

MONI—An Intelligent Infection Surveillance Software Package

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Abstract. *MONI is an intelligent database and surveillance system designed to aid infection control specialists in primary care hospitals. The system is based on a relational Oracle database; different application modules can flexibly be placed around it. In addition to providing administrator tools for setting database parameters and automatically transferring microbiology data from the hospital's central laboratory database to the MONI database, which is located on a separate server, the system offers modules for simple database queries. The new aspect of MONI is realized by developing active, intelligent surveillance tools. On data acquisition, these modules check newly generated microbiology results by applying knowledge-based monitoring rules. If one of the results applies to an incoming microbiology result, the system informs the infection control team by selectable modes of action. Such actions may consist of the storage of clustered results into a file, printing out the result, showing an alert message on the screen, or sending a message via the Internet to a specific e-mail address. By doing so, the system not only warns the infection control team in the event of alert organisms, but also when new clusters of microorganisms appear, giving truly intelligent alarms in clinical medicine. Since the system provides access to patient data, security is an important element of the design. User identification is required every time any module of the system is activated. Several user levels defined by restriction to specific data sections can be created.*

1. Introduction

Surveillance is an essential element in the control and prevention of nosocomial infections. The accumulation of nosocomial infections can be detected early by an established surveillance system and appropriate preventive measures can be taken. Furthermore, surveillance serves the quality assurance of hygiene activities in a hospital. It helps to plan meaningful and adequate management of medical resources by efficient estimation of potentially acute nosocomial problems.

Over the last decades, numerous modes of surveillance for nosocomial infections were conducted worldwide. The projects were mainly designed as descriptive prevalence studies, and their purpose was to outline the magnitude of the problem. They were conducted as prospective studies under substantial data acquisition effort, first manually, and later by the aid of computer systems [1–5]. Today, the extent of nosocomial infections is sufficiently well known in most industrial nations. The next step is to create national and international surveillance networks [6]. However, several efforts to establish continuous nosocomial infection surveillance systems have failed because they tried to perform, in a holistic fashion, a hospital-wide collection of all types of nosocomial infections in all medical areas and specialties—an approach today considered less effective. Such attempts also failed due to understaffed infection control teams and deficiencies in the infrastructure, mainly in terms of computer hardware.

The highly competitive possibilities of new computer systems and network infrastructures in modern hospitals, together with the development of professional relational database systems and standardization of the “structured query language” by introducing the SQL, have made it possible to conduct ongoing surveillance on a large scale. Today’s vision is to merge medical information derived from several different sources and to analyze them within an acceptable period of time. However, until this vision is realized, collection and analysis of routine microbiology results is the most practical method because it provides information that has been interpreted by medical professionals. Nosocomial infection surveillance based on microbiology results is conducted by continuous collection of these data in a central database. However, it is important that the information does not disappear into a “black hole”. It must remain selectively accessible at any time.

In the following we present MONI (Monitoring of Nosocomial Infections), an intelligent database and surveillance system developed by the Division of Hospital Hygiene in collaboration with the Section of Medical Expert and Knowledge-Based Systems of the Department of Medical Computer Sciences of the University of Vienna Medical School.

2. Design of MONI

MONI is an intelligent database and surveillance system for monitoring and detecting nosocomial infections. The heart of the system is a relational Oracle database in which microbiology results identified by the Division of Clinical Microbiology are stored (Figure 1). At present, only microbiology results obtained from blood cultures, faeces, and urine samples are available in electronic form. Immediately after the result is verified by a clinical microbiologist, it is downloaded to the hospital’s central laboratory database (CLD), stored and then forwarded to the sample sender. Simultaneously, the results are downloaded to the MONI database, which is located on a separate server.

