Published in final edited form as:
Health Serv Outcomes Res Methodol. 2006 December ; 6(3-4): 127–138.

Predicting the Length of Stay of Patients Admitted for Intensive Care Using a First Step Analysis

ADRIANA PEREZ* and **WENYAW CHAN**
The University of Texas Health Science Center at Houston, School of Public Health, Division of Biostatistics, 80 Fort Brown, SPH Rm N.200, Brownsville, TX 78520, USA.

RODOLFO J. DENNIS
Pontificia Universidad Javeriana, Clinical Epidemiology and Biostatistics Unit, HUSI, Cra 7 # 40-62 Piso 2, Bogotá, Colombia.

Predicting the Length of Stay of Patients Admitted for Intensive Care Using a First Step Analysis

For patients admitted to intensive care units (ICU), the length of stay in different destinations after the first day of ICU admission, has not been systematically studied. We aimed to estimate the average length of stay (LOS) of such patients in Colombia, using a discrete time Markov process. We used the maximum likelihood method and Markov chain modeling to estimate the average LOS in the ICU and at each destination after discharge from intensive care. Six Markov models were estimated, describing the LOS in each one of the Cardiovascular, Neurological, Respiratory, Gastrointestinal, Trauma and Other diagnostic groups from the ultimate primary reason for admission to ICU. Possible destinations were: the intensive care unit, ward in the same hospital, the high dependency unit/ intermediate care area in the same hospital, ward in other hospital, intensive care unit in other hospital, other hospital, other location same hospital, discharge from same hospital and death. The stationary property was tested and using a split-sample analysis, we provide indirect evidence about the appropriateness of the Markov property. It is not possible to use a unique Markov chain model for each diagnostic group. The length of stay varies across the ultimate primary reason for admission to intensive care. Although our Markov models shown to be predictive, the fact that current available statistical methods do not allow us to verify the Markov property test is a limitation. Clinicians may be able to provide information about the hospital LOS by diagnostic groups for different hospital destinations.

Keywords

discrete time; destination after intensive care unit; Markov chain

1. Introduction

Prognosis is one of the key facets of clinical medicine, especially for critically ill patients in need of intensive care. In this setting, valid information on probability of death and possible length of stay (both in intensive care and in the hospital) is of substantial relevance for physicians, administrators, and family alike. Prediction of duration of a patient's stay in the

adriana.perez@uth.tmc.edu
wenyaw.chan@uth.tmc.edu
rdennis@cable.net.co
*Author to whom correspondence should be addressed

Intensive Care Unit (ICU) however, is difficult[16] and less studied than the prediction of mortality[2,9-11]. Prolonged stay in the intensive care unit not only increases the overall costs and consumes more resources, but also limits the number of beds available for use. In addition, patients, families, physicians and managers demand more informed health care information [15].

Time spent in an ICU must be productive and cost-efficient for both the patient and the hospital [12]. Previous modeling strategies for length of stay do not incorporate the destinations after admission to a particular location. Many studies used linear regression, semi parametric and Bayesian approaches for estimating overall length of stay at a particular location. Nevertheless, the need for accurate estimation of length of stay (LOS) does not finish with intensive care. After ICU admission, the most frequent question from the patients' family member is about when they will be able to go home or how long it will take the patient to recover and move to different destinations within the hospital structure. Therefore, the ability to accurately predict LOS and length of time at any other destination after the ICU is an important component of prognosis in critical care.

To help address this important need, we present an application of discrete time Markov process to model the average LOS of patients admitted into intensive care in Colombia, as the patients move back and forth between hospital destinations, home or death after admission to ICU. We also aimed to evaluate the reliability of our results by applying them to a (different) validation dataset known as a split-sample analysis.

2. Description of the data

2.1. Study Design and Participants

The Evaluación de Cuidado Intensivo en Colombia (ECIC) study design, collection instrument, participants, sample and handling of missing values[3,4,13,14] has been documented previously with a brief summary provided here. A prospective cohort of consecutive patients admitted to twenty randomly selected intensive care units between July 1997 and October 1998 represents the largest intensive care cohort measured in Colombia. Patient's unit/hospital admission, demographic characteristics, first 24 hour physiology, medical history, surgical status, ultimate primary reason for unit admission, unit and hospital outcome and destination after intensive care were collected on this prospective cohort until hospital discharge or death. The 3066 admissions among the 3254 admissions collected during this period, were from patients 16 years old or older and these adult admissions where used for the current study.

