Visual Analysis for Hospital Infection Control using a RNN Model

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Figure 1: *Visual interface for exploration of RNN model results for infection control (ICM) in hospitals. V1) ICM confusion matrix, V2) ICM confusion matrix per ward, V3) ICM epidemic curve, V4) ICM infection transmission timeline, V5) ICM features, and V6) ICM patient list.*

Abstract
Bacteria and viruses are transmitted among patients in the hospital. Infection control experts develop strategies for infection control. Currently, this is done mostly manually, which is time-consuming and error-prone. Visual analysis approaches mainly focus disease spread on population level. We learn a RNN model for detection of potential infections, transmissions and infection factors. We present a novel interactive visual interface to explore the model results. Together with infection control experts, we apply our approach to real hospital data. The experts could identify factors for infections and derive infection control measures.

1. Introduction

Bacterial and viral infections endanger patients in hospitals worldwide. Among these, so-called multidrug-resistant pathognes such as vancomycin-resistant enterococci (VRE) or methicillin-resistant Staphylococcus aureus (MRSA) are difficult to treat and require the use of last-resort antibiotics [TC08, HSR*18].

Pathogens are transmitted among the hospital patients by direct patient contacts or via contaminated places in the same room or at the same ward. These infections obtained in hospitals are a threat to patients' health and increase treatment costs. As many infected patients do not have illness symptoms, dozens of the patients might get infected before the infection is detected [HSR*18]. Screening all patients is too costly. Thus, infection control experts (i.e., hy-

gienists, clinicians, hygiene experts) aim to develop strategies for early detection of pathogens in hospitals, identification of potential outbreaks, and prevention of pathogen transmission. The experts need to detect when and where higher than usual presence of pathogens occurs – an outbreak (*Task T1*). The experts need to identify patients that may be potentially infected, even though they are not ill (*Task T2*). They need to detect when (*Task T3*) and how (*Task T4*) pathogens could be transmitted, i.e., to identify factors supporting pathogen transmission. This helps them to determine preventive measures such as disinfection of rooms, or patient isolation.

Currently, the infection control experts perform these tasks mostly manually using long lists of infected patients. This is time-consuming and likely error-prone [HSR*18]. Current visual analytics approaches focus on disease spreading in large populations. They show the number of infected persons over time and the spatial distribution of infections [MLR*11, PL20]. Recent approaches [vLWB*19, WBvL*19] focus on the monitoring of the current situation in the hospital or projecting future disease spread. However, the development of infection control strategies requires an exploration of potential infection occurrence and factors supporting pathogen transmission.

We present a novel approach that we developed together with infection control (IC) experts in a project over a two year period. Our approach learns a *recurrent neural network* (RNN) for detecting potential infections across hospital wards and for determining factors that support pathogen transmission. Our novel interactive visual interface enables IC experts to explore the model results with respect to their tasks. IC experts employed our approach on data from a large German hospital. Our use case is a hospital infection by vancomycin-resistant enterococci (VRE) within the period of three years. The experts could identify time periods and wards with potentially higher than usual infection – i.e., outbreak. They could detect when and how transmission could happen for selected patients. This helps to improve infection control in the future.

2. Related Work

Visual Analysis of health data has recently gained large interest. Some works focus on visual analysis of health records [CCDW17, MLL*13, WGGP*11, HHO*16, RFG*17, RWA*13]. Recently also RNN models have been used for predicting medical data in this context [CBS*16, KCK*18]. Another research strain is disease surveillance and epidemiology [PL20]. The approaches focus on spatial and temporal character of the disease spreading on the population level [PL20], e.g., the dynamics of infections per geographic area [MHR*10, BWMM15, LAS14, BH13, YDH*17]. Tools such as NEMO [AKMR16], GEFSim [SVS*17], or COMSOL [LSSW10] simulate disease spreading and visualize population statistics – the number of infected patients. All these works focus on aggregate – population level. On individual level, visual analysis for infection spread in hospitals was proposed [WBvL*19]. It concentrates on prediction, rather than on infection control. In contrast to visual analysis for modeling experts [HKPC18], we focus on the challenge of showing model results to clinicians in an understandable and interpretable way [JCHG19, DVK17]. Thus, we build upon an existing system for infection control for hospitals [vLWB*19].

