Better antimicrobial resistance data analysis and reporting in less time

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Received 4 August 2022; accepted 21 December 2022

Objectives: Insights about local antimicrobial resistance (AMR) levels and epidemiology are essential to guide decision-making processes in antimicrobial use. However, dedicated tools for reliable and reproducible AMR data analysis and reporting are often lacking. We aimed to compare traditional data analysis and reporting versus a new approach for reliable and reproducible AMR data analysis in a clinical setting.

Methods: Ten professionals who routinely work with AMR data were provided with blood culture test results including antimicrobial susceptibility results. Participants were asked to perform a detailed AMR data analysis in a two-round process: first using their software of choice and next using our newly developed software tool. Accuracy of the results and time spent were compared between both rounds. Finally, participants rated the usability using the System Usability Scale (SUS).

Results: The mean time spent on creating the AMR report reduced from 93.7 to 22.4 min (P < 0.001). Average task completion per round changed from 56% to 96% (P < 0.05). The proportion of correct answers in the available results increased from 37.9% in the first to 97.9% in the second round (P < 0.001). Usability of the new tools was rated with a median of 83.8 (out of 100) on the SUS.

Conclusions: This study demonstrated the significant improvement in efficiency and accuracy in standard AMR data analysis and reporting workflows through open-source software. Integrating these tools in clinical settings can democratize the access to fast and reliable insights about local microbial epidemiology and associated AMR levels. Therefore, our approach can support evidence-based decision-making processes in the use of antimicrobials.

Introduction

Antimicrobial resistance (AMR) is a global challenge in healthcare, livestock and agriculture, and the environment alike. The silent tsunami of AMR is already impacting our lives and the wave is constantly growing.1,2 One crucial action point in the fight against AMR is the appropriate use of antimicrobials. The choice and use of antimicrobials have to be integrated into a well-informed decision-making process and supported by antimicrobial and diagnostic stewardship programmes.3,4 Next to essential (setting-specific) guidelines on appropriate antimicrobial use, the information on AMR rates and antimicrobial use through reliable data analysis and reporting is vital. While data on national and international levels are typically easily accessible through official reports, local data insights are often lacking, difficult to establish, and their generation requires highly trained professionals. This is often further complicated by very heterogeneous data structures and information systems within and between different settings.5,6 Yet, decision-makers in the clinical context need to be able to access these important data in an easy and rapid manner. Incorrect data or data analyses could even lead to biased/erroneous empirical antimicrobial treatment policies.

To overcome these hurdles, we previously developed new approaches to AMR data analysis and reporting to empower any expert on any level working with or relying on AMR data.7,8 We aimed for reliable, reproducible and transparent AMR data analysis. In addition, we demonstrated the application of this software package to create interactive analysis tools for rapid and user-friendly AMR data analysis and reporting.8 Thereby, we could fill an important gap, defined by the lack of available...
(free and open-source) software tools that fulfill all requirements such as incorporation of (inter-)national guidelines or reliable reference data.

However, while the use of our approach in research has been demonstrated,9–12 the impact on workflows for AMR data analysis and reporting in clinical settings is pending. AMR data analysis and reporting are typically performed in clinical microbiology departments in hospitals, in microbiological laboratories, or as part of multidisciplinary antimicrobial stewardship activities.

In this study, we aimed to demonstrate and study the usability of our developed approach and its impact on clinicians’ workflows in an institutional healthcare setting. The approach aimed for better AMR data analysis and reporting in less time.

Methods

The study was initiated at the University Medical Center Groningen (UMCG), a 1339 bed tertiary care hospital in the Northern Netherlands and performed across the UMCG and Certe (a regional laboratory) in the Northern Netherlands. It was designed as a comparison study to evaluate the efficiency, effectiveness and usability of a new AMR data analysis and reporting approach7,8 against traditional reporting.

Study setup

The setup of the study is visualized in Figure 1 and explained in the following sections.

The study was based on a task document listing general AMR data analysis and reporting tasks (Table 1). This list served as the basis to compare effectiveness (solvability of each task for every user) and efficiency (time spent solving each task) of both approaches. Tasks were grouped into five related questions (further referred to as five tasks). A maximum amount of time per task (group) was defined for each task. The list of tasks including correct results is available in Appendix A1, available as Supplementary data at JAC Online.

