvet.com.au; ronan.oneill@agriculture.gov.ie; anebo@sund.ku.dk	Web survey - SVA, IE, DK
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https://sites.google.com/site/hackoutwiki/participants	Open repositories
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Christoph.Staubach@fli.de	Web survey - FLI
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stm@fvst.dk	Web survey - Danish Veterinary and Food Administration
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jiscmail@jiscmail.ac.uk	Open repositories
mark@NOSPAM.brixtonhealth.com	Open repositories
a.conte@izs.it	Web survey - IZSAM
p.calistri@izs.it	Web survey - IZSAM
th.katsifoli@minagric.gr	Web survey - GREEK MINISTRY OF RURAL DEVELOPMENT AND FOOD

TOOL NAME

DESCRIPTION

Description of the tool

TOOL SPECIFICATIONS

Data Input Requirements (data format)

Data Input Format

Data Outputs Generated

Data Outputs format

Operating System (OS)

Programming Language

Framework

Interface

Natural Language

Development Status

Current stable release (as of December 1, 2018)

Last Updated (year)

License

Required IT Skills

Website or Repository

TOOL FEATURES

1. Calculation of epidemiological relevant indicators
2. Data aggregation according to temporal/spatial dimensions
3. Spatial representation of the data (e.g. maps or Web-GIS, contact networks)
4. Disease notification
5. Active/Passive/Syndromic surveillance
6. Risk factor analysis
7. Identification and analysis of clusters
8. Visualisation of control measures (e.g. zoning, vaccination status)
9. Temporal or spatial analysis of outbreaks
10. Integration of outcomes from other projects (e.g. ENETWILD, GISAID, Vectornet, WAHIS, EMPRES-i)
11. Scenarios/Simulations

ASF spatio-temporal model

R script for the calculation of the K-function on a set of ASF spatio-temporal data

dataset
.csv
report
.pdf
Unix/Linux, Mac OS, Windows
R
R Package & R shiny app
CLI, GUI
English
PS
0.2
2016
CC BY 4.0
Familiarity with R

https://zenodo.org/record/198181#.XF_2tPZFzmQ



The site is intended for use by epidemiologists and researchers involved in estimating disease prevalence or demonstrating freedom from disease through structured surveys, or in other epidemiological applications

dataset
raw data to paste in the web service
tables
.xlsx
Web-service
NA
Web-app
GUI
English
PS
NA
2019
NA
None

<http://epitools.ausvet.com.au/content.php?page=home>

●

●

BayesX

BayesX is a software tool for estimating structured additive regression models. The R package includes resources for constructing boundary and graph files from other geographical information systems. The R-package BayesXsrc allows to install BayesX via the package management of R while R2BayesX and BayesR provide convenient access from within R in the usual R fomular style.

dataset
.csv
maps, tables, graphs
.tex, png
Unix/Linux, Mac OS, Windows
R
R Package
CLI, GUI
English
PS
3.0.2
2015
GPL2
Familiarity with the R language

<http://www.uni-goettingen.de/de/bayesx/550513.html>



Bluetongue model

The model retains the strongly data-driven elements of the baseline model (Szmaragd et al., 2009), representing the on-farm transmission of bluetongue, and in particular the temperature dependence of the relevant midge infectivity and mortality, adding some new features.

dataset
.csv
maps, tables, graphs
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
C++, R
CLI
English
PS
NA
2016
CC BY 4.0
Familiarity with the R language

https://zenodo.org/record/168022#.XF_8RPZFzmQ

●

●

branchr

The package implements estimations of reproduction numbers from cluster size distribution

dataset, matrix
.csv
tables, graphs
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
R Package
CLI
English
B
0.1
2017

MIT + file [LICENSE](#)

Familiarity with the R language

<https://github.com/reconhub/branchr>

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Brugs

Fully-interactive R interface to the 'OpenBUGS' software for Bayesian analysis using MCMC sampling. Runs natively and stably in 32-bit R under Windows. Versions running on Linux and on 64-bit R under Windows are in ``beta" status and less efficient.