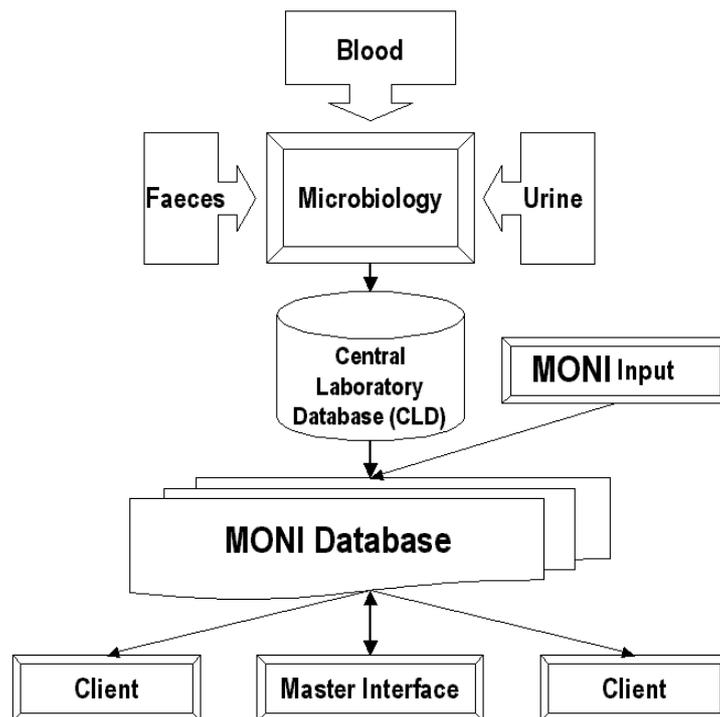


Figure 1: Data stream to the MONI database.

Various statistical and intelligent surveillance systems can be set up. While members of the Division of Hospital Hygiene have full access to all microbiology data, the access of MONI clients is confined to the reports of patients from their own unit.

There are three categories of applications, which in part represent the historical development of the system: administration tools (MONI Admin and MONI Input), query tools (MONI Stat and Flex Scan), and automatic microbiology result surveillance tools (monitoring of alert organisms and antibiotic resistance patterns, monitoring of cross infections, and monitoring of germ frequencies and trends). A fourth category is being planned: it will focus on nosocomial infection surveillance rather than on monitoring microbiology results.

2.1. Administration Tools

MONI Admin helps to control database settings and adjust parameters, as well as to transfer microbiology results from the hospital's CLD to the MONI database. MONI Input is a tool that permits manual input of microbiology results or input of further information to a dataset. The tool serves to collect and store microbiology results that are not available in electronic form. At present, all findings from specimen material other than blood, stool, or urine, that contain *Staphylococcus aureus*, are entered manually into the system. By this procedure, the hospital control unit can perform its surveillance on all *Staphylococcus aureus* isolates, one of the most relevant hospital germs causing nosocomial infections.

2.2. Query Tools

Today, query applications are a common part of any laboratory information system. Their principal use is to count off results or sets of database entries in accordance with specific restrictions (sender, germ, microbiology sample, antibiotic resistance pattern, patient information, and so on).

Queries conducted with these tools result in standard analyses of proportions of germs and cumulative antimicrobial susceptibility test data, stratified by ward or unit. With the help of such information, the resources of a hospital can be targeted towards areas in which intervention is most needed. Additionally, the information aids quality assurance at the microbiology laboratory.

MONI has two query tools, one (MONI Stat) to generate simple and standardized tabulations, and the other, (Flex Scan), that allows more extended queries by using Boolean operators. However, for rapid infection surveillance and for detection of possible outbreaks, tools like these are not perfectly suitable because of their retrospective character.

2.3. Automatic Surveillance Tools

One solution to the problem of time delay is on-line surveillance. In the latter, the system will continuously monitor for specific microbiology results previously defined in a knowledge base. If a defined alert organism or any cluster of germs occurs, the system informs the infection control team by different modes of action. Such reactions may consist of the storage of clustered results into a file, printing out the result, displaying a warning on the screen, or sending a message via the Internet to a specific e-mail address. MONI has three different applications for on-line monitoring, all serving different needs.