3. Infection Model

We model the infection likelihood and infection transmission for a pathogen using a recurrent neural network (RNN). RNN is an artificial neural network for classification along a temporal sequence [Sch15]. It enables us to classify each patient p in each time moment t as infected $y(p,t) = 1$ or non-infected $y(p,t) = 0$. The temporal facet of the modeling is important for determining who is likely infected (*T1 and T2*) and when patients get likely infected (*T3*). The RNN model also enables us to identify features that contribute to infection transmission (*T4*). We focus on the visual exploration of model results, not on creating best fitting model.

Model input We use time-dependent features that are available for each patient on hourly basis. Based on the tasks, clinical expertise, and data availability, we use the following features:
– *Type of patient's stay*, .e.g., "Change ward", "Hospitalization", or "Surgery". It may influence the pathogen transmission, e.g., transmission in a surgery may be more likely than in an entrance to hospital. We use 20 types in one-hot-encoding.
– *Ward* Patient location. We apply MDS on the organizational hierarchy to reduce one-hot-encoding from 668 to 10 features.
– *Room* The location of a patient. Encoding is similar to wards.
– *Current number of infected patients in the same ward* Direct and indirect contact on the same ward may lead to transmission. Higher number of infections means a higher likeness of an infection.
– *Recent number of infected patients in the same ward* Accumulated number of infected patients in the last 3, 6, and 12 days. This is interesting for pathogens with longer incubation times.
– *Current nr. of infected patients in the same room* – as for ward.
– *Recent nr. of infected patients in the same room* – as for ward.
All 63 features are normalized to $0 - 1$ interval so that larger wards do not get overproportionally high values.

Model training Figure 2 shows the used model structure, which resulted from several experiments. We used a standard loss function for a two class problems – the mean squared error [SC08] and the Softmax activation function [GBC16]. As training data, we used the real detected patient infections $y^R(p,t)$. We used the above-mentioned features and weighting for balancing between $y^R = 1$ and $y^R = 0$ classes. The training was performed offline before the visualization due to the long training duration of several hours.

Model result Model result is an infection likelihood per patient and time step $0 \leq \overline{y(p,t)} \leq 1$. An increase in the infection likelihood in two consecutive time steps $\Delta\overline{y(p,\tau)} > 0$ means a likelihood of infection at time τ. This detects likely time of infection τ and its likelihood $\Delta\overline{y(p,\tau)}$. Infection likelihood above a user-defined threshold is classified as an infection. The default value is 80%.

4. Interactive Visual Interface

We present a novel interactive visual interface for exploring model results for infection control (ICM) to be used by infection control experts in the hospital (see Figure 1). We extend an existing system [vLWB*19], which increases the acceptance and understandability of the approach. Our interface has five linked views V1–V5:

V1: ICM confusion matrix view (see Fig. 3) provides model results on the number of (in)correctly classified infections. We used
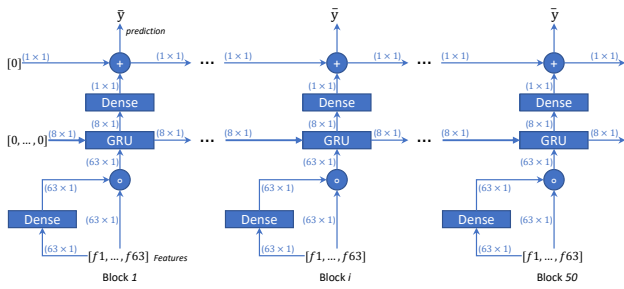
Figure 2: *Used RNN model structure.*

Figure 4: *ICM confusion matrix per ward*

it as the IC experts were familiar with a classic confusion matrix. A classic confusion matrix shows the number of classified cases (i.e., patients): true positive (*TP*), true negative (*TN*), false-positive (*FP*), and false negative (*FN*). However, as not all patients are screened, we needed to extend this matrix with an additional discrimination of false positive for screened (*FP-error*) and for non-screened patients (*FP-PUI*). We color-code all five cases consistently also in other views. The *FP-PUI* class is interesting for IC experts as it contains all patients identified as potentially infected, but not screened (*task T2*). These patients should be screened, or the screening strategy needs to be adjusted.

The sliders allow to interactively adjust model parameters: prediction threshold and *FP* threshold. The slider color indicates the effect of the slider changes, e.g., whether the model focuses on *FN* (red) or *FP* (yellow-green). This supports understandability of the model to the IC experts. This view can be used for filtering patients of an user-selected category, such as *TP* (dashed cell border).