dataset, matrix

all formats for import available in R

text

all formats for export available in R

Unix/Linux, Windows

R

R Package

CLI

English

PS

0.9

2017

GPL-2

Familiarity with the R language and OpenBUGS

<https://cran.r-project.org/web/packages/BRugs/BRugs.pdf>



The CAPS2 project portal is the access point to visualize and manage all the information about aquaculture, fishes and molluscs diseases in the Adriatic Sea. The Supranational Web GIS application is freely accessible, but the detailed disease information are available only for authorized user.

none

none

none

none

Unix/Linux, Mac OS, Windows

Javascript, server and client frameworks

Web-GIS Application

GUI

English

PS

0.9

2019

NA

None

<http://www.caps2.eu/caps2/>



C-TSEMM

The Cattle TSE Monitoring Model (C-TSEMM), developed for EFSA by a contractor, allows evaluating different bovine spongiform encephalopathy (BSE) monitoring regimes (implemented or hypothetical) in cattle and the ability of those schemes to detect either the re-emergence of BSE or the emergence of a new transmissible spongiform encephalopathy (TSE) disease in cattle, by estimating the trend of the current BSE epidemic within European Union Member States.

dataset, matrix
.csv
text
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
R Package & VBA interface
CLI, GUI
English
PS
3.0.2
2016
GPL2
Familiarity with the R language
https://zenodo.org/record/57079#.XGEbC_ZFzmQ



Cytoscape

Cytoscape is an open source software platform for visualizing complex networks and integrating these with any type of attribute data. A lot of Apps are available for various kinds of problem domains, including bioinformatics, social network analysis, and semantic web.

network file
SIF, GML, and XGMML
Reports, graphs
pdf, graphical outputs
Unix/Linux, Mac OS, Windows
Java
Java Desktop application
CLI, GUI
English
PS
3.7.1
2019
LGPL
None

<https://cytoscape.org/>



dibbler

dibbler provides tools for investigating food-borne outbreaks with (at least partly) known food distribution networks, and genetic information on the cases.

dataset, matrix
.csv
graph
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
R Package
CLI
English
PS
0.1
2017
MIT + file LICENSE
Familiarity with the R language
<https://github.com/reconhub/dibbler>



distcrete

The package takes a distribution and a set of parameters and returns a list object with functions as elements. Each one is the equivalent to the function calls we typically expect to be able to do in R for a given distribution:

- Density e.g. `dnorm`
 - Distribution function e.g. `pnorm`
 - Quantile function e.g. `qnorm`
 - Random generation e.g. `rnorm`
-
-

dataset, matrix

.csv

none

all formats for export available in R
Unix/Linux, Mac OS, Windows

R

R Package

CLI

English

PS

0.1

2017

MIT + file LICENSE

Familiarity with the R language

<https://github.com/reconhub/distcrete>



DTU-DADS-ASF

The DTU-DADS-ASF is used to simulate the spread of African swine fever between swine herds through animal movements, abattoir, low risk, and medium risk contacts, and through local spread. It also includes spread from wild boar to domestic pigs under the assumption of an endemic ASF situation in wild boar. The model runs in the basic R and it does not require downloading extra packages. It consists of 15 scripts that include the different functions of the model.

dataset
.csv
tables, graphs, maps
.txt,
Unix/Linux, Mac OS, Windows
R
R package
CLI
English
PS
0.16
2018
GPL3
Familiarity with the R language
<https://github.com/THalasa/DTU-DADS-ASF>



Davis Animal Disease Simulation model (DADS) that has been further developed at the Technical University of Denmark to DTU-DADS to simulate a hypothetical spread of FMD in Denmark

dataset

.csv

tables, graphs, maps

.txt

Unix/Linux, Mac OS, Windows

R

R package

CLI

English

PS

0.16

2018

GPL3

Familiarity with the R language

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5425474/>



earlyR

This package implements simple estimation of infectiousness, as measured by the reproduction number (R), in the early stages of an outbreak. This estimation requires:

- prior knowledge: the serial interval distribution, defined as the mean and standard deviation of the (Gamma) distribution. In general, these parameters are best taken from the literature.
 - data: the daily incidence of the disease, including only confirmed and probable cases.
-
-

dataset, matrix
.csv
graph
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
R Package
CLI
English
PS
0.1
2017
MIT + file LICENSE
Familiarity with the R language
<https://github.com/reconhub/earlyR>

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The project ECOSEA aims to promote, improve and protect the marine and coastal environments through sustainable management of fisheries. The Information System Ecosea is a technically - scientific support to the choices of governance of the fisheries sector.

