# Modelling the length of hospital stay in medicine and surgical departments

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## ABSTRACT

Healthcare Associated Infections are among the world's leading public health problems and the most serious complications for hospitalized patients that can impact length of stay (LOS). In this work, medical record data of 24365 patients admitted to general surgery and clinical medicine wards were used collectively with the aim of creating models capable of predicting overall LOS, measured in days, considering clinical information. Multiple linear regression analysis was performed with IBM SPSS, the coefficient of determination ($R^2$) was equal to 0,288. A regression analysis with ML algorithms was performed with the Knime Analysis Platform. The $R^2$ were quite low for both multiple linear regression and ML regression analyses. The use of these techniques showed that there is a relationship between clinical variables and overall LOS. The results constitute a valid support tool for decision makers to provide the turnover index for the benefit of health policy in the management of departments.

## CCS CONCEPTS

• **Computing methodologies** → Modeling and simulation; Model development and analysis; Model verification and validation.

## KEYWORDS

Machine learning algorithms, Multiple Linear Regression, Healthcare Associated Infections

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## 1 INTRODUCTION

Healthcare-associated infections (HAI) are the most frequent and serious complication for patients, representing one of the main public health concerns worldwide and causing an increase in morbidity, mortality and costs [1]. The difficulty of medical care, the use of antibiotics for prophylactic or therapeutic purposes due to resistant bacterial strains and the high prevalence of multidrug-resistant organisms transmissible through healthcare professionals or the hospital environment have led to a focus on better management and prevention of infections [2]. Healthcare professionals are those at increased risk of nosocomial infections with respiratory, blood and other infections causing increased rates of illness, absenteeism and even death among healthcare workers as well as a large financial cost to the healthcare system [3]. Diabetes mellitus, malignant tumors, human immunodeficiency virus are conditions that can favor the onset of ICA [4]. The number of infections could be kept under control using effective management tools to improve health performance. Among the approaches to improve the quality of healthcare services, simulation and modeling, multicriteria decision making methods, and, not least, Lean Six Sigma (LSS) have been employed [5–11]. In particular, LSS has been used for dealing with hospital issues related to the length of hospital stay (LOS) [12–16]: Improta et al. and Cesarelli et al. used LSS methodology to reduce the risk of nosocomial infections in the clinical medicine areas and in the Neonatal Intensive Care Unit of the Federico II University Hospital of Naples. LSS has proved to be an effective tool in recognizing the variables that influence HAI risk and in implementing corrective actions to optimize the performance of the care process [17, 18]. The same methodology was found to be useful for reducing the number of days of hospitalization of patients with sentinel bacterial infections who are at risk for HAI in the general surgery department [19].

An interesting goal would be the capacity to predict the results of patients in order to be able to intervene and proceed with the best treatment to avoid adverse phenomena and complications. Geneves et al. opened the way to the use of artificial intelligence techniques for the construction of analysis systems through machine learning (ML) models, making predictions at the time of hospital admission [20]. Revuelta-Zamorano et al. presented a ML approach to predict

HAI in an intensive care unit by combining heterogeneous data from longitudinal electronic health records and the microbiology laboratory [21]. The use of ML applications in healthcare is on the rise and could profoundly influence the field of healthcare in fact in the literature there are studies that demonstrate its use [22–24]. Daghistani et al. used this approach to predict LOS in heart patients [25], others have used it in the field of oncology to optimize the quality and efficiency of patient care [26–29]. ML models were used to effectively predict the timing of surgery and for infected necrotizing pancreatitis [30].

In this work, the goal is to create models capable of predicting LOS, measured in days, considering the clinical variables of hospitalized patients at risk of HAI. These models will be able to verify if there is a relationship between clinical variables and LOS. The aim is to support decision makers in assessing the hospitalization of patients at risk for HAI.

For this purpose, a pilot study was conducted by collecting the data from the medical records of patients hospitalized collectively in the general surgery and clinical medicine departments. The study started with multiple linear regression to understand how the variables interact with each other to predict LOS and, subsequently, ML regression analyses were performed as more powerful modelling techniques. The large dataset we analysed in this paper should be considered one of its main strength.