V2: ICM confusion matrix per ward in Figure 4 allows the IC expert to assess the classification results per ward. It shows whether there are wards with exceptional results (*Task T4*), such as wards with a high number of misclassifications (*FN*) or with a high number of potentially infected persons (*FP-PUI*). The number of patients in each cell is shown as text and as color. Hue shows the type of information and saturation shows the relative number of patients. This normalization was needed for a consistent comparison of large and small wards in one view. This normalization is shown with saturation. Dark colored wards show a potential local outbreak – a high number of infections. The IC experts can select rows (i.e., wards) or cells (i.e., patient categories) to filter patients of interest. They can be shown in other views. e.g., patient list.

(a) *Whole dataset* **(b)** *Summer 2011*

Figure 3: *ICM confusion matrix*

V3: ICM epidemic curve view is an extension of a standard epidemic curve, which shows the number of really detected infected patients over time $\sum y^R(t)$. It helps to detect outbreaks by a higher than usual number of infected patients (*Task T1*). Our extended curve shows the model results as a stacked bar chart. It differentiates between true positive and false negative of the real infections. It thus shows the model quality over time, i.e., whether there are time periods of higher/lower model performance. The curve also shows the two categories of false positives: *FP-PUI* and *FP-Error*. This is novel and important. The IC experts can see the dynamics in the number of infected persons together with the dynamics of potentially infected persons (*FP-PUI*). Thus, they can see how many persons should have been screened in different time periods.

The interactive view allows the IC expert to focus on selected time periods. The curve on the top shows the whole analyzed time period. The curve on the bottom shows details for a user-selected time period. The details also show the seven-day-moving average of the number of patients per category as a line. This is needed, as the data may fluctuate strongly, e.g., due to working-day effect. The time selection is used to filter patients in other views.

V4: ICM infection transmission timeline view shows the model results for pathogen transmission events τ and their likelihood $\Delta \overline{y}(p, \tau)$ for a user-selected patient *p* (see Fig. 6) (*Task T3*). This information is integrated to the already existing view on the patient history from the input data.

The existing view shows the time spent in hospital with the background color indicating the infection status. Patient's location at wards is shown via horizontal colored lines. Long vertical lines show the time moment of screening. The color of these lines shows the screening result, i.e., the really detected infection status. White color means non-infected and red is infected. The length of the vertical line shows the resistance class of the pathogen.

We overlay this view with model results. We keep the visual metaphor of colored vertical lines for infection results. Therefore, we show an additional vertical bar at time of likely transmission event τ (*Task T3*). Transmission likelihood is shown as as color from light (low) to dark (high). In this way, the IC experts can see when the model detects possible transmissions and how much they can trust in this result. The IC expert can assess the possible transmission causes of this transmission event in the ICM feature view. Additionally, for each transmission event, we show also the pos-
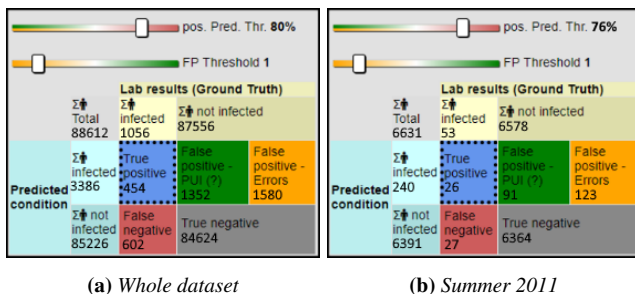
Figure 5: *ICM epidemic curve*
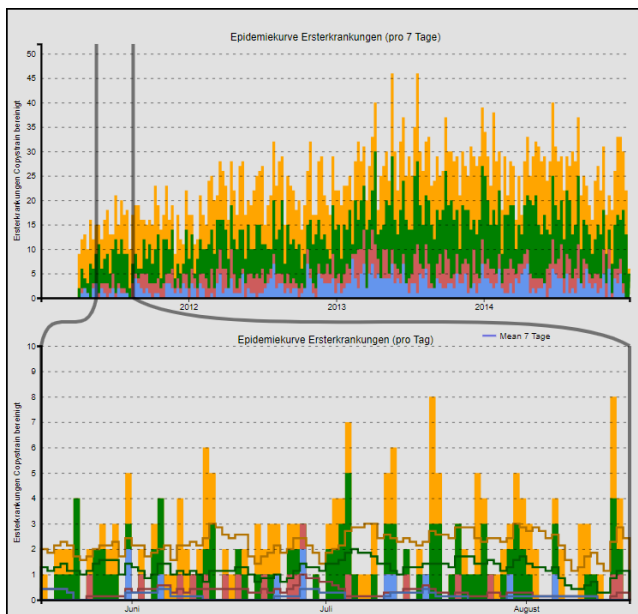

Figure 6: *ICM infection transmission hypothesis and features*

sible causes of this transmission – contact patients (*Task T4*). The number of contact patients is shown directly as an icon with a number. The full list of contact patients is shown on demand in a tooltip. A selection of a patient in this tooltip enables the IC expert to further investigate the infections of the selected contact patient.