Parameters
Numeric values
maps
dynamic maps
Unix/Linux, Mac OS, Windows
Mapserver and client framework
Web-GIS Application
GUI
Italian
PS
NA
2019
NA
None

http://mapserver.izs.it/gis_ecosea/



epicontacts

The package aims to facilitate manipulation, visualisation and analysis of epidemiological contact data.

Such datasets inherently have network components, in which nodes are typically cases and reported contacts or exposures are (directed or undirected) edges. This package provides a convenient data structure as well as functionality specific to handle these data.

dataset

.csv

graphs

all formats for export available in R

Unix/Linux, Mac OS, Windows

R

R package & R shiny Web-App

CLI, GUI

English

PS

0.2

2017

MIT + file LICENSE

Familiarity with R

<https://github.com/reconhub/epicontacts>



EpicontactTrace

Routines for epidemiological contact tracing and visualisation of network of contacts. The output from the analysis is available as a dataset, but moreover, the tool automatically generates a report on farm level. The report both contains an overview of the situation on the farm, including a graph, as well as detailed information including dates of movements on group or individual level on all contacts.

dataset
all formats for import available in R
report
.pdf
Unix/Linux, Mac OS, Windows
R
R package & R shiny Web-App
CLI, GUI
English
PS
0.2
2017

Familiarity with R

<https://github.com/stewid/EpiContactTrace>



EpiEstim

A tool to estimate time varying instantaneous reproduction number during epidemics

This tool is described in the following paper: A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics Anne Cori, Neil M. Ferguson, Christophe Fraser and Simon Cauchemez American Journal of Epidemiology 2013.

dataset

all formats for import available in R

graphs

all formats for export available in R

Unix/Linux, Mac OS, Windows

R

R package

CLI

English

PS

0.1

2017

MIT + file LICENSE

Familiarity with R

<https://github.com/annecori/EpiEstim>

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epiflows

Epiflows is a package for predicting and visualising spread of infectious diseases based on flows between geographical locations, e.g., countries. epiflows provides functions for calculating spread estimates, handling flow data, and visualization

dataset

all formats for import available in R

graphs

all formats for export available in R

Unix/Linux, Mac OS, Windows

R

R package

CLI

English

PS

0.1

2018

MIT + file LICENSE

Familiarity with the R language

<https://github.com/reconhub/epiflows>



epimaps

This package provides a set of tools and wrappers useful for mapping infectious diseases.

dataset
.csv
maps
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
R package
CLI
English
PS
0.1
2018
MIT + file LICENSE
Familiarity with the R language
<https://github.com/reconhub/epimaps>



epimatch

It is a package for displaying and recording suggested patient row matches across datasets for epidemiology workers in the field. It was specifically designed for field workers who will be attempting to find duplicated patient records within a single or multiple tabular datasets, such as csv files.

dataset
.csv
None
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
R package
CLI
English
PS
0.1
2016
MIT + file LICENSE
Familiarity with the R language
<https://github.com/Hackout3/epimatch>



EpiModel

EpiModel is an R package that provides tools for simulating and analyzing mathematical models of infectious disease dynamics. Supported epidemic model classes include deterministic compartmental models, stochastic individual contact models, and stochastic network models. Disease types include SI, SIR, and SIS epidemics with and without demography, with utilities available for expansion to construct and simulate epidemic models of arbitrary complexity.

dataset
.csv
graphs, tables
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
R Package
CLI
English
PS
1.7.2
2018
GPL-3
Familiarity with the R language
<http://www.epimodel.org/index.html>



epinet

A collection of epidemic/network-related tools. Simulates transmission of diseases through contact networks. Performs Bayesian inference on network and epidemic parameters, given epidemic data.

dataset
.csv
graphs, tables
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
R Package
CLI
English
PS
1.7.2
2018
GPL-2
Familiarity with the R language
<https://github.com/cran/epinet>



Online application implementing statistical methods for estimating disease prevalence or demonstrating freedom from disease through structured surveys, or in other epidemiological applications

dataset
none / raw data to paste in the web service
tables
.xlsx
Unix/Linux, Mac OS, Windows
NA
Web-app
GUI
English
PS
NA
2017
NA
None

