

Development of an interactive open source software application (RadaR) for infection management / antimicrobial stewardship

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Abstract

Objectives

Analysing process and outcome measures for patients suspected of or having an infection in an entire hospital requires processing large datasets and accounting for numerous patient parameters and treatment guidelines. Rapid, reproducible and adaptable analyses usually need substantial technical expertise but can yield valuable insight for infection management and antimicrobial stewardship (AMS) teams. We describe a software application (RadaR - Rapid analysis of diagnostic and antimicrobial patterns in R) for infection management allowing user-friendly, intuitive and interactive analysis of large datasets without prior in-depth statistical or software knowledge.

Methods and Results

RadaR was built in R, an open source programming language, making it free to use and adaptable to different settings. Shiny, an additional open source package to implement web-application frameworks in R, was used to develop the application. RadaR was developed in the context of a 1339-bed academic tertiary referral hospital to handle data of more than 180,000 admissions.

RadaR visualizes analytical graphs and statistical summaries in an interactive manner within seconds. Users can filter large patient groups by 17 different criteria and investigate antimicrobial use, microbiological diagnostic use and results, and outcome in length of stay. Results can easily be stratified and grouped to compare individually defined patient groups. Finally, datasets of identified patients / groups can be downloaded for further analyses.

Conclusion

RadaR facilitates understanding and communication of trends in antimicrobial use, diagnostic use and patient outcome by linking and aggregating individual patient data in one user-friendly application. RadaR can produce aggregated data analysis while preserving patients' features in the data to adjust and stratify results in detail. AMS teams can use RadaR to identify areas, both for diagnostic and therapeutic procedures, within their institutions that might benefit from increased support and to target their interventions.

Introduction

In times of rising antimicrobial resistances (AMR) worldwide efforts focus on the preservation of antimicrobials as a precious non-renewable resource. Infection management in the form of antimicrobial stewardship (AMS) programmes, defined as "a coherent set of actions which promote using antimicrobials responsibly", is an effective way to tackle this global health problem (1). Appropriate use of antimicrobials based on appropriate and timely diagnostics are important tools for successful infection management. Stewardship efforts aim at improving quality of care and patient safety as a top priority of any intervention. Thereby, the contribute to efforts in fighting AMR through optimizing the use of antimicrobials. They are focused both on individual patients (personalized medicine, consulting) and patient groups/clinical syndromes (guidelines, protocols, IT infrastructure/clinical decision support systems, etc.).

AMS setups in hospitals are often heterogeneous but audit and feedback to assess the goals are an essential part of most programmes and are included in international guidelines and reviews (2–7). Important data for AMS programmes include for example days of therapy (DOT), daily defined doses (DDD), admission dates, length of stay (LOS) and adherence to local or national treatment guidelines (1). Clinical outcomes, quality of care or consumption of hospital resources can be measured in mortality or surrogate parameters like length of stay. Widespread electronic health records (EHR) and administrative data facilitate data collection. Administrative data has also been shown to be a reliable source for assessing clinical outcomes (8).

EHR usually offer quick insights into useful data for AMS on the individual patient level. However, easy access to analyse patient groups (e.g. stratified by departments or wards,

specific antimicrobials or diagnostic procedures used) is difficult to implement in daily practice. Rapid analysis of larger patient populations (e.g. spread over multiple specialties) is even more challenging although this information might be available. Yet, this is vital for meaningful analysis, including possible confounders, and pattern recognition across different populations. Even when aggregated data is available it is often not possible to trace back individual patients and analysis lack the ability to be further adjusted or stratified.

AMS teams are multidisciplinary and act beyond the borders of single specialties (9). They are usually understaffed (10), with limited IT support. They therefore need user-friendly and time-saving IT resources, without the need for profound technical expertise once the system is set up. To aggregate and link data of diagnostic compliance, antimicrobial use, guideline adherence, and clinical outcomes on the institutional level can build the basis for important insights for these teams. These could be used to identify areas within hospitals that might benefit most from supportive AMS interventions (e.g. subspecialties with lower guideline adherence, low diagnostic compliance or unusual patterns of antimicrobial use). Feedback from this data could also help physicians to better understand their patient population as a whole and administrative departments could allocate resources in a more targeted fashion.