AMR data

Data were collected retrospectively and permission was granted by the local ethical committee (METc 2014/530). Anonymized microbiological data were obtained from the Department of Medical Microbiology and Infection Prevention at the UMCG. The data consisted of 23 416 records from 18 508 unique blood culture tests that were taken between 1 January 2019 and 31 December 2019, which were retrieved from the local laboratory information system (LIS). The exemplified data structure is presented in Table 2.

AMR data analysis, agile workflow and reporting

We used our previously developed approach7,8 to create a customized browser-based AMR data analysis and reporting application. This application was used in this study and applied to the AMR data analysis and reporting tasks (Table 1). The development of the application followed an agile approach using scrum methodologies and involved two developers, a clinical microbiologist and an infection preventionist.14 Scrum is a framework for project management in which work is split into short-term achievable goals, which has been proven to help with the integration of roles and knowledge to a project. Also, in medical research, scrum has been shown to efficiently empower quality, technology and implementation in scientific projects.15 Very recently, researchers showed that scrum can complement established quality assurance and software engineering practices by promoting ‘a social environment that is conducive to creating high-quality software’.16 The resulting application was designed as an interactive web-browser based dashboard (Figure 2). The prepared dataset was already loaded into the system and interaction with the application was possible through any web browser.

Analyses of AMR data in the participating departments is a regular task and comprises data from within departments (from and within local
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Data analysis tools (in this manuscript: traditional tools) for regular analysis available to study participants were tools such as IBM SPSS Statistics software (SPSS) and Microsoft Excel to allow for raw data processing (in particular in multicentre approaches to overcome interoperability issues).

Study participants

Participants in this study were recruited from the departments of Medical Microbiology, Critical Care Medicine and Paediatrics, to reflect heterogeneous backgrounds of healthcare professionals working with AMR data. Members of the development team did not take part in the study.

Study execution and data

First, study participants were asked to fill in an online questionnaire capturing their personal backgrounds, demographics, software experience and experience in AMR data analysis and reporting. Next, participants were provided the task document together with the AMR data (csv or xlsx format). The participants were asked to perform a comprehensive AMR data report following the task document using their software of choice (round 1). Task results and information on time spent per task were self-monitored in a structured report form. Lastly, participants repeated the tasks using the new AMR data analysis and reporting application (round 2). Task results and information on time spent per task were again self-monitored in a structured report form. Round 2 was evaluated using a second online questionnaire. The study execution process is illustrated in Figure 1.

Evaluation and study data analysis

The utility of the new AMR data analysis and reporting application was evaluated according to ISO 9241-11:2018. This international standard comprises several specific metrics to quantify the usability of a tool with regard to reaching its defined goals (Figure 3). In this study the goal was a comprehensive AMR data report and comprised several tasks. The equipment was the focus of this study (traditional AMR data analysis and reporting approach versus newly developed AMR data analysis and reporting approach).

The three ISO standard usability measures were defined as follows in this study. Effectiveness was determined by degree of task completion coded using three categories: (1) completed; (2) not completed (task not possible to complete); and (3) not completed (due to given time limits). In addition, effectiveness was assessed by the variance in the task results stratified by study round. Deviation from the correct results was measured in absolute percent from the correct result. Efficiency was determined by timing each individual task. Time on task started when the user started performing the task, all data was loaded and the chosen