<https://epitools.fp7-risksur.eu/>

●

This package implements small helper functions usefull in infectious disease modelling and epidemics analysis.

dataset
.csv
graphs, tables
all formats for export availble in R
Unix/Linux, Mac OS, Windows
R
R Package
CLI
English
PS
0.2.2
2019
MIT + file LICENSE
Familiarity with the R language
<https://github.com/reconhub/epitrix/>



Ersatz

Ersatz is a bootstrap add-in for Microsoft Excel for Windows. It allows the user to do uncertainty analysis (aka 'riskanalysis', 'Monte Carlo simulation', 'probabilistic sensitivity analysis', 'bootstrapping'), microsimulation, and probabilistic bias quantification in Excel.

Ersatz was originally developed as a low-cost alternative to @Risk™ and Crystal Ball™. The Ersatz program has additional features included for users who are interested in health economic evaluation modeling and/or microsimulation.

dataset
xlsx
graphs, tables
all graphical and data formats available for export in Excel
Windows only
VBA
Microsoft Excel plug-in
GUI
English
PS
5.3
2016
Free + Copyright
None

http://www.epigear.com/index_files/ersatz.html

●

●

freedom

An R package to calculate probability of freedom from disease in a population based on surveillance data. This is used for Demonstrating Disease Freedom (DDF) and as foundation for affecting and maintaining trade relationships as well as trade restrictions to avoid future introductions. These calculations have been successfully done in @risk software which is add-on toolset to the Microsoft Excel spreadsheet package. In order to make these calculations more reproducible and based on openly available tools, this package is being produced in R.

dataset
.csv
graphs, tables
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
R Package
CLI
English
PS
0.2.2
2019
GPL-3
Familiarity with the R language
<https://github.com/SVA-SE/freedom>



A collection of R functionalities to define where to place a sampling site trap. expert opinions based (AHP) on the Corine Land Cover classification

dataset
.csv
graphs, tables, shapefiles
.csv, .shp, and all available graphical formats
Unix/Linux, Mac OS, Windows
R
R Scripts
CLI
English
I
NA
2017
MIT
Familiarity with the R language

<https://github.com/IZSVenezie/GISEntoTrap>

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Web-GIS application showing the global bluetongue geographical distribution. The data shown in the application are not official.

They are collected and managed by the staff of the IZSA&M, and derived from the information published by OIE.

It is possible to run ad-hoc queries to filter the hosted data both temporally and spatially.

none

none

none

none

Unix/Linux, Mac OS, Windows

Mapserver and client framework

Web-GIS Application

GUI

Italian

PS

NA

2019

NA

None

http://mapserver.izs.it/gis_oiemaps/



incidence

Provides functions and classes to compute, handle and visualise incidence from dated events for a defined time interval. Dates can be provided in various standard formats. The class 'incidence' is used to store computed incidence and can be easily manipulated, subsetted, and plotted. In addition, log-linear models can be fitted to 'incidence' objects using 'fit'.

dataset
.csv
graphs
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
R package & R shiny Web-App
CLI, GUI
English
PS
0.2
2017
MIT + file LICENSE
Familiarity with R
<https://github.com/reconhub/incidence>



MetaXL

MetaXL is an add-in for meta-analysis in Microsoft Excel for Windows. It supports all major meta-analysis methods, plus, uniquely, the inverse variance heterogeneity and quality effects models. Starting with v4.0, it also implements a powerful, yet easy to use way to do network meta-analysis.

dataset
xlsx
graphs, tables
all graphical and data formats available for export in Excel
Windows only
VBA
Microsoft Excel plug-in
GUI
English
PS
5.3
2016
Free + Copyright
None

http://www.epigear.com/index_files/metaxl.html

●

●

mill

An R package for grinding together docx files to generate a pdf report.

text
.docx, .txt
report
pdf
Unix/Linux, Mac OS, Windows
R
R package
CLI
English
PS
0.0.12
2018
EUPL
Familiarity with R and Latex
<https://github.com/SVA-SE/mill>



OIEparser

An R package to create SQLite database from the OIE reports

dataset, matrix
sqlite
tables, maps
.shp, .kml, .html
Unix/Linux, Mac OS, Windows
R
R Package
CLI
English
PS
0.1
2017
GPL-3
Familiarity with the R language