Moreover, aggregated data and simultaneous analysis of multiple areas (e.g. antimicrobial and diagnostic use) present an extensive insight into large patient populations. This also enables comprehensive and multidisciplinary approaches of infection management combining treatment and diagnostic perspectives (1,9,11). Unfortunately, this kind of analyses still requires substantial statistical knowledge and software skills while being time consuming.

Technology, data science, and application development can bring solutions to complex data handling problems like those described above. Application development for medical and epidemiological (research) questions has found many important answers during the last years alone. Applications at hospital emergency departments (ED) in form of a software dashboard have been shown to improve efficiency and quality of care for patients requiring emergency admission to hospital. These applications are used to communicate clearly defined clinical problems like mortality ratio, number of cardiac arrests or re-admission rate to the ED (12). This approach led to a decreased length of stay and mortality at the ED. Other applications can rapidly and interactively display geographical locations of tuberculosis cases without the need of technical expertise improving the understanding of transmission and detection (13). Data driven fields like genomics are front runners in developing new innovative software applications to handle large datasets, in close collaboration with bioinformatics (14).

It is of importance to note that all of these examples have been created in an open source approach. The underlying source code can be shared, modified and freely distributed through open repositories like GitHub (<https://github.com>), taking open source software license obligations into account. This facilitates collaboration and easy adaptation to many different settings and IT systems and supports the use of advanced data visualization to users with minimal experience in programming and little or no budget for professional database engineers (11).

However, to the best of our knowledge, there is no such open-source approach described for applications working with antimicrobials use and diagnostic data in the field of infection management.

We followed principles of open knowledge (15) to address the need for an interactive, easy-to-use tool that allows users to investigate antimicrobial use, microbiological diagnostic use and patient outcomes at an institutional (hospital) level. We describe the development and use of a software application (RadaR - Rapid analysis of diagnostics and antimicrobial patterns in R). It enables rapid and reproducible data analysis without extensive technical expertise in a graphically appealing way while being adaptable to different settings. Analyses are based on datasets of individual patients. Therefore, also aggregated results can be stripped down and additional patient features can be investigated. With this application we aim at supporting data-driven hospital insights and decision making for actors in the field of antimicrobial stewardship.

Methods

RadaR was developed in R, an open source programming language (16), and RStudio (<https://www.rstudio.com>). To build this web-browser based application we used the Shiny package for R (17). Shiny allows R users to build interactive web applications without extensive knowledge in web design and its programming languages. They can be run and hosted online for free (<https://www.shinyapps.io>), on local or cloud-based servers or on personal computers.

This open source approach has great advantages over traditional methods like Excel or SPSS. Hughes et al. described those in their report of an application for RNA-sequencing data analysis (14). They highlight aspects that were also fundamental for the development of RadaR. Firstly, R allows transparent, reproducible and sustainable data analysis through scripts that can easily be shared and changed. This can build the basis for collaboration and enforces the spirit of open science (also through the strong collaborative R community online). Secondly, R is open source and free to use, therefore, enabling use in resource-limited settings, too. Finally, Shiny empowers users to interact with the data making even very large datasets quickly interpretable.

The functionality of R can be easily extended by installing additional packages. Especially the dplyr and ggplot packages are to be mentioned as they are used to transform the data and to create most plots in RadaR (18,19). All packages used for the development of RadaR are listed in Table 1. RadaR is developed in an open source environment and licensed under GNU General Public License v2.0 giving options to change, modify and adapt RadaR to both personal and commercial users' needs while requiring the need to document code changes.

Table 1. Required R packages fo RadaR

R package	Minimal Version
AMR	0.2.0
broom	0.4.4
DT	0.4.0
ggrepel	0.8.0
ggridges	0.5.0
lubridate	1.7.4
plotly	4.7.1
RColorBrewer	1.1-2
rintrojs	0.2.0
shiny	1.1.0
shinyBS	0.61
shinycssloaders	0.2.0
shinydashboard	0.7.0
shinyjqui	0.2.0
shinyjs	1.0.0
shinyWidgets	0.4.3
sjPlot	2.4.1
survival	2.41-3
survminer	0.4.2
tidyverse	1.2.1
viridis	0.5.1

RadaR can be used to perform statistical tests for explanatory analysis. Differences in length of stay are displayed by a Kaplan-Meier curve in conjunction with a log-rank test using the survminer package (20). Users can further build a Cox regression model for length of stay and a multiple logistic regression model for the likelihood of performing microbiological

diagnostic tests. The underlying calculations are done using the survival package and the base stats package respectively (16,21).