## 2 MATERIAL AND METHODS

The study was conducted at the University Hospital "Federico II" of Naples, collecting data from January 2011 to December 2016: the number of patients analysed was 24365.

The following variables are considered in the study since they are always immediately and easily available to clinicians:

- Age ($0 \leq Age \leq 103$);
- Preoperative LOS (measured in days);
- Diagnosis Related Group (DRG) weight, provides a measure of the average consumption of resources associated with hospitalization pertaining to each DRG: the greater the weight, the higher the care load of the corresponding case series;
- Number of medical or surgical procedures (from 1 to 6);
- Infection (Yes; No), i.e. the presence of an infection in a patient.

Team members include physicians of the Healthcare Directorate, biomedical and managerial engineers, biologists and economist.

### 2.1 Multiple Linear Regression

A multiple linear regression model explains the dependent variable Y as a function of k independent variables, with $k > 2$. The multiple linear regression model that predicts the natural logarithm of LOS (dependent variable) as a function of the 5 independent variables (age, preoperative LOS, DRG weight, colonization and number of procedures), can be defined as follows in equation:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_4 + \beta_5 x_5$$

Where y is predicted LOS, $\beta_0$ is intercept value, $x_i$ are independent variables and $\beta_i$ estimated regression coefficients of respective variables.

Before creating the model, it was necessary to diagnose it by testing six hypotheses (more details on the hypotheses are shown in the supplementary material). To solve the violation of the linearity hypothesis, the dependent variable (LOS) was transformed into a natural logarithm (ln).

- The relationship between independent and dependent variables is linear. One way to verify this hypothesis is to produce a scatter plot and a partial regression plot. This hypothesis is verified for all variables.
- The absence of multicollinearity is the assumption that the predictors are not too closely related to each other. This is tested with a Pearson's Bivariate Correlation test, correlations of more than 0.8 may be problematic. We can also test this assumption by looking at Variance Inflation Factor (VIF) and Tolerance. In general, a VIF greater than 10 or a Tolerance less than 0.2 indicate high multicollinearity which can cause concern;
- The values of the residuals are independent. We test this assumption using the Durbin-Watson statistic with a value between 1 and 3;
- The variance of the residuals is constant. This is called homoscedasticity and is the assumption that the variation in the residuals (or amount of error in the model) is similar at each point across the model. The scatter plot does not show a clear correlation between residuals and expected values;
- The values of the residuals are normally distributed. This can be tested with a P-P plot (Probability-Probability plot). This graph allows to evaluate how similar two data sets are, by plotting the two Cumulative Distribution Function on a graph;
- Outlier detection. It was necessary to verify that all Cook's distance values are less than 1. Cook's distance is used in regression analysis to find influential outliers in a set of predictive variables. The measurement is a combination of the leverage of each observation and the residual values; the greater the leverage and residues, the greater the distance from the cook.

Multiple linear regression was implemented with the IBM SPSS (Statistical Package for Social Science) statistics software version 25.

### 2.2 Machine Learning

The ML regression analysis was performed by using Knime Analytics Platform (v.4.2.0). It is a well-known data mining and business intelligence platform allowing users to create workflows by combining nodes. Several biomedical studies have been performed by using it: in oncology for radiomics studies [30, 31], for foetal monitoring [32, 33], in ophthalmology for congenital nystagmus investigations [34, 35], after the use of gait analysis [36-39] and recently also for applications on COVID-19 [40, 41]

The following algorithm were implemented in Knime: decision tree (DT) and k nearest neighbour (KNN) [42, 43]. DT is the most interpretable and easy algorithm in literature while KNN has a different functional principle since it is an instance-based algorithm, which allocates a label to the test record on the basis of its distance