Table 1. AMR data analysis and reporting tasks

| Task | Task description | Maximum given time per task (min) |
|------|------------------|----------------------------------|
| 1    | Total number of blood culture sets per year | 15 |
| 2a   | Total number of positive blood culture sets per year | 20 |
| 2b   | Total number of negative blood culture sets per year | 20 |
| 3    | Top 10 isolated microorganisms per year including isolate count (first isolates) | 20 |
| 4a   | Resistance profile (S/I & R) in Escherichia coli (first isolates) for selected antimicrobials | 30 |
| 4b   | Resistance profile (S/I & R) in Klebsiella pneumoniae (first isolates) for selected antimicrobials | 30 |
| 4c   | Resistance profile (S/I & R) in Staphylococcus aureus (first isolates) for selected antimicrobials | 30 |
| 5a   | Empirical treatment coverage for E. coli and K. pneumoniae (first isolates only for both) with a combination of cefuroxime and tobramycin | 30 |
| 5b   | Empirical treatment coverage for E. coli and K. pneumoniae (first isolates only for both) with a combination of amoxicillin + clavulanic acid + tobramycin OR amoxicillin + clavulanic acid + gentamicin | |
| 5c   | Empirical treatment coverage for E. coli and K. pneumoniae (first isolates only for both) with a combination of ceftriaxone + tobramycin OR ceftriaxone + gentamicin | |

S = susceptible; I = susceptible, increased exposure; R = resistant.

The maximum given time was the same for round 1 and round 2. If more time was spent than is stated here, this number was used as a maximum.

Table 2. Raw data example

| Patient ID | Date         | Sample ID | Specimen | Microorganism | PEN | AMX | CXM |
|------------|--------------|-----------|----------|---------------|-----|-----|-----|
| 0001       | 8 March 2019 | 100       | blood    | esccol        | R   | I   | S   |
| 0001       | 9 March 2019 | 101       | blood    | esccol        | R   | I   | S   |
| 0002       | 8 March 2019 | 102       | blood    | staaur        | R   | S   | —   |
| 0003       | 8 March 2019 | 103       | blood    | pseaer        | R   | R   | R   |

S, susceptible; I, susceptible, increased exposure; R, resistant; PEN, penicillin; AMX, amoxicillin; CXM, cefuroxime; esccol, E. coli; staaur, S. aureus; pseaer, Pseudomonas aeruginosa.
analysis software was up and running. Time on task ended when the task reached one of the endpoints, as described above. The mean time for each task and the mean total time for the complete report across users was calculated. Statistically significant difference was tested using paired Student’s t-test. Outcomes of tests were considered statistically significant for \( P < 0.05 \). All analyses were performed in R.\(^\text{18}\) Accuracy of the reported results per task and round were studied by calculating the deviation of the reported result in absolute percent from the correct result. Satisfaction was measured using the System Usability Scale (SUS), a 10-item Likert scale with levels from 1 (strongly disagree) to 5 (strongly agree, see Appendix A3).\(^\text{19}\)

**Results**

**Study participants**

In total, 10 participants were recruited for this study. Most participants were clinical microbiologists (in training) (70%). The median age of the participant group was 40.5 years with a median field experience of 8.0 years. The relevance of AMR data as part of the participants’ job was rated with a median of 5.0 (scale 1–5). AMR data analysis was part of 60% of all participants’ jobs. Participants reported to be experienced in interpreting AMR data structures (median 5.0, scale 1–5). Participants were less experienced in epidemiological data analysis (median 3.0, scale 1–5). All participant characteristics are summarized in Table 3.

The participants reported a diverse background in software experience for data analysis, with most experience reported for Microsoft Excel (Figure 4).

**Effectiveness and accuracy**

Average task completion between the first round and the second round changed from 56% (SD: 23%) to 96% (SD: 6%) \((P < 0.05)\). Task completion per question and round is displayed in Figure 5. Variation in responses for each given task showed significant differences between the first and second round.
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Table 3. Study participant characteristics

| Characteristics                                      | Overall (n=10) |
|------------------------------------------------------|---------------|
| Age (years), median (min–max)                        | 40.5 (32.0–61.0) |
| Working experience (years), median (min–max)         | 8.00 (1.00–22.0) |
| Job description, n (%)                               |               |
| Infection preventionist                              | 1 (10.0)      |
| Intensivist                                          | 1 (10.0)      |
| Clinical microbiologist                              | 4 (40.0)      |
| Paediatrician                                        | 1 (10.0)      |
| Resident clinical microbiology                       | 3 (30.0)      |
| Worked with AMR data before, n (%)                   |               |
| No                                                   | 1 (10.0)      |
| Yes                                                  | 9 (90.0)      |
| Relevance of AMR data as part of the job (1=not relevant at all; 5=very relevant), median (min–max) | 5.00 (3.00–5.00) |
| AMR data analysis as part the job, n (%)             |               |
| No                                                   | 4 (40.0)      |
| Yes                                                  | 6 (60.0)      |
| Familiarity with AMR data structure (1=not familiar at all; 5=expert) |               |
| Median (min–max)                                     | 4.00 (1.00–5.00) |
| Missing, n (%)                                       | 1 (10.0)      |
| Experience in interpreting AMR data (e.g. antibiograms) (1=no experience; 5=very experienced), median (min–max) | 5.00 (3.00–5.00) |
| Experience in epidemiological data analysis (1=no experience; 5=very experienced), median (min–max) | 3.00 (2.00–5.00) |
| Experience in working with AMR data (1=no experience; 5=very experienced), median (min–max) | 3.50 (1.00–5.00) |