RadaR has been developed in macOS High Sierra (1.4 GHz, 4 GB RAM) and its use in Windows 7 and Linux (Ubuntu 16.04.4 LTS) was tested without any difficulties. A running example version has been deployed to shinyapps.io (<https://ceefluz.shinyapps.io/radar/>).

The entire source code of RadaR is freely accessible on Github (<https://github.com/ceefluz/radar>). The development will continue with more suggestions and improvements coming from its users and the R community. Further comments and suggestions for RadaR can be submitted at <https://github.com/ceefluz/radar/issues>.

Results and discussion

We have developed RadaR, a dashboard application providing an intuitive platform for rapid analysis of large datasets containing information about patients' admission, antimicrobial use, and results of microbiological diagnostic tests. This application can help users (i.e. professionals involved in antimicrobial stewardship programmes) to find answers to questions like: "What are the most commonly used antimicrobials at an institution/specialty/department and have they changed over time?", "Were adequate microbiological diagnostics performed at the start of antimicrobial treatments?", "What are the most frequent microorganisms found in different departments?", "Can we identify priority areas within a hospital where antimicrobial or microbiological diagnostic use has the largest room for improvement?"

Application design

RadaR is designed in form of a browser-based dashboard that most users are familiar with from typical websites and online tools (Fig. 1). The basis of RadaR's functionality is filtering datasets and producing analytical graphs according to selection criteria defined by the user. Any calculations and data aggregation is based on single observations of individual patients. To identify and analyze groups of patients, 17 different selection criteria can be found in the sidebar (Table. 2). The output of RadaR is grouped into four panels (patient, antimicrobials, diagnostics, and outcome) that each consist of three to four output boxes displaying the results.