2.3.1. Monitoring of Alert Organisms and Antibiotic Resistance Patterns

This tool checks the MONI database as to whether specific germs with defined resistance patterns exist within the newly downloaded datasets (e.g., vancomycin-resistant enterococci, methicillin resistant *Staphylococcus aureus*, as well as alert organisms such as *Campylobacter species*, or *Salmonella species*) (see Figure 2).

The example in Figure 3 illustrates such “clustering” for *Campylobacter jejuni*. The first isolate was retrieved on 10 January 2000 at the outpatient clinic of the pediatrics department. It was isolated from a 9-year-old boy who had abdominal pain and bloody stools. The next day, a *Campylobacter jejuni* with an identical antibiotic resistance pattern was isolated in the stool sample of a 34-year-old woman who was admitted to the accident and emergency department because of abdominal pain and fever. She turned out to be the boy’s mother and a household transmission of the pathogen had occurred.

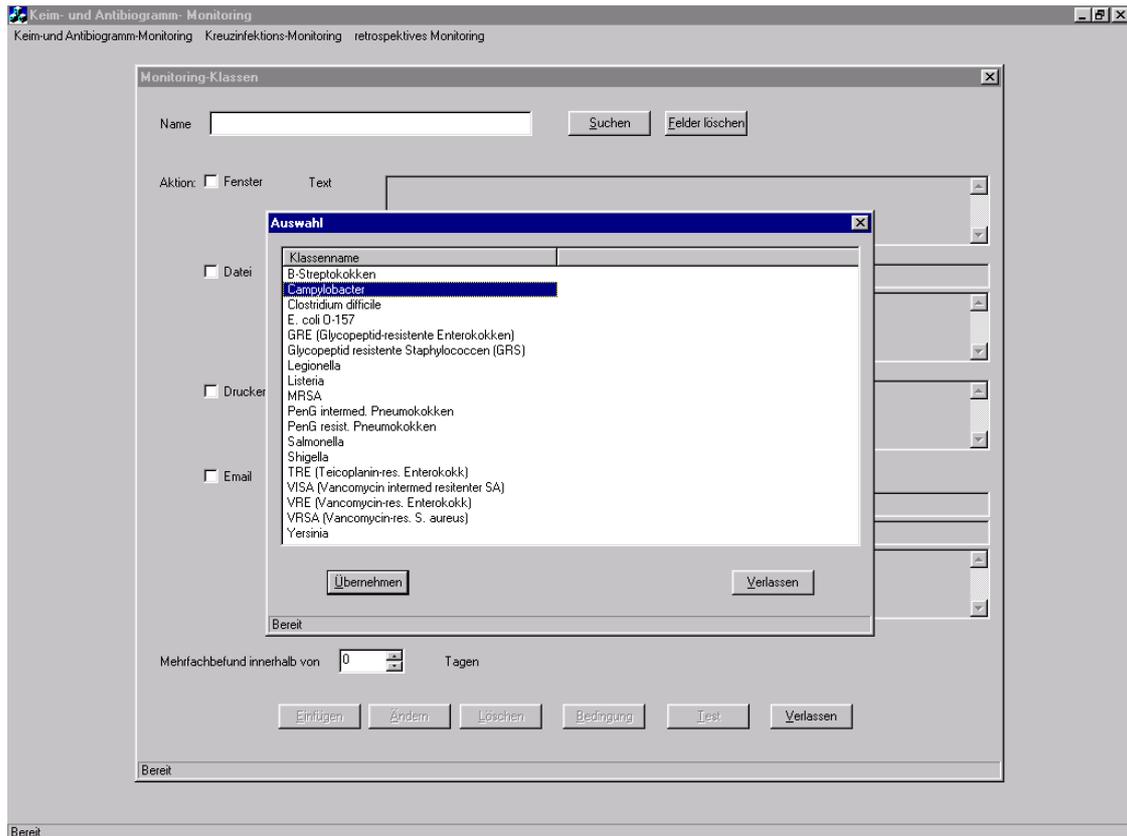


Figure 2: List of alert organisms together with the window for definition of actions.