![Data analysis software experience reported by study participants](image)

**Figure 4.** Data analysis software experience reported by study participants.

Figure 6 shows the deviation in absolute percent from the correct results from the correct result per round and task. The proportion of correct answers in the available results increased from 38% in the first round to 98% in the second round (P<0.001). A subanalysis of species-specific results for task 3 round 1 is available in Appendix A3.

**Efficiency**

Overall, the mean time spent per round was significantly reduced from 93.7 (SD: 21.6) to 22.4 (SD: 13.7) min (P<0.001). Significant time reduction was observed for tasks 2–5 (Figure 7). Analyses were further stratified to compare efficiency between participants.
who reported AMR data analysis as part of their job versus not part of their job. No significant time difference for completing all tasks was found between the groups. However, in both groups the overall time for all tasks significantly decreased between rounds, on average by 70.7 min ($P < 0.001$) in the group reporting AMR data analysis as part of their job and by 72.1 min ($P = 0.01$) in the group not reporting AMR data analysis as part of their job.

**Satisfaction**

Participants rated the usability of the new AMR reporting tool using the SUS, which takes values from 0 to 100 (Appendix A2). This resulted in a median of 83.8 on the SUS.

**Discussion**

This study demonstrates the effectiveness, efficiency and accuracy of using open-source software tools to improve AMR data analysis and reporting. We applied our previously developed approach to AMR data analysis and reporting \(^1\) in a clinical scenario and tested these tools with study participants working in the field of AMR. Comparing traditional reporting tools with our newly developed reporting tools in a two-step process, we demonstrated the usability and validity of our approach. Based on a five-item AMR data analysis and reporting task list and the provided AMR data, study participants reported significantly less time spent on creating an AMR data report (on average 93.7 versus 22.4 minutes; $P < 0.01$). Task completion increased significantly from 56% to 96%, which indicates that with traditional reporting approaches common questions around AMR are hard to answer in a limited time. The accuracy of the results greatly improved using the new approach, implicating that erroneous answers are more common when relying on non-AMR-specific traditional software solutions. The usability of our approach was rated with a median of 83.8 on the SUS. The SUS is widely used in usability assessments of software solutions. A systematic analysis of more than 1000 reported SUS scores for web-based applications across different fields has found a mean SUS score of 68.1.\(^2\) The results thus demonstrate good usability of our approach.
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The task list used in this study reflects standard AMR reporting tasks. More sophisticated tasks, such as the detection of multidrug resistance according to (inter-)national guidelines were not included. However, these analyses are vital in any setting but restrained since the required guidelines are not included in traditional tools (e.g. Microsoft Excel, SPSS etc.). Notably, the underlying software used in this study does provide methods to easily incorporate (inter-)national guidelines.