Figure 1. Design of RadaR in a browser-based dashboard format

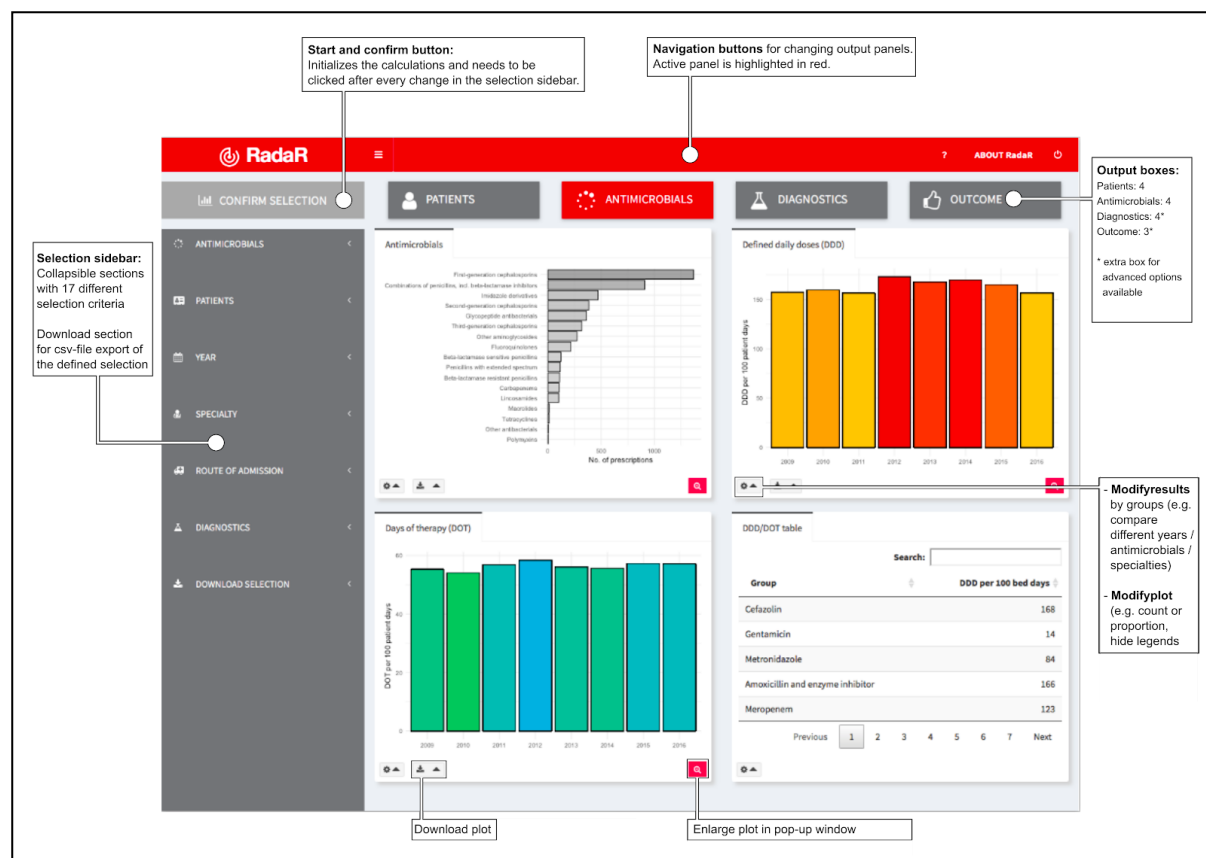


Table 2. Selection criteria in sidebar

Tab name	Criteria	Functionality
Antimicrobials	Start of antimicrobials (in relation to start of admission)	Select patients starting treatment in a defined time period
	Minimum duration of treatment (days) - all antimicrobials	Select patients with a minimum treatment duration
	Minimum duration of prescription (days) - single antimicrobial	Define the minimum duration of a prescription for any selected antimicrobial
	Administration route	Intravenous or oral
	First antimicrobial only	Filter patients for first prescribed antimicrobial

		only or any (based on all other selection criteria)
	Groups of antimicrobials	4th level of the WHO ATC classification system**
	Antimicrobials	5th level of the WHO ATC classification system**
Patients	Gender	Female or male
	Age	As available in the data
Year	Year	Years available in the data
Specialty	Specialty	Internal medicine, surgery or other
	Minimum number of patients per subspecialty	0, 10, 100, 1 000 or 10 000
	Include only this subspecialty	All other subspecialties will be excluded
	Exclude subspecialty	Define single subspecialties to be excluded
Admitting department	Admitting department	As available in the data
Diagnostics	Type of diagnostics	Blood culture or urine culture test
	Days to first test (in relation to start of antimicrobials)	Define time period for tests to be performed in
Advanced options*	Logistic regression analysis [†]	Select input variables to build a logistic regression model
	Cox regression analysis [‡]	Select input variables to build a Cox regression model

* only available in panels: Diagnostics, Outcome

** (22)

[†] only available in panel: Diagnostics

[‡] only available in panel: Outcome

All output is based on the selection criteria defined by the user in the sidebar. By default, all available options are set to include the maximum number of patients. Each new selection and any change needs to be confirmed by clicking the confirm selection button (Fig. 1). Users can navigate between the different analysis panels through clicking the respective button. The active panel is highlighted by a change in color of the selected button.

Results are shown in bar charts, combined histogram and density plots, a bubble plot and a Kaplan-Meier curve for length of stay in hospital. Each panel further displays a table summarizing the respective data analyses. All output boxes and their content are described in Table 3. Most output boxes include modification options that can be identified by small gear icons (Fig. 1). These clickable icons allow for further specification of the generated plots and tables. Users can compare different groups (e.g. antimicrobial use by antimicrobial agent or length of stay by specialty) or modify the plots (e.g. switch from count to proportion, show or hide a histogram in density plots, show or hide the legend or highlight outliers). The combination of different options results in a total of 75 different plots that can be generated for a single selection defined in the sidebar.