**Table 1: Standardized and Unstandardized coefficients with p-values of the multiple linear regression analysis**

| Variable | Unstandardized Coefficients | | Standardized Coefficients Beta | t | Sign. |
|---|---|---|---|---|---|
| | B | Std. Error | | | |
| Intercept | 1.130 | 0.010 | - | 116.507 | |
| | | | | | <0.001 |
| Age | -0.001 | 0.000 | -0.031 | -5.416 | |
| | | | | | <0.001 |
| LOS pre-operative | 0.073 | 0.001 | 0.312 | 55.065 | |
| | | | | | <0.001 |
| DRG weight | 0.135 | 0.004 | 0.194 | 32.472 | |
| | | | | | <0.001 |
| N. procedures | 0.113 | 0.002 | 0.262 | 45.305 | |
| | | | | | <0.001 |
| Colonization | 0.450 | 0.034 | 0.072 | 13.146 | |
| | | | | | <0.001 |

**Table 2: Evaluation metrics for the ML regression analysis**

| Algorithm | DT | KNN |
|---|---|---|
| $R^2$ | 0.264 | 0.162 |
| Mean absolute error | 0.459 | 0.500 |

from similar training data. In the following analysis, the k was fixed to 3 and the distance among records was not weighted.

The evaluation metrics of the ML analysis were the coefficient of determination ($R^2$) and the mean absolute error [44]. The models were trained by employing a hold-out validation in light of the large amount of available data while all the metrics were, of course, computed only on the test set.

## 3 RESULTS

A multiple linear regression analysis was performed, the coefficient of determination ($R^2$) was equal to 0.288. The coefficients of the multiple linear regression and t-test are shown in Table 1. The t-test verifies the significance of the regression coefficients ($\beta_i$) at the level of significant $\alpha = 0.05$. The hypotheses tested are $H_0$: $\beta_i = 0$ (no linear relationship between xi and y) and $H_1$: $\beta_i \neq 0$ (There is a linear relationship between $x_i$ and y). The null hypothesis ($\beta_i = 0$) is rejected when the p-value <0.05 and the coefficients are statistically significant other than 0, i.e., the independent variables ($x_i$) affect the LOS (y).

The regression coefficients ($\beta_i$) express, based on the model (1), how much the dependent variable (LOS) increases or decreases for each unit increase of the independent variables (clinical variables).

The dataset was then divided into a training and a test set (respectively, 80% and 20% of the total) for the ML regression analysis. The evaluation metrics for the ML regression analysis are shown in Table 2.

## 4 DISCUSSION AND CONCLUSION

In this article, a pilot study was conducted using some variables collected from the medical records of patients at risk of HAI. First, a Multiple linear regression analysis was performed to predict LOS measured in days because, although the assumptions cannot be perfectly verified in a medical scenario, it is the simplest model to preliminary deal with data. Then, ML regression was performed for the same task because ML models are more powerful and have no assumptions compare with the multiple linear regression.

The dataset may represent an obvious limitation due to the few variables collected that do not allow an accurate prediction of LOS, although 20 thousand patients can be considered a large dataset. Indeed, the results obtained show all the $R^2$ were quite low for both multiple linear regression and ML regression analyses.

Despite this, the study provided models capable of linking LOS using some clinical information of patients, thus demonstrating the relationship between LOS and clinical variables.

Several studies used ML to predict LOS in different healthcare sectors. Turgeman et al. applied a regression tree model (cubist) for the prediction of LOS, based on static inputs, i.e. values known at the time of admission and which do not change during the patient's hospital stay. The cubist model was chosen because it produced more accurate predictions than other models according to those authors [45]. In cardiac patients, as suggested by Daghistani et al., a ML model was validated to predict LOS accurately. The random forests model outperformed other ML models and achieved high accuracy [25].

Finally, future development to improve the results mentioned above, the LOS could be grouped by weeks and a classification analysis could be performed. Future goals are to employ other algorithms such as Random Forests and Gradient Boosting Tree. Of course, ML algorithms cannot fit all the frameworks required for modeling, no single model can outperform all other models for all datasets in a specific domain. However, in this scenario, random forests and, in general, tree-based algorithms could have significant feasibility in predicting LOS as well as in other clinical settings [33, 35–39].

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