A total of 3059 patients were used for analysis after accounting for patient readmissions as part of the total patient length of stay among those 3066 admissions. All patients admitted to ICU were followed daily including their destinations after discharge from ICU. November 30, 1998 was the closing date of the study. Patients that were not discharged by that date contributed to the overall LOS from admission until the closing date. In total, these 3059 patients represent 62322 patients-days. The mean and median length of stay of these patients was 20 and 13 days respectively. Due to the heavy tails of the LOS and to improve the estimation of the LOS on the different destinations after ICU, LOS greater than 30 days were truncated from the analysis. This study received institutional review approval by the Ethics and Research Committee of the school of Medicine at Javeriana University in Bogotá.

2.2. Split-Sample Analysis: Development and Validation Datasets

The Intensive Care National Audit and Research Centre coding method (ICM)[17], a systematic method for recording the reason for admission to intensive care, was used in this study. A brief summary is provided here. The ICM code is a five-tiered hierarchical method. Physicians assign the ICM code to each admission. The first tier is type, whether the patient

patients had a surgical or non-surgical admission. The second tier is the body anatomic system affected from the primary reason for ICU admission: (i) respiratory, (ii) cardiovascular, (iii) gastrointestinal, (iv) neurological, (v) trauma and (vi) other anatomic system, which includes dermatological, endocrine, metabolic, thermoregulation, poisoning, genitor-urinary, hematological, immunological, musculoskeletal and psychiatric conditions. The third, fourth and fifth tiers of ICM identify the anatomical site, the physiological or pathological process, and the condition necessitating admission, respectively[17]. The third, fourth and fifth tiers are known as the precipitating factors for the primary indication for ICU admission[17].

From the second tier of the ICM, each one of these six body anatomic system databases was randomly divided into two equal datasets. The first dataset for each body anatomic system is the development dataset. Patient data in the development dataset were utilized for estimating transition probabilities of the discrete time Markov Chain model. The second dataset for each body anatomic system is the validation dataset. Patient information in the validation dataset was utilized to evaluate the reliability of the model derived using the information on patients from the development dataset[8].

The total number of possible unique combinations of first, second and third tiers, representing anatomical sites, is 134. Fifteen of these unique anatomical sites had only one patient, 87 had more than one patient and 32 had no patients. All fifteen patients with a unique anatomical site were combined and this one constituted the 88^{th} precipitating factor. We employed a stratified sampling procedure by unique precipitating factors (88), sex and age (<45 years old and greater or equal to 45 years old) to guarantee their distribution within the development and validation datasets. Patients in these strata were likewise randomized into the two datasets. While randomizing, if a strata had an odd number of patients the extra patient was allocated randomly to the development or the validation dataset. Data validation and analysis were carried out using SAS Version 8.2. No personal or hospital identifiers were included in the analysis files.

3. Markov model

3.1. States of the Markov Chain Model

Eight possible destinations after the first day of admission to the intensive care unit were evaluated for each ICU patient: Ward same hospital (W); Other hospital's ward, not ICU or being at other hospital after discharge from ICU to other hospital (B); Other hospital's ICU (O); High dependency unit same hospital or Intermediate care area same hospital (U); same ICU or other ICU within the same hospital (I); other location same hospital (H), House/hospice/rehabilitation unit=Exit (E) and Death (D). Each destination identifies a state in the Markov chain.

We built a sequence or chain of each patient's stay in the hospital. The chain is composed of ‘W’s, ‘I’s, ‘B’s, ‘O’s, ‘U’s, ‘H’s, and either E or D. This chain represents the destination where the patient was located each day. For example, a sequence of the form HIIIIIWWWWBBE represents a patient who spent a total of 14 days in the hospital and his/her first day was in the hospital in a location different from the Ward, the following five days this patient was in the ICU, the following five days this patient was in a Ward in the same hospital where he/she was admitted into ICU, the following two days this patient was in the ward of another hospital and the patient was discharged home/hospice/rehabilitation unit on day 14. We included in our analysis the days of hospital stay before the first day of admission of ICU patients within each chain because the time spent somewhere else in the hospital is known in the literature as a predictor of death and/or of longer ICU stays.