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### Figure 6
Deviation from the correct result by task and round in absolute percent from correct result. Only completed tasks (n) are shown.

| Task 1          | Task 2               | Task 3               | Task 4               | Task 5               |
|-----------------|----------------------|----------------------|----------------------|----------------------|
| (Total blood culture count) | (Positive/negative blood culture count) | (Top 10 isolated microorganisms) | (Resistance profile for selected isolates & antimicrobials) | (Empiric susceptibility rate for combination of two antimicrobials) |
| n=8             | n=7                  | n=7                  | n=2                  | n=5                  |
| n=9             | n=9                  | n=10                 | n=10                 | n=10                 |

#### Percent off correct value
- 0-5%
- 5-10%
- 10-15%
- >15%

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### Figure 7
Mean time spent per task in minutes in each round. Statistical significance was tested using two-sided paired t-tests. All results were included irrespective of correctness of the results.

| Task 5 | Task 4 | Task 3 | Task 2 | Task 1 | All tasks |
|--------|--------|--------|--------|--------|-----------|
| (Empiric susceptibility rate for combination of two antimicrobials) | (Resistance profile for selected isolates & antimicrobials) | (Top 10 isolated microorganisms) | (Positive/negative blood culture count) | (Total blood culture count) | Mean time spent (minutes) |

#### Mean
- Round 1
- Round 2

#### Standard deviation around the mean
- Round 1
- Round 2

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*) p < 0.05; **) p < 0.01; ***) p < 0.001
such as the definitions for (multi)drug resistance and country-specific (multi)drug-resistant organisms. The increase in task completion rate and accuracy of the results demonstrated that our tools empower specialists in the AMR field to generate reliable and valid AMR data reports. This is important as it enables detailed insights into the state of AMR on any level. These insights are often lacking. Our approach could fill this gap by democratizing the ability for reliable and valid AMR data analysis and reporting.

This need is exemplified in the worrisome heterogeneity of the reporting results using traditional AMR reporting tools in round 1. Only 37.9% of the results in round 1 were correct. Together with a task completion rate of 56%, this demonstrates that traditional tools are not suitable for AMR reporting. The inability of working in reproducible and transparent workflows further aggravates reporting with traditional tools. All participants in the study should be able to produce standard AMR reports and 90% indicated that they worked with AMR data before. Sixty percent reported AMR data analysis to be part of their job, but no efficiency difference between groups was found. Our results show that AMR data analysis and reporting is challenging and can be highly error-prone. But an approach such as the one we developed can lead to correct results in a short time while being reproducible and transparent.

Our approach was inspired by others not in the AMR field that describe the use of reproducible open-source workflows in ecology. We found that open-source software enables the transferability of methodological approaches across research fields. This transfer is a great example of the strength in the scientific community when working interdisciplinary and sharing reliable and reproducible workflow.

This study also has limitations. Only 10 study participants were recruited. Although low participant numbers are frequently observed in usability studies and reports show that only five participants suffice to study the usability of a new system, a larger sample size would be desirable. In addition, other evaluation methods (e.g. ‘think aloud’ method) beyond the single use of the SUS would further improve insights in the usability of our approach but were not possible in the study setting. Although the introduction of new AMR data and reporting tools made use of an already available approach, implementation still requires staff experienced in R. Reporting requirements also differ per setting and tailor-made solutions incorporating different requirements are needed.

References
1 O’Neill J. Review on Antimicrobial Resistance: Tackling a Crisis for the Health and Wealth of Nations. 2014. https://wellcomecollection.org/works/rdpck35v/items.
2 OECD. Stemming the superbug tide. 2018. https://doi.org/10.1787/9789264307599-en
3 Dyar OJ, Huttner B, Schouten J et al. What is antimicrobial stewardship? Clin Microbiol Infect 2017; 23: 793–8. https://doi.org/10.1016/j.cmi.2017.08.026
4 Morjaria S, Chapin KC. Who to test, when, and for what: why diagnostic stewardship in infectious diseases matters. J Mol Diagn 2020; 22: 1109–13. https://doi.org/10.1016/j.jmoldx.2020.06.012
5 Tacconelli E, Sifakis F, Harbarth S et al. Surveillance for control of antimicrobial resistance. Lancet Infect Dis 2018; 18: e99–106. https://doi.org/10.1016/S1473-3099(17)30485-1
6 Limmuthuotsakul D, Dunachie S, Fukuda K et al. Improving the estimation of the global burden of antimicrobial resistant infections. Lancet Infect Dis 2019; 19: e392–8. https://doi.org/10.1016/S1473-3099(19)30276-2
7 Berends MS, Luz CF, Friedrich AW et al. AMR: an R package for working with antimicrobial resistance data. J Stat Softw 2022; 104: 1–31. https://doi.org/10.18637/jss.v104.i03
8 Luz CF, Berends MS, Dik J-WH et al. Rapid analysis of diagnostic and antimicrobial patterns in R (Radar): interactive open-source software app for infection management and antimicrobial stewardship. J Med Internet Res 2019; 21: e12843. https://doi.org/10.2196/12843
9 Le Guerr R, Titecat M, Loiez C et al. Comparison of time-to-positivity between two blood culture systems: a detailed analysis down to the genus-level. Eur J Clin Microbiol Infect Dis 2021; 40: 1399–404. https://doi.org/10.1007/s11987-021-04175-9
10 Kim S, Yoo SJ, Chang J. Importance of susceptibility rate of “the first” isolate: evidence of real-world data. Medicina 2020; 56: 507. https://doi.org/10.3390/medicina56100507
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11 Tenea GN, Jarrin-V P, Yepez L. Microbiota of wild fruits from the Amazon region of Ecuador: linking diversity and functional potential of lactic acid bacteria with their origin. In: Mikkola HJ, ed. Ecosystem and Biodiversity of Amazonia. IntechOpen, 2021. https://doi.org/10.5772/intechopen.94179