Table 3. Output boxes for analysis results

Output panel	Output box	Output type	Content	Modification options
Patients	Subspecialties in selection	Bubble chart†	Number of patients per subspecialty	• Show top ten by number of patients
	Subspecialties - table	Table	Total number of patients and per subspecialty	
	Patient age	Density plot (distribution)	Age distribution in selection	• Group by gender
	Number of patients per year	Bar chart	Count or proportion in selected years	• Group by gender□ • Count or proportion
Antimicrobials	Antimicrobials	Bar chart	(Group of) antimicrobials sorted by	• Single antimicrobials or groups□

			prescription, DDD or DOT	<ul style="list-style-type: none"> • Select prescription count, DDD or DOT
	Defined daily doses (DDD)	Bar chart	DDD per 100 bed days per group	<ul style="list-style-type: none"> • Group by: year, specialty, subspecialty, admitting department <input type="checkbox"/> • Show top 3 outliers <input type="checkbox"/> • Hide legends
	Days of therapy (DOT)	Bar chart	DOT per 100 bed days per group	<ul style="list-style-type: none"> • Group by: year, specialty, subspecialty, admitting department <input type="checkbox"/> • Show top 3 outliers <input type="checkbox"/> • Hide legends
	DDD/DOT table	Table	Summary of DDD/DOT per 100 bed days per group	<ul style="list-style-type: none"> • DDD or DOT <input type="checkbox"/> • Group by: antimicrobial (group), year, specialty, subspecialty, admitting department
Diagnostics	Diagnostics in selected patients	Bar chart	Diagnostics taken vs. not taken in specified timespan	<ul style="list-style-type: none"> • Count or proportion <input type="checkbox"/> • Year or Quarter per year
	Diagnostics - timing	Bar chart	Time of diagnostics performed in days after treatment start	
	Diagnostics in relation	Bar chart [†]	Absolute difference from average proportion of diagnostics performed	<ul style="list-style-type: none"> • Group by: antimicrobial (group), year, specialty, subspecialty, admitting department <input type="checkbox"/> • Show legends
	Table - Proportion performed	Table	Summary of proportion of	<ul style="list-style-type: none"> • Group by: antimicrobial (group), year, specialty,

			diagnostics performed	subspecialty, admitting department
	Microorganisms found	Bar chart	Microorganisms sorted by frequency	• Group by: antimicrobial (group), year, specialty, subspecialty, admitting department
	Advanced options*	Text output	Summary multiple logistic regression model	
Outcome	Length of stay	Density plot (plus histogram)	Distribution of length of stay per group	<ul style="list-style-type: none"> • Group by: all, gender, year, antimicrobial (group), diagnostics performed, specialty, subspecialty, admitting department <input type="checkbox"/> • Show histogram <input type="checkbox"/> • Show legend
	Length of stay - Kaplan-Meier	Kaplan-Meier curve	Kaplan-Meier curve per group	• (Groups shown as selected in Length-of-stay-box)
	Length of stay - table	Table	Summary of length of stay per group	• Group by: gender, year, antimicrobial (group), diagnostics performed, specialty, subspecialty, admitting department
	Advanced options*	Text output	Summary Cox regression model	

* Needs to be selected in sidebar

† Interactive plot showing additional information when hovering over plot

The panels for diagnostics and outcome have additional advanced options available in the sidebar. Users can use RadaR to build a logistic regression model to study the effect of different selection criteria on the likelihood of performing the selected microbiological diagnostic test in the defined time period. Similarly, the outcome panel gives the option to investigate the likelihood of discharge from hospital through a Cox regression model. The results are shown in odds and hazard ratios respectively including summary statistics to assess and compare the models. These advanced options should be used carefully and require background statistical knowledge. When implementing this application these options could be disabled depending on the local requirements.

Finally, a dataset of the user-defined selection can be downloaded from the sidebar menu in a csv-file format (comma-separated value) for further analysis (e.g. retrieving a list of patient numbers of the selected patient group)

Development process

RadaR has been developed in close contact with infection management team at the University Medical Center Groningen, Groningen, the Netherlands, to meet the needs and requirements of this user group. Subsequently, all members of the European Society of Clinical Microbiology and Infectious Diseases Studygroup for Antimicrobial stewardship (ESGAP) were asked to evaluate and test the application through a running online example of RadaR and by filling out an online survey. The ESGAP comprises around 200 members coming from more than 30 countries worldwide. Twelve members took part in the evaluation. This yielded important information on user experiences with the application and led to further improvements that are reflected in the version we present in this report. In a next phase, RadaR will be tested in different settings of ESGAP members and other interested partners using locally available data.