<https://solymosin.github.io/OIEparser/>



outbreaker2

R package that implements a Bayesian framework for integrating epidemiological and genetic data to reconstruct transmission trees of densely sampled outbreaks. It re-implements, generalises and replaces the model of outbreaker, and uses a modular approach which enables fine customisation of priors, likelihoods and parameter movements

dataset
.Rdata, .csv
graphs, tables
all formats for export available in R
Unix/Linux, Mac OS, Windows
R Package
R Package
CLI
English
PS
1.1.0
2018
MIT + file LICENSE
Familiarity with the R language
<https://github.com/reconhub/outbreaker2>

●

●

projections

This package uses data on daily incidence, the serial interval (time between onsets of infectors and infectees) and the reproduction number to simulate plausible epidemic trajectories and project future incidence

dataset
.Rdata, .csv
graphs, tables
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
R Package
CLI
English
PS
0.3.1
2019

MIT + file LICENSE
Familiarity with the R language

<https://github.com/reconhub/projections>

●

●

Online application implementing statistical methods for estimating the sample size, global (and group) sensitivity and probability of freedom from disease.

numerical parameters
None
tables, graphs
all formats for export available in R
Unix/Linux, Mac OS, Windows
R
R package & R shiny Web-App
GUI
English
PS
0.1
2016
CC BY 4.0
No skills required

<https://zenodo.org/record/2541541#.XGCVRfZFzmQ>

●

●

Analysis of small scale infectious disease data using stochasticSusceptible-Exposed-Infectious-Recovered (SEIR) models. The R package wraps functionality of the Java program LadyBug, i.e. a Java virtual machine has to be installed on your computer.

dataset, matrix
.csv
tables, graphs
all formats for export available in R
Unix/Linux, Windows
R (need Java virtual machine installed)
R Package
CLI
English
PS
0.7-2
2014
CC BY 4.0
Familiarity with the R language

https://r-forge.r-project.org/R/?group_id=1868



QMRA model

The QMRA model is set up using a modular approach. It consists of the following modules: farm, transport & lairage, slaughter and processing, preparation and consumption. The outcome of the latter module is fed into the dose-response model to predict the risk. The model uses Monte Carlo sampling as a means for dealing with variability in the parameters. A user-friendly interface has been developed for the QMRA model for Salmonella in pigs.

Model parameters

numerical values

tables

.txt

Unix/Linux, Mac OS, Windows

Matlab

executable (.exe)

GUI

English

PS

NA

2016

CC BY 4.0

Familiarity with the Matlab language

<https://zenodo.org/record/154724#.XGCQLfZFzmQ>

●

●

SaTScan (Rsatscan)

SaTScan(TM) (<http://www.satscan.org>) is software for finding regions in Time, Space, or Time-Space that have excess risk, based on scan statistics, and uses Monte Carlo hypothesis testing to generate P-values for these regions. The rsatscan package provides functions for writing R data frames in SaTScan-readable formats, for setting SaTScan parameters, for running SaTScan in the OS, and for reading the files that SaTScan creates.

dataset
.csv, .txt, .Rdata
shapefiles, tables
.dbf, .shp
Unix/Linux, Mac OS, Windows
C++,R
R package
GUI, CLI
English
PS
9.6 (0.3.9200)
2018 (2016)
GPL-3
none/Familiarity with the R language
<https://www.satscan.org/>

•

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The package provides an efficient and very flexible framework to conduct data-driven epidemiological modeling in realistic large scale disease spread simulations. The framework integrates infection dynamics in subpopulations as continuous-time Markov chains using the Gillespie stochastic simulation algorithm and incorporates available data such as births, deaths and movements as scheduled events at predefined time-points.

dataset

All possible import formats available in R
graphs, maps, tables

All possible export formats available in R
Unix/Linux, Mac OS, Windows

R

R package

CLI

English

PS

NA

2016

GPL-3

Familiarity with the R language

<https://github.com/stewid/SimInf>

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SpatialEpi

Package of data and methods for spatial epidemiology.