V5: ICM feature view shows the attention features for the whole model and for the user-selected transmission event in a bar chart (see Fig. 6 bottom right). Features with high weights (i.e., long bars) indicate possible causes of pathogen transmission (*Task T4*). Inspired by [MCZ*17], we show the difference between feature weights of the whole model (black bars) and the feature weights of the selected transmission event. Blue bar means a higher feature weight of the transmission event, and red means a lower weight.

5. Use Case

In cooperation with infection control experts, we apply our approach to real world data on infections by vancomycin-resistant enterococci (VRE) in a large German hospital. This pathogen is relevant for hospital infections worldwide.

We used 88,612 patient cases over three years. RNN training was done on 80% and testing on the 20% of the data. We evaluated standard performance measures: area under ROC curve score (92%) [HL05], DP as $y_1 = 0.3$, and $y_0 = 0.003$. Together with the confusion matrix, the results show a good model quality. We note, that our goal was not to create the best fitting model, but rather to investigate the usefulness of using and showing RNN results for infection control.

In this use case, the IC expert wants to detect the potentially infected patients and the causes of VRE transmission in order to derive strategies for better disease control in the future. The expert wants to analyze the increase of high VRE infection in summer
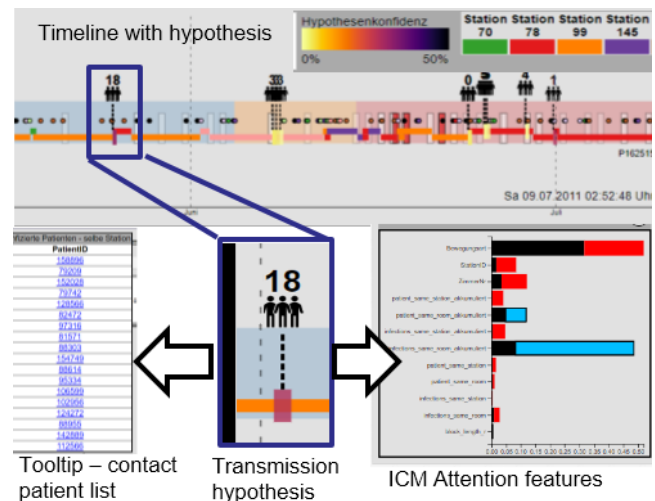
2011. Therefore, the time filters were set to that period in the ICM epidemic curve view (Fig. 5). He looks at the confusion matrix to detect possible infections. In order to have a low number of false negative results, and high detection rate, he sets the threshold in the red area at 75% (Fig. 3). The matrix for Summer 2011 shows 53 already known cases and also 91 additional potentially infected patients. So the outbreak was possibly larger than already known (*T1*). A look at the wards discovers the *ward 70* in the *area 1026* with an elevated number of potential patients (Fig. 4). This ward is a potential location of the outbreak (*T4*). The patients list gives an overview of all patients at that ward. The transmission timeline view (Fig. 6) reveals that the model detected a high likelihood of the first transmission event (dark vertical bar) already 2 weeks before the first positive screening was monitored (orange background) (*T3*). This indicates that the patient was earlier infected than known and thus he could have infected other patients. This motivates an earlier screening of patients for VRE on this ward. The expert is interested in factors supporting the VRE transmission. Thus, he looks at the the feature list. It shows a long blue bar next to the feature "accumulative number of infected patients in room". This means that this room is a potential cause of the infection transmission and thus needs to be disinfected (*T4*). The effect of this intervention needs to be analyzed in a follow-up study.

6. Conclusion and Future Work

We presented a new visual analytics approach to support infection control in hospitals. It learns a RNN model and shows its results in a new interactive visualization. The evaluation with infection control experts showed advantages of this approach. In the future, we wish to extend the model and visual interface with additional information, e.g., input data uncertainty.

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