Workflow

RadaR was developed and tested with a dataset of all patients receiving systemic antimicrobials admitted to our institution, a 1339-bed academic tertiary referral hospital, within the years of 2009 to 2016 comprising 181,078 admissions with a total of 635,227 observations/rows. For simulation purposes and online user testing we have created a test dataset of 60,000 simulated patients that do not represent real patients. This dataset cannot be used for any meaningful results but allows testing of RadaR's functionality.

A typical example workflow with RadaR comprises six steps (with examples from the test dataset):

1. Define the selection: For example, patients receiving intravenous cefuroxime for at least two days starting on the day of hospital admission from any specialty in all years in the dataset.
2. Patients panel: Identify the total number of patients and the subspecialties with the highest number of included patients (example: 188 patients selected in total with 41 patients from internal medicine and 32 from surgery). Investigate patients' gender and age distribution.
3. Antimicrobials panel: Identify the total use of antimicrobials in DDD and DOT per 100 bed days (example: 152 and 51 respectively). Stratify the results by year and subspecialty and identify those with the highest number of DDD and DOT per 100 bed days (example: highest use by DDD and DOT in year 2011 and subspecialty pediatrics).
4. Diagnostics panel: Check if the selected microbiological diagnostic test (e.g. blood culture test) has been performed on the same day as start of cefuroxime. Investigate the proportion of performed tests over the years and which subspecialty performs

best compared to others (example: surgery ICU). Check which microorganism was the most common overall and compare differences between subspecialties.

5. Outcome panel: Check for patterns of differences in LOS in the defined patient group by subspecialties or performed diagnostics (example: highest mean LOS of 12.0 days in Urology).
6. Refine the selection: Investigate a subgroup of the original selection. For example, select only the top three subspecialties by number of patients and repeat step two to five.

Customization

RadaR uses common csv-files (comma-separated values) as input. The current state of RadaR doesn't provide any capabilities to be immediately connected to electronic medical records. Therefore, these data still needs to be extracted manually. However, this option shall be implemented in future versions to provide the optimal use for IT staff and users.

We have documented the entire workflow of data cleaning and preparation for use with RadaR in an online accessible Rmarkdown-file

(https://github.com/ceefluz/radar/blob/master/RadaR_data_preparation.Rmd). These steps are based on data from our institution and can be adjusted to fit the needs of different settings. The data should be structured in a dataset format where each variable is one column and each observation is one row. This follows the concept of tidy data by Hadley Wickham (23). Table 4 displays the final set of variables underlying RadaR's functionality.

Table 4. Input variables for RadaR

Variable	Detail
ab_days	Duration of single prescription in days
ab_days_all	Duration of overall antimicrobial treatment
ab_first	First antimicrobial (TRUE/FALSE)

ab_group	Antimicrobial group according to ATC classification
ab_route	Route of administration
ab_start_all	Start of treatment (YYYY-MM-DD)
ab_start_date	Start of prescription (YYYY-MM-DD)
ab_stop_all	Stop of treatment (YYYY-MM-DD)
ab_stop_date	End of prescription (YYYY-MM-DD)
ab_timing	Difference in days between start of admission and start of antimicrobial therapy
ab_type	Name of antimicrobial
adm_end_date	End of admission (YYYY-MM-DD)
adm_route	Admitting department
adm_start_date	Start of admission (YYYY-MM-DD)
adm_weekday	Weekday (TRUE/FALSE)
age	Patients' age
atc_code	ATC code of antimicrobial
bc_date	Time of the first blood culture (YYYY-MM-DD)
birth_date	Birth date (YYYY-MM-DD)
ddd_per_prescription	Defined daily dose per prescription
ddd_sum	Defined daily dose for all antimicrobials per treatment
fullname	Microbiological test result (if available)
gender	Gender
id	Patient ID or study ID
LOS	Length of stay
material	Microbiological test material
patient_death	Death during hospital stay (TRUE/FALSE)
specialty	General specialty (Internal medicine, Surgery, Other)
sub_specialty	Subspecialty
test_date	Microbiological test date
uc_date	Date of the first urine culture
uc_timing	Difference in days between start of antimicrobials and first urine culture
year	Year
yearquarter	Year and quarter (YYYY-Q)