spatial dataset
.csv, .txt
maps
jpeg
Unix/Linux, Mac OS, Windows

R Package
CLI
English
PS
1.2.3.9000
2018
GPL-2
Familiarity with the R language

<https://github.com/rudeboybert/SpatialEpi>

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•

STEM

STEM is a standalone rich client platform (RCP).
STEM requires atleast Java 1.6. Java JREs from Oracle and IBM are supported.

dataset

Unix/Linux, Mac OS, Windows

Java

Java toolkit

GUI

English

PS

4.0.0

2019

[http://www.eclipse.org/legal/epl-2.0.](http://www.eclipse.org/legal/epl-2.0)

None

<https://www.eclipse.org/stem/downloads.php>

●

●

Svamap

Routines for reading and reshaping data to produce an R spatial dataset (i.e. Spatial(*)DataFrame object), export the data to geojson format and write it to a .js file THis .js file is then passed to a template designed with the javascript library Leaflet to create an interactive webmap.

.csv

.csv

map

.html

Unix/Linux, Mac OS, Windows

R

R package

CLI

English

PS

0.1

2018

GPL-3

Familiarity with R

<https://github.com/SVA-SE/svamap>



SVAMP

An R package that generates a geographic summary report for farm data in Sweden. Useful for monitoring the status of the farms and as a management tool during outbreaks events

dataset

.csv

maps, tables, graphs

.html

Unix/Linux, Mac OS, Windows

R

R package & Web-App

CLI, GUI

English

I

0.1

2016

GPL-3

No skills required

<https://github.com/SVA-SE/svamp>



SVASSS (vetsyn)

Veterinary syndromic surveillance from classified data to interface. Detailed tutorials are included with the package. It provides ready-to-use codes to automatize the process of converting pre-classified animal health data into epidemiological information. Functions to monitor data daily and weekly are available.

dataset
.csv
report
.pdf
Unix/Linux, Mac OS, Windows
R
R package & R shiny Web-App
CLI
English
PS
???
2018
GPL-3
Familiarity with R
<https://github.com/nandadorea/vetsyn>



TemporalNetworkAccessibility

Unfolding Accessibility Provides a Macroscopic Approach to Temporal Networks

dataset
.dat
list
.txt
Unix/Linux, Mac OS, Windows
Python 3
Python script
CLI
English
B
0.1
2019
NA
Familiarity with Python language

<https://github.com/hartmutlantz/TemporalNetworkAccessibility#temporalnetworkaccessibility>



TSA

Developed and applied by the EFSA Working Group on *Listeria monocytogenes* contamination of ready-to-eat foods. The analyses are implemented in R. The analyses are explained step by step in the R script.

dataset
.csv
NA
NA
Unix/Linux, Mac OS, Windows
R
R scripts
CLI
English
PS
0.1
2018
CC 4.0
Familiarity with R

https://zenodo.org/record/1117639#.XF_xAvZFzmQ

●

VetEpiGIS-Tool

A QGIS plugin, Spatial functions for vet epidemiology

Spatial dataset

lat/long

shapefiles, tables

.shp, .txt

Unix/Linux, Mac OS, Windows

Python

QGIS plug-in

GUI

English

PS

NA

2019

GPL-2

Familiarity with Python and QGIS

<https://github.com/IZSVenezie/VetEpiGIS-Tool>

●

●

The Danish Veterinary and Food Administration monitors the occurrence of wild boar in Denmark in collaboration with the Danish Nature Agency and the DTU Veterinary Institute. Wild boars that has been killed by hunting or found dead are examined for a number of diseases, among other things African Swine Fever. This Web-GIS service shows where live wild boar or traces of these have been found.

Parameters

Numeric values

maps

dynamic maps

Unix/Linux, Mac OS, Windows

Mapserver and Open layer framework

Web-GIS Application

GUI

Danish

PS

NA

2019

NA

None

https://www.foedevarestyrelsen.dk/Nyheder/Aktuelt/Sider/Pressemeddelelser_2018/Meld-vildsvin-med-ny-app.aspx



vimes

The package provides tools for integrating various types of surveillance data for detecting disease outbreaks and clusters.

dataset
.csv
graphs
all available graphical options in R
Unix/Linux, Mac OS, Windows
R
R package
CLI
English
PS
1.0.0
2018
GPL>=2
Familiarity with R

<https://github.com/reconhub/vimes>

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