

Monitoring of Germs and Antibiotic Sensitivity Patterns, Crossinfections, and Nosocomial Infections by Applying Knowledge-Based Techniques

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Background

Surveillance of nosocomial infection is one of the prominent tasks for infection control teams in hospitals [1]. Efficient surveillance needs to address various data sources within the hospital such as patient administration, laboratory and other diagnostics, clinical patient data management and patient care documentation. With such enormous data loads epidemiological alerts tend to pass unrecognised if these data are not managed by computer programs.

Objective

The goal of this system is a knowledge-based monitoring of incoming data [2,3]. Two kinds of monitoring are performed in this system: Monitoring of major collectives of patients (monitoring of germs and antibiotic sensitivity patterns, monitoring of crossinfections) and patient-oriented monitoring of suspected nosocomial infections. For the first kind only microbiological data are of concern, for the second kind clinical patient data are essential as well.

Material and Methods

Monitoring of Germs and Antibiotic Sensitivity Patterns

Initially, the user must specify which organisms with which antibiotic sensitivity patterns he is interested in. Whenever a corresponding isolate occurs, the computer gives a message. The user defines for specific groups of organisms which types of warnings shall be released. So far, the alternatives provided by the program are a window on the screen, an entry in a file, a printed document, an e-mail, or combinations of these. All parameters (texts, filenames, addresses) are specified by the user. Any term in a text field that is surrounded by curly brackets is interpreted as a variable (Fig. 1). When a warning actually occurs, these variables are replaced by the current values.

The user also defines how to ignore repetitive reportings, in other words, he defines the time period within which no warnings are released when an identical isolate is reported from the same patient.

The second step is the definition of the "alert organism" to be observed. The user selects the microbial species he is interested in and may or may not define an antibiotic sensitivity pattern as well as restrictions concerning specimens and senders.

Possible entries for antibiotic sensitivity are: - (resistant), + (sensitive), ± (intermediate), * (not indicated), # (not tested).

An antibiotic which is not part of the defined antibiotic sensitivity pattern may have any of these values.

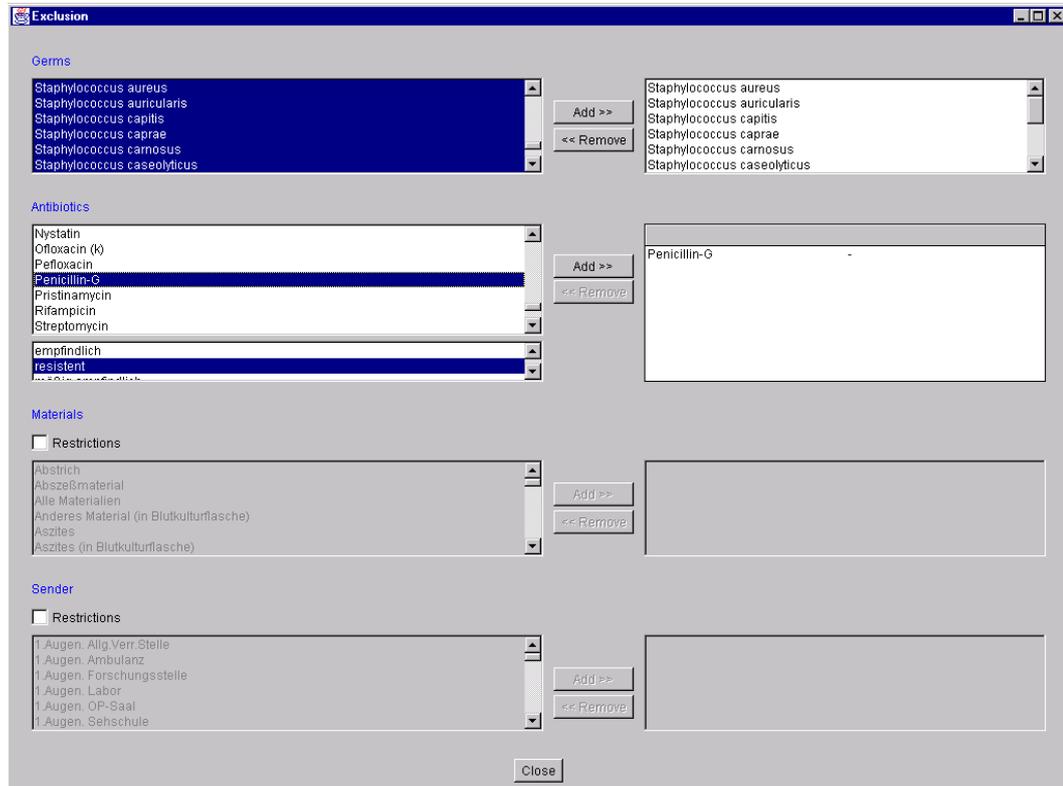


Fig.1: Exclusion screen in English (the original program is in German)

Monitoring of Crossinfections

A crossinfection is the transmission of a germ from one person to another. The isolation of the same germ with the same or a very similar antibiotic sensitivity pattern from both persons is strongly indicative for such occurrences. Classes of such matching microbiological results are classes of possible crossinfections. A physician still has to check the elements of the classes to verify real crossinfections.