Two exiting and absorbing states comprise the Markov Chain. Dead patients will reach their exiting state ‘D’ in their chain. Discharged (to home, hospice or rehabilitation unit) patients

will reach their exiting state ‘E’ in their chain. A total of 3059 chains were built and either the ‘D’ or the ‘E’ state must appear at the end of each chain.

3.2. The Transition Probability Matrix

$p_{ij}(n) \equiv$ the probability that a patient who is in state i upon entry into the system (intensive care unit) will be in state j , n time units later, i = H, I, B,O,W,U and j = H, I, B,O,W,U, E, D. A patient can not start at the E or D state. Note that $p_{ij}(n)$ can be easily obtained as the (i, j) th element in the transition probability matrix (P^n). This matrix is of size 8 by 8. $X_{ij}(m) \equiv$ indicator variable such that

$$X_{ij}(m) = \begin{cases} 1 & \text{if a patient who is in state } i \text{ upon entry into the intensive care unit is in the state } j, \\ & m \text{ time units later,} \\ 0 & \text{otherwise} \quad (i = H, I, B, O, W, U, E, D \text{ and } j = H, I, B, O, W, U, E, D) \end{cases} \tag{3.1}$$

Then

$$E\{X_{ij}(n)\} = p_{ij}(n). \tag{3.2}$$

Let $v_{ij}(n) \equiv$ the random variable representing the number of times state j is entered in n transitions when at the beginning of the transitions the system was in state i . Since the absorbing states ‘E’ and ‘D’ may be entered only once, $v_{iE}(n)$ and $v_{iD}(n)$ will indicate the length of time a patient has already spent in state ‘E’ and ‘D’ respectively, since entry. Then,

$$v_{ij}(n) = \sum_{m=0}^{n} x_{ij}(m). \tag{3.3}$$

and the expectation of $v_{ij}(n)$ is

$$E\{v_{ij}(n)\} = \sum_{m=0}^{n} p_{ij}(m). \tag{3.4}$$

The first step analysis allows one to analyze the possibilities that can arise at the end of the first transition, and then use the law of total probability and the Markov property to establish the relationship among variables during subsequent steps. Note that $\sum_{k=1}^{n} P^k$ represents the matrix whose elements represent the average length of time spent in the various states in n units ($n \equiv 1,2,\ldots$) of time as a function of the starting state. The upper limit in the summation is set to 30 since the maximum duration of stay in the dataset was truncated at 30 days. The probability matrix from each of the development datasets were calculated using a first-step analysis[6] which is equivalent to the maximum likelihood estimation procedure[7]. The state occupancy probabilities at time k in the future are obtained by pre-multiplying P^k by the initial state probability vector A. In other words, the destination frequency distribution on the first day for each body anatomic system from the development datasets represented the initial state probability vector. The elements of this new vector A P^k represent the probability of being in any particular state on the k th transition.

3.3. Assumptions of the Markov Model

The Markov chain model has two key assumptions: the Markov property and the stationary property[1,5]. A particular system holds the Markov property if the present state predicts future states as well as the whole history of past and present states does. This is also known as a memoryless process[1]. As far as we know, there is not an overall test capable of testing the adequacy of the Markov property itself. Some authors[2,3,7] indirectly assess this property by testing the order of the dependence. The length of the sequence has a large impact in this test, a short length of the sequence will have a low power to detect the adequateness of the model [1]. Our maximum sequence length is 30, which is too short for this approach. We used a

reliability method (the split-sample analysis) to empirically address the appropriateness of the Markov property[8].

The Markov chains estimated using the development datasets were combined with the initial state probability vector to generate the expected length of stay in each destination for each body anatomic system. These expected lengths of stay were compared with the observed length of stay from the validation datasets. The split-sample analysis uses a chi-square statistic to evaluate the goodness of fit of the Markov chain models from the development datasets, when used to fit the data from the validation datasets.

The stationary property in our data assumes that the flow of patients from one destination to another destination was independent of time and ruled by a constant transition probability matrix within each body anatomic system. We examined this stationary property by regressing time on the mean length of stay in each destination and calculating the percentage of cells within the 8 by 8 matrix where this property held. Statistical significance was established using a type I error level of 0.05.