12 Dutey-Magni PF, Gill MJ, McNulty D et al. Feasibility study of hospital antimicrobial stewardship analytics using electronic health records. JAC Antimicrob Resist 2021; 3: dlab018. https://doi.org/10.1093/jac/dam028

13 CLSI. Analysis and Presentation of Cumulative Antimicrobial Susceptibility Test Data—Fifth Edition: M39. 2022.

14 Schwaber K, Beedle M. Agile Software Development with Scrum. Prentice Hall, 2001.

15 Torrente G, Queiroz de Souza T, Tonaki L et al. Scrum framework and health solutions: management and result. Stud Health Technol Inform 2021; 284: 290–4. https://doi.org/10.3233/SHTI210725

16 Alami A, Krancher O. How scrum adds value to achieving software quality? Empir Softw Eng 2022; 27: 165. https://doi.org/10.1007/s10664-022-10208-4

17 International Organization for Standardization. Ergonomics of Human-System Interaction—Part 11: Usability: Definitions and Concepts (ISO 9241-11:2018). 2018. https://www.iso.org/standard/63500.html?

18 R Core Team. R: A Language and Environment for Statistical Computing. 2019. https://www.r-project.org/

19 Brooke J: SUS: A retrospective. J Usability Stud 2013; 8: 29–40.

20 Bangor A, Kortum PT, Miller JT. An empirical evaluation of the system usability scale. Int J Hum Comput Interact 2008; 24: 574–94. https://doi.org/10.1080/10447310802205776

21 Lowndes JSS, Best BD, Scarborough C et al. Our path to better science in less time using open data science tools. Nat Ecol Evol 2017; 1: 160. https://doi.org/10.1038/s41559-017-0160

22 Ledieu T, Bouzillé G, Thiessard F et al. Timeline representation of clinical data: usability and added value for pharmacovigilance. BMC Med Inform Decis Mak 2018; 18: 86. https://doi.org/10.1186/s12911-018-0667-x

23 Rubin J, Chisnell D. Handbook of Usability Testing: How to Plan, Design, and Conduct Effective Tests. Wiley, 2008.

24 Albert W, Tullis T. Measuring the User Experience: Collecting, Analyzing, and Presenting Usability Metrics. Morgan Kaufmann, 2013.

25 Iordatii M, Venot A, Duclos C. Design and evaluation of a software for the objective and easy-to-read presentation of new drug properties to physicians. BMC Med Inform Decis Mak 2015; 15: 42. https://doi.org/10.1186/s12911-015-0158-2

26 Bastien JMC. Usability testing: a review of some methodological and technical aspects of the method. Int J Med Inform 2010; 79: e18–23. https://doi.org/10.1016/j.ijmedinf.2008.12.004

27 Jaspers MWM. A comparison of usability methods for testing interactive health technologies: methodological aspects and empirical evidence. Int J Med Inform 2009; 78: 340–53. https://doi.org/10.1016/j.ijmedinf.2008.10.002