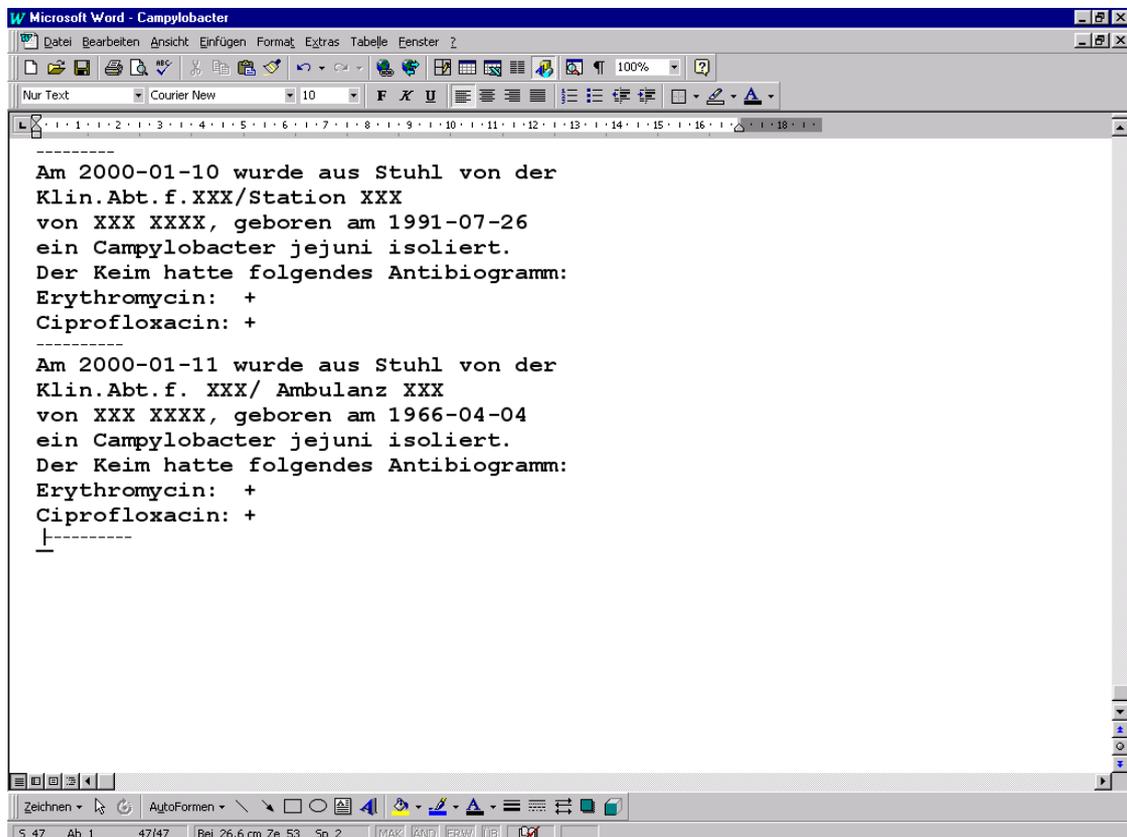


Figure 3: Result of cluster monitoring, showing two reports on *Campylobacter jejuni*.

The latter finding, however, was an incidental one, as the two findings were consecutively saved in the “Campylobacter file”. Usually, two possibly corresponding epidemiological findings are interrupted by other results, which makes the detection of cross infections uncertain. To overcome this difficulty, a specific tool for monitoring cross infection was designed.