4. Results

The sample sizes randomly selected in the development and validation datasets for each body anatomic system were: (i) respiratory 226 and 227, (ii) cardiovascular 505 and 505, (iii) gastrointestinal 175 and 175, (iv) neurological 322 and 323, (v) trauma 126 and 126 and (vi) other anatomic system 174 and 175 patients, respectively.

Table 1 presents the transition probability matrix (P) for each body anatomic system obtained from the development datasets. The elements in each Markov chain represent the probability of transition from one destination to another given that the patient was admitted to intensive care. For example, the number 0.059 that appears at the intersection of the second row and the fifth column in the respiratory Markov chain matrix is the probability of going from destination intensive care unit to ward in the same hospital in one day after being discharged from the ICU. Similarly, the number 0.105 that appears at the intersection of the first row and the second column in the respiratory Markov chain matrix, is the probability of returning to the intensive care unit from somewhere in the hospital different from the ward the day following discharge from the ICU. The sum of the elements in each Markov chain matrix in any row add up to one, because when a patient is in any one destination, the next transition may be into the same destination or to any of the other seven destinations.

The stationary property holds for the following percentages of the transition probabilities cells of the Markov Chain matrix in each body anatomic system: (i) respiratory 86%, (ii) cardiovascular 71%, (iii) gastrointestinal 100%, (iv) neurological 90%, (v) trauma 92% and (vi) other anatomic system 55%, respectively. It is appropriate to model the variability of the length of stay of these intensive care patients using a constant transition matrix within each body anatomic system except other anatomic system, which should be interpreted with caution. We consider these results adequate. Because the percentages of the transition probabilities cells where the regression on time holds are above 70%.

Table 2 summarizes the chi-square statistics comparing the observed and the expected length of stay using Markov chain models from the development datasets to fit the data from the validation datasets. Tables 3 to 5 present the comparison of the expected and observed length of stay by the number of days in the different destinations of these intensive care unit patients for the Respiratory, Cardiovascular and Neurological body anatomic system patients, respectively. For ease of presentation, we did not include all 30 days; we only present the first five days individually, and after that in intervals of five days. The observed and expected length of stays for the remaining body anatomic systems are available upon request from the authors.

An example of the interpretation of these tables is the following. For day 10 in the respiratory body anatomic system, on average a patient spends 4.68 days in the intensive care unit, 1.8 days somewhere in the hospital other than the ward, 2.09 days in the ward of the same hospital, 0 days in another ICU from another hospital, 0.29 days in the ward of another hospital, and 0.43 days in the exit destination before either going home or dying.

5. Conclusions

To the best of our knowledge, this is the first application of a Markov model to LOS by destination in patients in need of intensive care. The results presented in this study allow hospital managers or physicians in charge of patients admitted to the intensive care unit to provide the patient's family members (i) transition probabilities of destinations to the different areas in the hospital and (ii) predictions of the time they will be able to go home or how long it will take the patient to recover or to leave the intensive care unit given the ultimate primary reason for admission by body anatomic system.

We did not have enough evidence to declare a lack of goodness fit of the Markov models in the respiratory, cardiovascular and neurological body anatomic systems. In other words, we fail to reject the null hypothesis that the Markov chain models from the development datasets fits the data in the validation datasets. This provides us with indirect evidence about the appropriateness of the model. The predicted length of stay per destination from our Markov models predicted the observed length of stay well in these body anatomic systems. However, a concern may rise, when evaluating the individual differences between the observed and expected values on tables 3-5, those lengths of stay at Home and Death destinations tended to be overestimated. We did not have enough evidence to declare these differences to be statistical significant.

On the other hand, it is possible that the lack of goodness of fit of the Markov models from the gastrointestinal and trauma body anatomic systems is due to the reduced sample size and/or that the Markov property does not hold. These reasons as well as the lack of the stationary property may explain the lack of fit of the Markov model for the other body anatomic system.

Although, our chosen unit of analysis was days and the models seems to fit this unit in tables 3-5, we are aware that clinicians may be more interested in using half a day as a unit of analysis since discharges occur in the middle of the day. Further modeling may be warranted.

