The Impact of Extraneous Variables on the Performance of Recurrent Neural Network Models in Clinical Tasks

Eugene Laksana, BS, Melissa Aczon, PhD, Long Ho, BS, Cameron Carlin, MS, David Ledbetter, BS, Randall Wetzel, MBBS
The Laura P. and Leland K. Whittier Virtual Pediatric Intensive Care Unit
Children’s Hospital Los Angeles, Los Angeles, California, United States

Abstract

Electronic Medical Records (EMR) are a rich source of patient information, including measurements reflecting physiologic signs and administered therapies. Identifying which variables are useful in predicting clinical outcomes can be challenging. Advanced algorithms, such as deep neural networks, were designed to process high-dimensional inputs containing variables in their measured form, thus bypass separate feature selection or engineering steps. We investigated the effect of extraneous input variables on the predictive performance of Recurrent Neural Networks (RNN) by including in the input vector extraneous variables randomly drawn from theoretical and empirical distributions. RNN models using different input vectors (EMR variables only; EMR and extraneous variables; extraneous variables only) were trained to predict three clinical outcomes: in-ICU mortality, 72-hour ICU re-admission, and 30-day ICU-free days. The measured degradations of the RNN’s predictive performance with the addition of extraneous variables to EMR variables were negligible.

Introduction

Electronic Medical Records (EMR) are increasingly adopted by hospitals, resulting in a potential wealth of data for clinical and machine learning research. A patient’s EMR contains comprehensive records of their vital signs, laboratory test results, medications and interventions. Many of these variables may be unrelated to a particular outcome of interest, and in this sense, may be considered extraneous features or noise for the purposes of modeling that outcome.

Deep learning (DL) algorithms such as Recurrent Neural Networks (RNNs) were designed to extract salient information from high-dimensional data: the hidden units of each layer are features derived from the input variables to that layer during model training, and this process may be thought of as feature engineering, but automated within the neural network. Combined with regularization techniques such as LASSO regularization, dropout, and recurrent dropout, DL-based models can be robust even when using very high-dimensional input vectors. With their feedback loop architecture, RNNs integrate newly acquired data with information retained from previous times to make their decisions. These characteristics make them attractive and suitable for processing evolving streams of clinical data, as evidenced by their increasing use in medical applications.

Despite the growing popularity of RNNs with clinical data, there is a paucity of literature about the effect of potentially irrelevant data on RNN performance. We sought to assess this effect by adding extraneous data to RNN model inputs and evaluating the resulting performance.

Related Works

Several studies have examined the effect of removing variables and measuring the subsequent effect on model performance. Working on the premise that removing irrelevant or redundant data increases learning accuracy, Khalid, et. al surveyed several automated feature selection and extraction methods for dimensionality reduction.

Motivated by lowering patient discomfort and financial costs, AlNuaimi, et. al investigated the effect of reducing the number of lab tests on model performance. Starting with 35 lab variables as the original inputs for modeling patient deterioration, they repeatedly lowered the number of input variables and employed feature selection algorithms to identify the optimal set of variables. They reported that the Naive Bayes algorithm displayed discrimination improvements when a smaller subset of input features was used. In contrast, the discrimination of the Random Forest, J48 Decision Tree, and Sequential Minimal Optimization models were not improved by the reduction of input data. The study showed that different algorithms respond differently to feature set reduction, and that, excepting Naive Bayes, this reduction neither degraded nor improved their performance.
We previously reported performance comparisons of logistic regression, multilayer perceptron and RNN models for in-ICU mortality using different subsets of EMR variables: physiologic measurements (vital signs and lab tests) only, therapies only, and all combined. Correlations exist amongst all the variables, and therefore redundancy likely exists when all variables are used. Regardless of algorithm, performance minimally decreased (less than 1% decrease in AUC) when model input was reduced from all variables to physiologic variables only. Across the three algorithms, performance decreased significantly when model input was limited to therapy variables only. These results indicated that the physiologic variables contained most of the relevant information for mortality risk and that the therapy variables contained redundant information, but algorithm performance did not degrade when therapy variables were included in the model.