For each incoming microbiological result the program recognizes whether there are already matching results from different persons in the database. If a matching case is found, a new class of possible crossinfections is created. If the new germ fits in an already existing crossinfection class, it is added to it. The germ only fits to the respective class, if it is sufficiently similar to each member of the class.

Two germs are taken as matching when they share the species name and their sensitivity patterns are identical or differ only slightly. That means, at least x% (which is to be defined by the user) of the antibiotics must be tested on both germs (= definition of maximum percentage of "holes"), and maximum in y% of the antibiotics the sensitivity may differ slightly. What is a slight difference is also to be determined by the user.

As soon as a new class is created or a microbiological result is added to an existing class, the user gets a warning in the format he previously defines. This is similar to the definition for monitoring of germs and antibiotic sensitivity patterns, but there are different messages for the creation of a new class and the addition of a result to an existing class.

Some germs with specific antibiotic sensitivity patterns occur so often that the monitoring would respond too often (e.g., Staphylococci resistant to penicilline and sensitive to all other tested drugs). However, this occurrence rarely is of any epidemiological significance. The program offers the possibility to exclude such germs from monitoring (Fig. 1). A list of all crossinfection classes and lists of all microbiological results belonging to them can be viewed (Fig. 2,3).

The screenshot shows a software window with a search bar at the top containing 'Begin 1990-01-01' and a 'Find' button. Below is a table with columns: class, germ, begin, and end. The table lists several classes, with class 5, 'Staphylococcus epidermidis', highlighted in blue. Below this is another table with columns: material, department, date, P, OX, AMC, Cephi, CN, Netlin, AK, baci, E, DA, RD, VA, FD, OFX, CIP. This table shows test results for various materials like 'Blut' from different departments, with asterisks indicating specific antibiotic sensitivities.

Fig. 2: Lists of all crossinfection classes including microbiological test results

The screenshot shows a software window with patient information on the left and an antibiogram on the right. Patient info includes Surname, Firstname (Günther), Birthname, Birthdate (1928-02-28), Sex (m), Patient no, Analysis no, Date (1996-02-05), Material (Blut), and Sender (Klin. Abteilung f. Klin. Neurologie/Station 15K). The Germ is 'Staphylococcus epidermidis'. The Antibiogram table lists antibiotics and their results: Penicillin-G (-), Isoxazolylpenicillin (-), Aminobz. pen. + BLI (-), Cephalospor. I-IV (+), Gentamicin (-), Netilmicin (+), Amikacin (-), Erythromycin (-), Clindamycin (-), Rifampicin (+), Vancomycin (+), Fusidinsäure (+), Ofloxacin (-), Ciprofloxacin (-).

Fig. 3: Selected microbiological result

Monitoring of Nosocomial Infections

Clinical data are transferred from the patient data management system (HP CareVue™) that is in routine clinical use at the Department of Pediatrics, whereas microbiological data are obtained from the MONI system. The knowledge-based analysis of the collected data will be performed by the MedFrame system, that is currently under development at the Department of Medical Computer Sciences. A specific definition and adaptation of monitoring rules will be possible by using the MedFrame/KBuilder Toolkit (Fig. 4).

Results

All prototypes have been tested by the hospital infection control department for several months. The retrospective studies have shown that a routine use of the system for active monitoring could save much time for the members of the hospital infection unit. It reports immediately all the defined alerts from the microbiological lab. So urgent actions can be taken without loss of time. All other results are stored for further utilization, but the user

does not need to check them. At present the prototypes are being further developed and reimplemented for routine use.

For the monitoring of nosocomial infections a pilot study has been started at the Department of Pediatrics of the General Hospital of Vienna (Division of Neonatology and Intensive Care) to demonstrate the feasibility and the clinical impact of the system in monitoring of infected newborns.

Fig. 4: Example of data acquisition

Technical Specification

All current prototypes were implemented in Java (Symantec Visual Cafe) using ODBC for database access. They are designed to monitor the incoming data, but can also be used for retrospective studies. The second is especially useful during the evaluation period.

Conclusion

Retrospective studies have demonstrated the utility of the current prototypes. Together with the users these will be further developed and other prototypes will be designed.

References

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