Originally we started by modeling a markovian model for the entire cohort and the lack of fit was to be expected. We then stratified the datasets using sex only or age only or the precipitating factors only and we obtained similar results. We have decided to present the model with all three variables incorporated within the stratification process. Furthermore, it is not possible to use a constant Markov model for the entire cohort or across body anatomic systems, and for this reason we present each of them separately. Previous markovian models are available from the authors upon request.

There are advantages of this type of modeling in this situation, where the patient's length of stay and utilization of intensive care resources are highly correlated. The Markov chain matrices will serve to predict patient's demands on the destination over time, as long as the case-mix and treatment modalities remain unchanged. The Markov chains allow estimating the average length of stay at each destination by day accounting for the random fluctuations in patient's conditions.

One of the limitations of this markovian modeling strategy is the imprecision in estimating the length of stay by not taking into account meticulous adjustments by disease severity and case mix variability. The APACHE II[9] or III[10] classification systems, used regularly to account

for disease severity and case mix, correspond to our precipitating factors, which were used to guarantee dataset comparability for estimating the length of stay and to measure the model reliability within each body anatomic system. Ideally, clinicians may be interested in generating a model for each precipitating factor; however this will require a large sample size at each precipitating factor, which was not feasible with our data. Another limitation is that our models cannot be extrapolated to admissions that spend more than 30 days in the ICU, since they were truncated in our analysis. They are very difficult to model and further research is needed. Finally, although our Markov models shown to be predictive, the fact that current available statistical methods do not allow us to verify the Markov property is a limitation and these models should be interpreted cautiously.

Clinicians can provide information about the hospital length of stay based on body anatomic system for the reason of admission of the patient to the intensive care unit. Therefore, information from these models may have implications for the utilization, planning, and scheduling of beds and personnel in the hospital.

Acknowledgements

We thank all participating intensive care units which allowed the study team to follow the patients until hospital discharge: Clinics: Bautista, Fundadores, General del Norte, Nueva, Reina Sofía, San José, San Pedro Claver and San Rafael; Foundations: Carlos Ardila Lule, Valle de Lili and Santafe de Bogotá; Hospitals: Bocagrande, Erazmo Meoz, Federico Lleras Acosta, Hernando Moncaleano, Militar Central, San Juan de Dios, Simón Bolívar, Universitario San Ignacio and Universitario San Jorge. We want to express our gratitude to the referees and editors for comments that greatly improved this work. The Evaluación de Cuidado Intensivo en Colombia (ECIC) study was supported by Colciencias Grant # 080-99, Pontificia Universidad Javeriana Grant # 1203-04-954-98/12-24-01-290 and INCLEN Inc. The first' author's work was partially supported by a grant from the National Institutes of Health. National Center on Minority Health and Health Disparities (Grant: Creation of an Hispanic Health Research Center in the Lower Rio Grande Valley, Statistical and Economic Analysis Core # 1P20MD000170-019001).

References

1. Bhat, UN.; Miller, GK. Elements of applied stochastic processes. Third Edition. John Wiley & Sons Inc; Hoboken, New Jersey: 2002.
2. Copeland-Fields L, Griffin T, Jenkins T, Buckley M, Wise LC. Comparison of outcome prediction made by physicians, by nurses and by using the mortality prediction model. American Journal of Critical Care 2001;10:313–319. [PubMed: 11548564]
3. Dennis RJ, Metcalfe A, Pérez A, Londoño D, Gómez C, McPherson K, Rowan K. Cuidado intensivo en Colombia. Recurso humano y tecnológico. Acta Médica Colombiana 2000;25:211–217.
4. Dennis RJ, Pérez A, Rowan K, Londoño D, Metcalfe A, Gómez C, McPherson K. [Factors associated with hospital mortality in patients admitted to intensive care in Colombia]. Archivos de Bronconeumologia 2002;38:117–122. [PubMed: 11900688]
5. Hoel PG. A test for markov chains. Biometrika 1954;41:430–433.
6. Kapadia AS, Chan W, Sachdeva R, Moye LA, Jefferson LS. Predicting duration of stay in a pediatric intensive care unit: A markovian approach. European Journal of Operational Reseach 2000;124:353–359.
7. Kapadia AS, Vineberg SE, Rossi CD. Predicting course of treatment in a rehabilitation hospital: A markovian model. Computers and Operations Research 1985;12:459–469.
8. Kleinbaum, DG.; Kupper, LL.; Muller, KE.; Nizam, A. Applied Regression Analysis and Other Multivariable Methods. Third edition. Duxbury Press; Pacific Grove: 1998.
9. Knaus WA, Draper EA, Wagner DP, Zimmerman JE. APACHE II-a severity of illness classification system. Critical Care Medicine 1985;13:818–829. [PubMed: 3928249]
10. Knaus WA, Wagner DP, Draper EA, Zimmerman JE, Bergner M, Bastos PG, Sirio CA, Murphy DJ, Lotring T, Damiano A, Harrell FE. The APACHE III prognostic system: risk prediction of hospital mortality for critically ill hospitalized adults. Chest 1991;100:1619–1636. [PubMed: 1959406]