Material and Methods

Clinical Data Sources

Data were extracted from de-identified observational clinical data collected in Electronic Medical Records (EMR, Cerner) in the Pediatric Intensive Care Unit (PICU) of Children’s Hospital Los Angeles (CHLA) between January 2009 and October 2017. A patient record included static information such as demographics, diagnoses, and discharge disposition at the end of an ICU episode. An episode is defined as a contiguous admission in the PICU; a patient may have multiple episodes. Each episode also contained irregularly, sparsely and asynchronously charted measurements of physiologic observations (e.g. heart rate, blood pressure), laboratory results (e.g. creatine, glucose level), drugs (e.g. epinephrine, furosemide) and interventions (e.g. intubation, oxygen level). Episodes without discharge disposition were excluded, leaving 7,356 patients with 9,854 episodes.

Prior to any of the computational experiments, the episodes were randomly partitioned into datasets for model training (60%), validation for hyper-parameter tuning (20%), and performance evaluation (20%). To prevent biasing performance evaluation metrics, partitioning was done such that all episodes from a single patient belonged to only one of these sets.

Target Variables

We were interested in predicting three clinical outcomes:

1. Mortality: This binary task predicts in-ICU survival or death. The top portion of Table summarizes the number of episodes and mortality rates in the three datasets (training, validation and testing).

2. 72-hour ICU Re-admission: This binary task predicts whether or not a patient was re-admitted to the ICU within 72 hours after physical discharge. Episodes where patients died, were transferred to other ICUs, or were moved to a different hospital were excluded from this experiment. The middle portion of Table describes this outcome in the three datasets after the exclusion criteria were applied.

3. 30-day ICU-free Days: This regression task predicts the number of days that a patient was not in the ICU in the 30-day window following a particular time of interest. A patient who died within that window was assigned 0 ICU-free days. Episodes where patients were transferred to the operating room, another ICU, or another hospital were excluded from this experiment. The bottom portion of Table describes this outcome in the three datasets after the exclusion criteria were applied. Note that the number of ICU-free days was computed at different time points after ICU admission.

Input Variables

To leverage existing deep learning frameworks, each patient episode’s data were first converted to a matrix format illustrated in Figure. Details of this conversion process, which includes z-normalization and forward-fill imputation, are described in previous work. A list of all 392 variables in this baseline matrix (whose rows we refer to as EMR variables in the remainder of this paper) can be found in the Appendix. To simulate extraneous, i.e. irrelevant, features as model inputs, rows containing artificial data were generated by randomly drawing values from two categories of distributions.
Table 1: Descriptive statistics of datasets used for each clinical outcome.

|                          | Train     | Valid    | Test     |
|--------------------------|-----------|----------|----------|
| **Mortality**            |           |          |          |
| # Episodes               | 5913      | 1979     | 1962     |
| Mortality rate           | 4.19%     | 3.39%    | 4.33%    |
| **72-hour ICU Re-admission** |         |          |          |
| # Episodes               | 5556      | 1883     | 1839     |
| Re-admission rate        | 2.21%     | 1.81%    | 2.28%    |
| Median length of stay (hours) | 51.9      | 56.6     | 53.2     |
| **30-day ICU-Free Days** |           |          |          |
| # Episodes               | 5828      | 1953     | 1934     |
| Mean ICU-Free days       |           |          |          |
| @ 3rd hour               | 24.91     | 25.10    | 24.71    |
| @ 6th hour               | 25.02     | 25.20    | 24.83    |
| @ 9th hour               | 24.13     | 25.28    | 24.90    |
| @ 12th hour              | 25.20     | 25.33    | 24.94    |
| @ 24th hour              | 25.03     | 25.12    | 24.65    |

1. **Theoretical**: normal, log-normal, multivariate-normal, exponential, and power function distributions.

2. **Empirical**: population-level distributions of each of the 392 variables in the original patient matrix. Feature generation from these distributions is formulized in Algorithm 1.

At each time point in a patient episode matrix, three draws of artificial data were generated from each distribution. This process generated 1191 rows of extraneous features ((5 theoretical x 3) + (392 empirical x 3)) for each patient episode. Three different types of inputs were then used to train models: EMR variables only, EMR and extraneous variables, and extraneous variables only. In the second type, the 1191 rows of extraneous variables were appended to the original patient episode matrix, i.e. they comprised 75% of the input data.