For setting up RadaR in a new environment after data preparation, users only need to perform the following four steps:

1. Downloading R (<https://cran.r-project.org/>) and RStudio (<https://www.rstudio.com/products/rstudio/download/>), which are free to use and open source software.
2. Download or copy and paste RadaR's source code (<https://github.com/ceefluz/radar>) into three files in RStudio: global.R, server.R, and ui.R.
3. In global.R manually edit the path for the prepared data to be imported into RadaR. Only a single line of code needs to be edited.
4. Run the application in RStudio with the calling the function runApp() in the console or by clicking the green run app button. This will download and install the required R packages needed for the application if they have not been installed previously and create the final dataset for analysis. The RadaR interface will open in the RStudio viewer pane or in a new window of the standard browser of the user's operating system.

RadaR's appearance has been customized with using a CSS (Cascading Style Sheets) script (https://github.com/ceefluz/radar/blob/master/www/radar_style.css) that is loaded into the application upon its start. This script needs to be saved into a subdirectory of the directory of the three main files (global.R, server.R, ui.R) called "www". We recommend RStudio's project function to create a single project for RadaR and to store all information in this project directory. Users with experience in using CSS can fully alter RadaR's design by changing the underlying CSS script.

Ethical considerations

RadaR has been developed using data of patients admitted to the University Medical Center Groningen, Groningen, The Netherlands. Data was collected retrospectively and permission was granted by the ethical committee. RadaR can be used locally in protected environments. When deploying it as an online application measures have to be taken to guarantee data protection depending on national regulations.

Conclusion

We have developed a web-browser based application for rapid analysis of diagnostic and antimicrobial patterns that can support AMS teams to tailor their interventions. It has been designed to enhance communication of relevant findings while being easily accessible also for users without prior extensive software or statistical skills. In experience this system can be adapted to new settings within one day when the required data is available. RadaR has been developed in R, an open source programming language, making it free to use, share or modify according to different needs in different settings. Next steps will involve testing in multiple settings and forming a user and research group to continue and expand the use of open source technology and open science principles in infection management. This can lead to more transparency enhancing optimal quality of care and patient safety which is crucial in the light of new data-driven developments of using EHR (24).