11. Le Gall JR, Lemeshow S, Saulnier F. A new simplified acute physiology score (SAPS II) based on a European/North American multicenter study. Journal of the American Medical Association 1993;270:2957–2963. [PubMed: 8254858]
12. Marcin JP, Slonim AD, Pollack MM, Ruttimann UE. Long-stay patients in the pediatric intensive care unit. Pediatric Critical Care 2001;29:652–657.
13. Pérez A, Dennis RJ, Gil JFA, Rondon MA, Lopez A. Use of the mean, hot deck and multiple imputation techniques to predict outcome in intensive care unit patients in Colombia. Statistics in Medicine 2002;21:3885–3896. [PubMed: 12483773]
14. Pérez A, Dennis RJ, Rondon MA, Metcalfe MA, Rowan KM. Intensive care mortality ratios are better in private versus public Colombian hospitals. Journal of Clinical Epidemiology 2006;59:94–101. [PubMed: 16360567]
15. Vicente FG, Lomar FP, Melot C, Vincent JL. Can the experiences ICU physician predict ICU length of stay and outcome better than less experienced colleagues? Intensive Care Medicine 2004;30:655–659. [PubMed: 14735235]
16. Weissman C. Analyzing intensive care unit length of stay data: Problems and possible solutions. Critical Care Medicine 1997;25:1594–1600. [PubMed: 9295838]
17. Young JD, Goldfrad C, Rowan K. Development and testing of a hierarchical method to code the reason for admission to intensive care units: the ICNARC Coding Method. British Journal of Anaesthesia 2001;87:543–548. [PubMed: 11878722]

Table 1

Markov chain of intensive care unit patients by body anatomic system, indicating probability of change between each destination after first day of admission in the hospital.

	H	I	B	O	W	U	E	D
				RESPIRATORY				
H	.891	.105	.000	.000	.000	.000	.000	.004
I	.013	.888	.002	.001	.059	.006	.001	.030
B	.049	.089	.837	.000	.000	.000	.025	.000
O	.000	.087	.043	.870	.000	.000	.000	.000
W	.008	.013	.000	.000	.883	.000	.088	.008
U	.000	.008	.000	.000	.000	.921	.055	.016
E	*	*	*	*	*	*	1	*
D	*	*	*	*	*	*	*	1
				CARDIOVASCULAR				
H	.884	.110	.000	.000	.000	.000	.000	.006
I	.003	.838	.002	.008	.099	.008	.008	.034
B	.012	.044	.880	.000	.000	.000	.064	.000
O	.000	.042	.042	.839	.000	.000	.077	.000
W	.000	.012	.002	.000	.825	.000	.156	.005
U	.000	.000	.006	.000	.000	.877	.111	.006
E	*	*	*	*	*	*	1	*
D	*	*	*	*	*	*	*	1
				GASTROINTESTINAL				
H	.905	.095	.000	.000	.000	.000	.000	.000
I	.000	.880	.002	.000	.068	.008	.000	.042
B	.000	.036	.936	.010	.000	.000	.018	.000
O	.000	.000	.000	1.00	.000	.000	.000	.000
W	.000	.005	.000	.000	.876	.000	.117	.002
U	.000	.019	.000	.000	.000	.916	.065	.000
E	*	*	*	*	*	*	1	*
D	*	*	*	*	*	*	*	1
				NEUROLOGICAL				
H	.895	.104	.000	.000	.000	.000	.000	.001
I	.016	.851	.000	.002	.074	.022	.003	.032
B	.011	.070	.908	.000	.000	.000	.011	.000
O	.100	.000	.100	.600	.000	.000	.100	.100
W	.001	.004	.000	.000	.887	.000	.100	.007
U	.000	.011	.000	.000	.000	.863	.126	.000
E	*	*	*	*	*	*	1	*
D	*	*	*	*	*	*	*	1
				TRAUMA				
H	.821	.161	.000	.000	.000	.000	.000	.018
I	.004	.909	.000	.001	.049	.016	.000	.021
B	.000	1.00	.000	.000	.000	.000	.000	.000
O	.000	.000	.000	.500	.000	.000	.000	.500
W	.000	.009	.000	.000	.918	.000	.067	.006
U	.000	.005	.000	.000	.000	.962	.033	.000
E	*	*	*	*	*	*	1	*
D	*	*	*	*	*	*	*	1
				OTHER				
H	.879	.121	.000	.000	.000	.000	.000	.000
I	.009	.895	.002	.001	.056	.008	.003	.026
B	.043	.043	.878	.007	.000	.000	.029	.000
O	.000	.050	.050	.900	.000	.000	.000	.000
W	.000	.003	.000	.000	.888	.000	.107	.002
U	.000	.000	.000	.000	.000	.914	.086	.000
E	*	*	*	*	*	*	1	*
D	*	*	*	*	*	*	*	1