**Algorithm 1: Generating extraneous features**

\[ F = \text{set of theoretical and empirical feature distributions} \]
\[ E = \text{set of all episodes, with each episode being a matrix as described in Figure 1} \]

\[
\text{for } f \in F \text{ do} \\
\text{for } e \in E \text{ do} \\
\hspace{1em}\|e\| = \text{number of recordings in episode } e \\
\text{for } i \in \text{range}(0, 3) \text{ do} \\
\hspace{2em} X = \text{random draw of } \|e\| \text{ samples from } f \\
\hspace{2em} \text{mask random values in } X \text{ to emulate missing data frequency in } f \\
\hspace{2em} \text{add } X \text{ to } e's \text{ feature set} \\
\text{end} \\
\text{end} \\
\text{end}
\]

**Model Development and Assessment**

RNN models with Long Short-Term Memory (LSTM) architecture were implemented and trained using the Keras Deep Learning library. The models were trained to make predictions at each time point where a measurement was available. Model weights were derived from the training set, while hyper-parameters (Table 2) were optimized using the validation set. For each clinical outcome, three iterations of RNN model training were performed to better evaluate...
Figure 1: Matrix representation for a single patient episode. A row of data corresponds to measured and imputed values of a single feature, while a column contains values of all features at a single point of time. Static information such as gender is repeated at each time point. Adapted with permission.

Table 2: Hyper-parameters of RNN models for the three clinical outcomes.

|                         | Mortality                  | 72-hour Readmission | ICU-Free Days          |
|-------------------------|----------------------------|----------------------|------------------------|
| Number of LSTM Layers   | 3                          | 2                    | 2                      |
| Hidden Units in LSTM Layers | 128, 256, 256             | 420, 375             | 512, 375               |
| Batch Size              | 128                        | 100                  | 100                    |
| Learning Rate           | 1e-5                       | 1e-4                 | 1e-4                   |
| Loss                    | binary cross entropy       | binary cross entropy | mean squared error      |
| Optimizer               | rmsprop                    | rmsprop              | rmsprop                |
| Dropout                 | 0.2                        | 0.2                  | 0.2                    |
| Recurrent Dropout       | 0.2                        | 0.2                  | 0.2                    |
| Regularizer             | 1e-4                       | 1e-4                 | 1e-6                   |
| Output Activation       | sigmoid                    | sigmoid              | linear                 |

Results

All performance metrics reported here were computed on the test set. Table displays the mean and standard deviation of model performance from the three training iterations for each outcome. Figure illustrates mortality and ICU-free days model performances as a function of prediction hour.
In-ICU Mortality Task. The RNN model using only the extraneous variables had the lowest discrimination, with AUCs ranging from 0.46 to 0.66 and peaking between the 6th and 9th hours. The simple model using only the number of measurements between ICU admission and prediction time achieved AUCs ranging from 0.66 to 0.81. The RNN model using only EMR variables had AUCs ranging from 0.870 (at the 3rd hour) to 0.935 (at the 24th hour). Adding extraneous variables to the EMR variables decreased the RNN’s AUCs anywhere from 0.005 to 0.008, representing 0.57% to 0.89% degradation in performance. For all input types except for extraneous variables only, longer observation time resulted in higher AUCs.

72-Hour ICU Re-admission. The model using only the extraneous features attained an AUC of 0.489, while the model using only EMR variables had an AUC of 0.644. This AUC did not change when extraneous variables were added to the EMR variables.

30-Day ICU-Free Days. The MAE of the baseline reference value was about 5 days across all prediction times, corresponding to about 20% of the mean target value. The RNN model using only extraneous features reduced this baseline MAE by more than half a day, except at the 24th hour, where the difference was insignificant. The RNN model using only EMR features had MAE ranging from 3.3 to 3.7 days. Adding extraneous variables to the EMR features increased the MAE by small fractions of a day (0.056 to 0.133, representing 1.6% to 4% performance degradation); these two RNN models saw their MAE decrease with longer observation time.

Discussion

Including extraneous variables alongside true EMR variables, with the extraneous features comprising 75% of the input, degraded the RNN’s performance only slightly: less than 1% on the in-ICU mortality and re-admission tasks, and 2%-4% on the 30-day ICU-free days task. Even on the third task, the difference meant small fractions in absolute days. These results demonstrate the RNN’s ability to manage extraneous information when predicting the clinical outcomes. Incorporating techniques such as dropout, recurrent dropout, and LASSO regularization help mitigate overfitting effects when high dimensional data are involved\cite{16}. Recent work has even suggested that, when done properly, adding noise to models can be a regularization technique\cite{13}.