2.3.2. Monitoring of Cross Infections

This application was designed to check clusters of identical results by means of bacterial species and corresponding antibiotic resistance patterns from different patients within a defined period. For instance, if three *Staphylococcus aureus* with identical resistance patterns are isolated within a period of two weeks from different patients from a ward, there is a strong suspicion of cross infection (Figure 4).

Klasse	Name	Keim	Anfangsdatum	Enddatum
160		<i>Pseudomonas aeruginosa</i>	1999-12-15	2000-01-11
119		<i>Pseudomonas aeruginosa</i>	1999-12-15	2000-01-11
152		<i>Pseudomonas aeruginosa</i>	1999-12-15	1999-12-21
141		<i>Pseudomonas aeruginosa</i>	1999-12-15	1999-12-16
153		<i>Pseudomonas aeruginosa</i>	1999-12-15	2000-01-05
133		<i>Pseudomonas aeruginosa</i>	1999-12-15	2000-01-04
138		Spindalze	1999-12-19	1999-12-22
151		<i>Staphylococcus aureus</i>	1999-12-16	2000-01-02
124		<i>Staphylococcus aureus</i>	1999-12-15	2000-01-17
148		<i>Staphylococcus epidermidis</i>	1999-12-17	2000-01-10
163		<i>Staphylococcus epidermidis</i>	2000-01-04	2000-01-13
134		<i>Staphylococcus epidermidis</i>	1999-12-24	2000-01-10
129		<i>Staphylococcus epidermidis</i>	1999-12-21	2000-01-02
120		<i>Staphylokokken Koag.neg (nicht S. saprophyticus)</i>	1999-12-22	1999-12-22
161		<i>Staphylokokken Koag.neg (nicht S. saprophyticus)</i>	1999-12-23	2000-01-10
154		<i>Staphylokokken Koag.neg (nicht S. saprophyticus)</i>	2000-01-03	2000-01-05
156		<i>Staphylokokken Koag.neg (nicht S. saprophyticus)</i>	1999-12-23	2000-01-13
125		<i>Staphylokokken Koag.neg (nicht S. saprophyticus)</i>	1999-12-25	2000-01-14
171		<i>Staphylokokken Koag.neg (nicht S. saprophyticus)</i>	2000-01-13	2000-01-14
126		<i>Staphylokokken Koag.neg (nicht S. saprophyticus)</i>	1999-12-20	1999-12-28
121		<i>Staphylokokken Koag.neg (nicht S. saprophyticus)</i>	1999-12-16	2000-01-10

Patient	Ma.	Station	Abnahme	Penicillin-G	Isowazolpericillin	Genlamicin (e)	Amkacin	Erythromycin (j)	Clindamycin	Vancomycin	Fuz
	Blut		1999-12-16	-	+	+	+	+	+	+	+
	Blut		1999-12-17	-	+	+	+	+	+	+	+
	Stuhl		1999-12-21	-	+	+	+	+	+	+	+
	Blut		1999-12-28	-	+	+	+	+	+	+	+
	Stuhl		2000-01-01	-	+	+	+	+	+	+	+
	Blut		2000-01-02	-	+	+	+	+	+	+	+

Figure 4: List of detected clusters of organisms with identical antibiotic susceptibility patterns.

2.3.3. Monitoring of Frequencies and Trends

The aim of this tool is to monitor whether a presented threshold of microbiology results is surpassed by actual results (e.g., the number of weekly isolates of a common clone of methicillin-susceptible *Staphylococcus aureus* (MSSA)). To allow for different epidemic patterns, we define two alert bounds: a lower one which must be surpassed at least three times in a row, indicating a continuous

rise, and a higher one which signals a possible epidemic and, for that reason, triggers an acute epidemic alarm when surpassed for the first time (Figure 5).