H= other location same hospital; I= same ICU or other ICU within the same hospital; B= Other hospital's ward, not ICU or being at other hospital after discharge from ICU to other hospital; O= Other hospital's ICU; W= Ward same hospital; U=High dependency unit same hospital or Intermediate care area same hospital; E=House/hospice/rehabilitation unit and D=Death.

* indicates a logical zero and it was not estimated.

Table 2

Chi square test statistic, sample size and conclusion when testing the null hypothesis that the Markov chain models, from the development datasets, fit the data from the validation datasets, by body anatomic system.

Body anatomic system	Sample size	Test Statistic	Conclusion
Respiratory	216	237.49	Not statistically significant
Cardiovascular	475	423.86	Not statistically significant
Gastrointestinal	172	384.46	Statistically significant
Neurological	319	334.66	Not statistically significant
Trauma	120	220.72	Statistically significant
Other	168	453.61	Statistically significant

Table 3

Observed and expected length of stay in each hospital destination by the number of days in the Respiratory body anatomic system.

	H		I		B		O		W		U		E	
Day	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**
1	0.35	0.32	0.51	0.50	0.04	0.04	0.00	0.00	0.05	0.04	0.02	0.05	0.01	0.03
2	0.63	0.61	1.00	0.98	0.07	0.07	0.01	0.01	0.17	0.11	0.06	0.10	0.02	0.07
3	0.88	0.88	1.47	1.44	0.10	0.09	0.00	0.01	0.28	0.20	0.09	0.15	0.07	0.11
4	1.06	1.13	2.00	1.88	0.15	0.12	0.02	0.02	0.46	0.30	0.15	0.20	0.06	0.17
5	1.38	1.35	2.29	2.30	0.17	0.14	0.00	0.02	0.69	0.42	0.25	0.24	0.08	0.24
...														
10	1.80	2.26	4.68	4.13	0.29	0.21	0.00	0.03	2.09	1.14	0.72	0.46	0.29	0.82
...														
15	1.94	2.90	6.39	5.54	0.28	0.25	0.00	0.04	4.86	1.90	0.97	0.65	0.28	1.80
...														
20	2.56	3.35	8.46	6.61	0.51	0.28	0.00	0.05	6.92	2.61	1.03	0.81	0.00	3.17
...														
25	4.72	3.68	7.55	7.41	0.47	0.30	0.00	0.06	8.96	3.20	2.36	0.94	0.47	4.88
...														
30	5.14	3.93	14.57	8.01	0.00	0.31	0.00	0.06	7.71	3.69	2.57	1.04	0.00	6.88

Exp=Expected; Obs=observed; H= other location same hospital; I= same ICU or other ICU within the same hospital; B= Other hospital's ward, not ICU or being at other hospital after discharge from ICU to other hospital; O= Other hospital's ICU; W= Ward same hospital; U=High dependency unit same hospital or Intermediate care area same hospital; E=House/hospice/rehabilitation unit and D=Death.