Not surprisingly, among the RNN models, those using only extraneous variables as inputs had the worst performance across all outcomes. The RNN model using only extraneous variables to predict ICU re-admission displayed random discrimination. The RNN model using only extraneous variables to predict ICU-free days performed about the same or slightly better than the baseline reference, indicating that this RNN model learned the population mean. For the in-ICU mortality task, the RNN model using only extraneous variables performed better than random (AUC > 0.5). Previous research has shown that nurse charting frequencies reflect clinicians’ anticipation of clinical outcomes\cite{17,18}. These findings are consistent with the range of AUCs (0.65 to 0.81) from a classifier that used only the number of recorded measurements between ICU admission and prediction time (fourth row of Table \ref{3a}). By construction, the temporal sampling of the extraneous features matched the temporal sampling of the charted measurements, which...
Table 3: Model performances on the three target outcomes

| Input                      | 3      | 6      | 9      | 12     | 24      |
|----------------------------|--------|--------|--------|--------|--------|
| Extraneous only            | 0.463 ±0.015 | 0.654 ±0.011 | 0.657 ±0.003 | 0.627 ±0.009 | 0.585 ±0.017 |
| EMR only                   | 0.875 ±0.003 | 0.911 ±0.005 | 0.913 ±0.004 | 0.921 ±0.005 | 0.942 ±0.005 |
| EMR + Extraneous           | 0.870 ±0.010 | 0.903 ±0.004 | 0.906 ±0.003 | 0.914 ±0.003 | 0.935 ±0.004 |
| Recording freq.            | 0.656 ±0.000 | 0.722 ±0.000 | 0.750 ±0.000 | 0.756 ±0.000 | 0.809 ±0.000 |

(a) Mortality Model AUC

| Input                      | AUC±std |
|----------------------------|---------|
| Extraneous only            | 0.489 ±0.008 |
| EMR only                   | 0.644 ±0.016 |
| EMR + Extraneous           | 0.644 ±0.017 |

(b) 72-Hour Readmission Model AUC

| Input                      | 3      | 6      | 9      | 12     | 24      |
|----------------------------|--------|--------|--------|--------|--------|
| Extraneous only            | 4.397 ±0.009 | 4.373 ±0.016 | 4.416 ±0.024 | 4.512 ±0.026 | 5.153 ±0.150 |
| EMR only                   | 3.683 ±0.036 | 3.502 ±0.061 | 3.419 ±0.081 | 3.345 ±0.108 | 3.326 ±0.173 |
| EMR + Extraneous           | 3.754 ±0.015 | 3.560 ±0.009 | 3.475 ±0.009 | 3.478 ±0.033 | 3.429 ±0.100 |
| Target mean from train set | 5.088 ±0.000 | 5.099 ±0.000 | 5.113 ±0.000 | 5.124 ±0.000 | 5.166 ±0.000 |

(c) 30-Day ICU-Free Days Model MAE (in days)

may explain the better than random performance of the RNN mortality model that used only extraneous features. This would suggest that the RNN learned some correlation between charting frequency and mortality risk from random values that had nothing to do with an individual patient but, when presented as a sequence, implicitly contained nurse charting frequency for that patient.

This study is limited by the single-center nature of the data used in the experiments. Future work will extend these experiments to other clinical tasks and algorithms, such as the multilayer perceptron, random forest, and logistic regression, to assess these algorithms’ robustness against extraneous or superfluous data.

Conclusion

This study demonstrated that RNN models with LSTM architecture can robustly manage high-dimensional data even when the majority of that data contain irrelevant information. The experiments focused on three clinical outcomes: in-ICU mortality, 72-hour ICU re-admission, and ICU-free days. RNNs can be trained for these clinically relevant tasks without model developers spending additional meticulous efforts on feature selection.

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References

1. Henry J, Pylypchuk Y, Searcy T, Patel V. Adoption of electronic health record systems among US non-federal acute care hospitals: 2008-2015. ONC Data Brief. 2016;35:1–9.

2. LeCun Y, Bengio Y, Hinton G. Deep learning. nature. 2015;521(7553):436.

3. Trevor H, Robert T, JH F. The elements of statistical learning: data mining, inference, and prediction. New York,
4. Srivastava N, Hinton G, Krizhevsky A, Sutskever I, Salakhutdinov R. Dropout: a simple way to prevent neural networks from overfitting. The Journal of Machine Learning Research. 2014;15(1):1929–1958.