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References

1. Dyar OJ, Huttner B, Schouten J, Pulcini C, ESGAP (ESCMID Study Group for Antimicrobial stewardshipP). What is antimicrobial stewardship? *Clin Microbiol Infect*. 2017 Nov;23(11):793–8.
2. Barlam TF, Cosgrove SE, Abbo LM, MacDougall C, Schuetz AN, Septimus EJ, et al. Implementing an Antibiotic Stewardship Program: Guidelines by the Infectious Diseases Society of America and the Society for Healthcare Epidemiology of America. *Clin Infect Dis*. 2016 May 15;62(10):e51–77.
3. Davey P, Marwick CA, Scott CL, Charani E, McNeil K, Brown E, et al. Interventions to improve antibiotic prescribing practices for hospital inpatients. *Cochrane Database Syst Rev*. 2017 Feb 9;2:CD003543.
4. NICE. Antimicrobial stewardship: systems and processes for effective antimicrobial medicine use [Internet]. [cited 2018 Mar 28]. Available from: <https://www.nice.org.uk/Guidance/NG15>
5. Schuts EC, Hulscher MEJL, Mouton JW, Verduin CM, Stuart JWTC, Overdiek HWPM, et al. Current evidence on hospital antimicrobial stewardship objectives: a systematic review and meta-analysis. *Lancet Infect Dis*. 2016 Jul;16(7):847–56.
6. SWAB. SWAB Guidelines for Antimicrobial Stewardship [Internet]. 2016 [cited 2018 Mar 28]. Available from: [http://www.swab.nl/swab/cms3.nsf/uploads/FAF701FBF4FCBDD6C12580EC0037D292/\\$FILE/20161228%20SWAB%20Guidelines%20for%20Antimicrobial%20Stewardship%200-definitief.pdf](http://www.swab.nl/swab/cms3.nsf/uploads/FAF701FBF4FCBDD6C12580EC0037D292/$FILE/20161228%20SWAB%20Guidelines%20for%20Antimicrobial%20Stewardship%200-definitief.pdf)
7. Pulcini C, Binda F, Lamkang AS, Trett A, Charani E, Goff DA, et al. Developing core elements and checklist items for global hospital antimicrobial stewardship programmes: a consensus approach. *Clin Microbiol Infect* [Internet]. 2018 Apr 3; Available from: <http://dx.doi.org/10.1016/j.cmi.2018.03.033>
8. Sarkies MN, Bowles K-A, Skinner EH, Mitchell D, Haas R, Ho M, et al. Data collection methods in health services research: hospital length of stay and discharge destination. *Appl Clin Inform*. 2015 Feb 18;6(1):96–109.
9. British Society for Antimicrobial Chemotherapy. Antimicrobial Stewardship: From Principal to Practice [Internet]. Birmingham, United Kingdom: British Society for Antimicrobial Chemotherapy; 2018. Available from: <http://bsac.org.uk/antimicrobial-stewardship-from-principles-to-practice-e-book/>
10. Pulcini C, Morel CM, Tacconelli E, Beovic B, de With K, Goossens H, et al. Human resources estimates and funding for antibiotic stewardship teams are urgently needed. *Clin Microbiol Infect*. 2017 Nov;23(11):785–7.
11. Dik J-WH, Poelman R, Friedrich AW, Panday PN, Lo-Ten-Foe JR, van Assen S, et al. An integrated stewardship model: antimicrobial, infection prevention and diagnostic (AID). *Future Microbiol*. 2016;11(1):93–102.

12. Staib A, Sullivan C, Jones M, Griffin B, Bell A, Scott I. The ED-inpatient dashboard: Uniting emergency and inpatient clinicians to improve the efficiency and quality of care for patients requiring emergency admission to hospital. *Emerg Med Australas*. 2017 Jun;29(3):363–6.
13. Smith CM, Hayward AC. DotMapper: an open source tool for creating interactive disease point maps. *BMC Infect Dis*. 2016 Apr 12;16:145.
14. Hughes LD, Lewis SA, Hughes ME. ExpressionDB: An open source platform for distributing genome-scale datasets. *PLoS One*. 2017 Nov 2;12(11):e0187457.
15. Molloy JC. The Open Knowledge Foundation: open data means better science. *PLoS Biol*. 2011 Dec;9(12):e1001195.
16. R Core Team. R: A Language and Environment for Statistical Computing [Internet]. Vienna, Austria: R Foundation for Statistical Computing; 2017. Available from: <https://www.R-project.org/>
17. Chang W, Cheng J, Allaire JJ, Xie Y, McPherson J. shiny: Web Application Framework for R [Internet]. 2017. Available from: <https://CRAN.R-project.org/package=shiny>
18. Wickham H. ggplot2: Elegant Graphics for Data Analysis [Internet]. Springer-Verlag New York; 2009. Available from: <http://ggplot2.org>
19. Wickham H, Francois R, Henry L, Müller K. dplyr: A Grammar of Data Manipulation [Internet]. 2017. Available from: <https://CRAN.R-project.org/package=dplyr>
20. Kassambara A, Kosinski M. survminer: Drawing Survival Curves using “ggplot2” [Internet]. 2018. Available from: <https://CRAN.R-project.org/package=survminer>
21. Therneau TM. A Package for Survival Analysis in S [Internet]. 2015. Available from: <https://CRAN.R-project.org/package=survival>
22. WHO Collaborating Centre for Drug Statistics Methodology. Guidelines for ATC classification and DDD assignment. Oslo, Norway; 2018.
23. Wickham H. Tidy data. *J Stat Softw*. 2014;59(10):1–23.
24. Xiao C, Choi E, Sun J. Opportunities and challenges in developing deep learning models using electronic health records data: a systematic review. *J Am Med Inform Assoc* [Internet]. 2018 Jun 8; Available from: <http://dx.doi.org/10.1093/jamia/ocy068>