Table 4

Observed and expected length of stay in each hospital destination by the number of days in the Cardiovascular body anatomic system.

	H		I		B		O		W		U		E	
Day	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**
1	0.23	0.21	0.59	0.52	0.03	0.03	0.04	0.04	0.07	0.07	0.01	0.02	0.02	0.02
2	0.42	0.40	1.01	0.98	0.06	0.05	0.08	0.07	0.30	0.19	0.03	0.04	0.05	0.07
3	0.53	0.56	1.31	1.39	0.11	0.08	0.11	0.11	0.71	0.32	0.04	0.05	0.09	0.15
4	0.70	0.71	1.64	1.76	0.13	0.10	0.13	0.14	1.03	0.48	0.08	0.08	0.20	0.25
5	0.78	0.84	2.09	2.09	0.14	0.13	0.15	0.17	1.32	0.64	0.12	0.10	0.36	0.39
...														
10	1.48	1.32	3.46	3.29	0.30	0.24	0.25	0.29	3.42	1.46	0.30	0.20	0.63	1.60
...														
15	2.79	1.60	5.57	4.01	0.43	0.33	0.43	0.37	4.39	2.10	0.54	0.28	0.86	3.56
...														
20	3.58	1.76	7.37	4.43	0.42	0.41	0.63	0.42	5.89	2.54	0.84	0.33	0.84	6.07
...														
25	4.04	1.86	10.66	4.69	0.74	0.46	1.10	0.45	5.51	2.83	0.37	0.38	1.47	8.96
...														
30	6.35	1.91	11.54	4.85	0.58	0.49	1.15	0.47	9.23	3.01	0.58	0.40	0.58	12.08

Exp=Expected; Obs=observed; H= other location same hospital; I= same ICU or other ICU within the same hospital; B= Other hospital's ward, not ICU or being at other hospital after discharge from ICU to other hospital; O= Other hospital's ICU; W= Ward same hospital; U=High dependency unit same hospital or Intermediate care area same hospital; E=House/hospice/rehabilitation unit and D=Death.

Table 5

Observed and expected length of stay in each hospital destination by the number of days in the Gastrointestinal body anatomic system.

	H		I		B		O		W		U		E	
Day	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**	**Obs**	**Exp**
1	0.37	0.34	0.49	0.45	0.03	0.03	0.01	0.01	0.06	0.04	0.03	0.06	0.01	0.04
2	0.57	0.65	1.03	0.88	0.06	0.05	0.02	0.01	0.15	0.12	0.08	0.13	0.04	0.09
3	0.84	0.93	1.37	1.28	0.08	0.07	0.03	0.01	0.36	0.21	0.20	0.19	0.03	0.16
4	1.10	1.19	1.76	1.65	0.11	0.10	0.04	0.02	0.59	0.33	0.26	0.25	0.07	0.26
5	1.23	1.44	2.16	1.99	0.13	0.11	0.04	0.02	0.76	0.46	0.34	0.32	0.19	0.37
...														
10	2.08	2.38	3.91	3.39	0.15	0.19	0.10	0.03	2.39	1.21	0.66	0.61	0.41	1.28
...														
15	2.77	3.01	5.14	4.36	0.10	0.24	0.00	0.03	5.14	1.98	1.54	0.86	0.21	2.77
...														
20	3.60	3.43	7.03	5.03	0.36	0.27	0.00	0.04	6.31	2.64	1.80	1.04	0.90	4.79
...														
25	4.17	3.71	8.89	5.49	0.56	0.29	0.00	0.04	8.89	3.18	1.67	1.18	0.83	7.23
...														
30	4.68	3.90	10.52	5.80	0.78	0.31	0.00	0.04	11.30	3.59	2.34	1.27	0.00	9.99

Exp=Expected; Obs=observed; H= other location same hospital; I= same ICU or other ICU within the same hospital; B= Other hospital's ward, not ICU or being at other hospital after discharge from ICU to other hospital; O= Other hospital's ICU; W= Ward same hospital; U=High dependency unit same hospital or Intermediate care area same hospital; E=House/hospice/rehabilitation unit and D=Death.