5. Gal Y, Ghahramani Z. A theoretically grounded application of dropout in recurrent neural networks. In: Advances in neural information processing systems; 2016. p. 1019–1027.

6. Lipton ZC, Kale DC, Elkan C, Wetzel R. Learning to diagnose with LSTM recurrent neural networks. arXiv preprint arXiv:151103677. 2015.;

7. Aczon M, Ledbetter D, Ho L, Gunny A, Flynn A, Williams J, et al. Dynamic mortality risk predictions in pediatric critical care using recurrent neural networks. arXiv preprint arXiv:170106675. 2017.;

8. Rajkomar A, Oren E, Chen K, Dai AM, Hajaj N, Hardt M, et al. Scalable and accurate deep learning with electronic health records. npj Digital Medicine. 2018;1(1):18.

9. Liang Z, Zhang G, Huang JX, Hu QV. Deep learning for healthcare decision making with EMRs. In: Bioinformatics and Biomedicine (BIBM), 2014 IEEE International Conference on. IEEE; 2014. p. 556–559.

10. Saqib M, Sha Y, Wang MD. Early Prediction of Sepsis in EMR Records Using Traditional ML Techniques and Deep Learning LSTM Networks. In: 2018 40th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC). IEEE; 2018. p. 4038–4041.

11. Khalid S, Khalil T, Nasreen S. A survey of feature selection and feature extraction techniques in machine learning. In: Science and Information Conference (SAI), 2014. IEEE; 2014. p. 372–378.

12. Al Nuaimi N, Masud M, Mohammed F. Examining The Effect of Feature Selection on Improving Patient Deterioration Prediction. International Journal of Data Mining & Knowledge Management Process. 2015 11;5:13–33.

13. Ho LV, Ledbetter D, Aczon M, Wetzel R. The Dependence of Machine Learning on Electronic Medical Record Quality. In: AMIA Annual Symposium Proceedings. vol. 2017. American Medical Informatics Association; 2017. p. 883.

14. Hochreiter S, Schmidhuber J. Long short-term memory. Neural computation. 1997;9(8):1735–1780.

15. Chollet F. Keras (2.2.2). GitHub; 2018.

16. Noh H, You T, Mun J, Han B. Regularizing Deep Neural Networks by Noise: Its Interpretation and Optimization. In: Advances in Neural Information Processing Systems; 2017. p. 5109–5118.

17. Donabedian A. Evaluating the quality of medical care. The Milbank memorial fund quarterly. 1966;44(3):166–206.

18. Donabedian A. The quality of care: how can it be assessed? Jama. 1988;260(12):1743–1748.
### Table 4: EMR variables (demographics, vitals and labs) in patient episode matrix. Demographics such as gender and race/ethnicity were encoded as binary variables.

#### Demographics and Vitals

| Variable                                | Value                                      |
|-----------------------------------------|--------------------------------------------|
| Age                                     |                                            |
| Sex                                     | F, M                                       |
| race                                     | Caucasian/European Non-Hispanic, Hispanic  |
| Abdominal Girth                          | FLACC Pain Face                            |
| Activity Level                          | FLACC Pain Intensity                       |
| Bladder pressure                        | FLACC Pain Legs                            |
| Capillary Refill Rate                   | Foley Catheter Volume                      |
| Central Venous Pressure                 | Gastrostomy Tube Volume                    |
| Cerebral Perfusion Pressure             | Glasgow Coma Score                         |
| Diastolic Blood Pressure                | Head Circumference                         |
| EtCO2                                   | Heart Rate                                 |
| Extremity Temperature Level             | Height                                     |
| Eye Response Level                      | Hemofiltration Fluid Output                |
| FLACC Pain Activity                     | Intracranial Pressure                      |
| FLACC Pain Consolability                | Left Pupil Size After Light                |
| FLACC Pain Cry                          | Left Pupil Size Before Light               |
| Demographics                            |                                            |
| Sex, M                                  |                                            |
| race_Hispanic                           |                                            |
| race_African American                   |                                            |