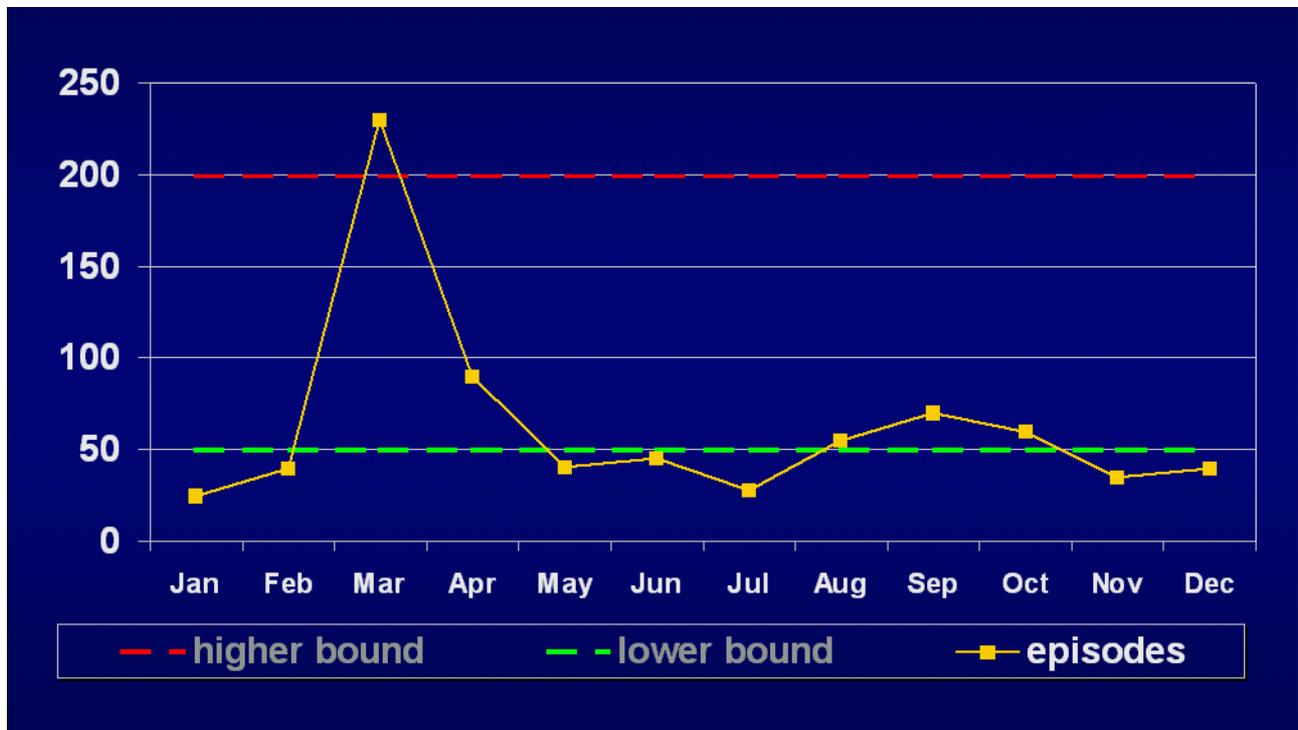


Figure 5: Principle of monitoring for microbiology report frequencies and trends.

3. Discussion

Efficient electronic-based surveillance of nosocomial infections is mainly hindered by the fact that the required data and parameters are not available in electronic form for the intelligent surveillance system. Fever, for instance, is an important but not exclusive feature of infection. The parameter “fever” is frequently not stored electronically and is therefore not accessible to surveillance systems.

The next problem occurs in the presence of gaps in the “chain of information”, such as a physician deciding not to take microbiological samples simply because he is certain he already has enough information to initiate therapy. Hence, the quality and continuity of data need to be assured when running intelligent knowledge-based systems. Finally, difficulties in linking different data structures derived from different sources should also be mentioned.

Until solutions for these problems are found, alternative approaches to infection control must be evaluated. By using mobile electronic data acquisition, it should be possible to collect necessary data in electronic form, e.g., by applying standardized collection protocols on mobile hand units such as Personal Digital Assistants (PDAs).

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