#### Labs

| Variable                                | Value                                      |
|-----------------------------------------|--------------------------------------------|
| ABG Base excess                         | CBG PCO2                                   |
| ABG FiO2                                | CBG PO2                                    |
| ABG HCO3                                | CBG TCO2                                   |
| ABG O2 sat                              | CBG pH                                     |
| ABG PCO2                                | CSF Bands %                                |
| ABG PO2                                 | CSF Glucose                                |
| ABG TCO2                                | CSF Lymphs %                               |
| ABG pH                                  | CSF Protein                                |
| ALT                                     | CSF RBC                                    |
| AST                                     | CSF Segs %                                 |
| Albumin Level                           | CSF WBC                                    |
| Alkaline phosphatase                    | Calcium Ionized                            |
| Amylase                                 | Calcium Total                              |
| Anti-Xa Heparin                         | Chloride                                   |
| B-type Natriuretic Peptide              | Complement C3 Serum                        |
| BUN                                     | Complement C4 Serum                        |
| Bands %                                 | Creatinine                                 |
| Basophils %                             | Culture Blood                              |
| Bicarbonate Serum                       | Culture CSF                                |
| Bilirubin Conjugated                    | Culture Fungus Blood                       |
| Bilirubin Total                         | Culture Respiratory                        |
| Bilirubin Unconjugated                  | Culture Urine                              |
| Blasts %                                | Culture Wound                              |
| C-Reactive Protein                      | D-dimer                                    |
| CBG Base excess                         | ESR                                        |
| CBG FiO2                                | Eosinophils %                              |
| CBG HCO3                                | Ferritin Level                             |
| CBG O2 sat                              | Fibrinogen                                 |
| CBG O2 sat                              | GGT                                        |
| CBG PO2                                 | Glucose                                    |
| CBG TCO2                                | Haptoglobin                                |
| Complement C3 Serum                    | Hemoglobin                                 |
| Complement C4 Serum                    | INR                                        |
| Creatinine                              | Lactate                                    |
| Culture Blood                           | Lactate Dehydrogenase Blood               |
| Culture CSF                             | Lactic Acid Blood                          |
| Culture Fungus Blood                    | Lipase                                     |
| Culture Respiratory                     | Lipase                                     |
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| Culture Blood                           | Lipase                                     |
| Culture CSF                             | Lipase                                     |
| Culture Fungus Blood                    | Lipase                                     |
| Culture Respiratory                     | Lipase                                     |
| Culture Urine                           | Lipase                                     |
| Culture Wound                           | Lipase                                     |
| Creatinine                              | Lipase                                     |
| Culture Blood                           | Lipase                                     |
| Culture CSF                             | Lipase                                     |
| Culture Fungus Blood                    | Lipase                                     |
| Culture Respiratory                     | Lipase                                     |
| Culture Urine                           | Lipase                                     |
| Culture Wound                           | Lipase                                     |
| Creatinine                              | Lipase                                     |
| Culture Blood                           | Lipase                                     |
| Interventions                                                                 | Drugs                                                                 |
|------------------------------------------------------------------------------|----------------------------------------------------------------------|
| **Abdominal X Ray**                                                         | Diversional Activity iv  NIV Mode  Range of Motion Assistance Type    |
| **Arterial Line Site**                                                      | ECMO Hours  NIV Set Rate  Sedation Intervention Level                |
| **CT Abdomen Pelvis**                                                       | EPAP  Nitric Oxide  Sedation Response Level                         |
| **CT Brain**                                                                | FiO2  Nurse Activity Level Completed  Tidal Volume Delivered        |
| **CT Chest**                                                                | Gastrostomy Tube Location  O2 Flow Rate  Tidal Volume Expiratory     |
| **Central Venous Line Site**                                                | HFOV Amplitude  Oxygen Mode Level  Tidal Volume Inspiratory         |
| **Chest Tube Site**                                                         | HFOV Frequency  Oxygen Therapy  Tidal Volume Set                     |
| **Chest X Ray**                                                             | Hemiflation Therapy Mode  PEEP  Tracheostomy Tube Size               |
| **Comfort Response Form**                                                   | IPAP  Peak Inspiratory Pressure  Ventilator Rate                    |
| **Continuous EEG Present**                                                  | Inspiratory Time  Peritoneal Dialysis Type  Ventriclecotomy Site     |
| **Diversional Activity Books**                                             | MRI Brain  Pharmacological Comfort Measures Given  Visitor Mood Level |
| **Diversional Activity music**                                              | Mean Airway Pressure  Position Support Given  Visitor Present         |
| **Diversional Activity Play**                                               | Mechanical Ventilation Mode  Position Tolerance Level  Volume Tidal  |
| **Diversional Activity Toys**                                               | MultiDisciplinary Team Present  Pressure Support                    |