## Predicting mortality of ICU patients

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## Mortality Prediction of ICU Patients - PhysioNet Computing in Cardiology Challenge 2012\*



\*https://physionet.org/challenge/2012

#### **QUESTION**

Can information collected during the first two days of an ICU stay predict in-hospital mortality?

#### **OUTCOME**

Logistic regression model based on ICU data predicts inhospital mortality with

- 83% AUC
- 76% sensitivity, 74% specificity
- 32% precision

Model performs significantly better than current measures of mortality (SOFA/SAPS-I based models)

### Data description

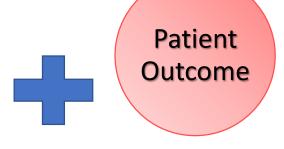
 Predictors (acute physiological measures as time-series data + general descriptors as non-time series data) along with survival outcomes on 4000 patients data

### Acute physiological measures on up to 37 features over 48 hours ICU stay such as:

- Respiratory rate
- Heart rate
- Glucose level
- Blood urea nitrogen
- Coma score
- Additional health/physiological measures

### General patient level descriptors collected at time of ICU admission such as:

- Record ID
- Age (years)
- Gender (0: female, 1: male)
- Height (cm)
- ICU type (1: Coronoary care, 2: Cardiac surgery recovery, 3: Medical ICU, 4: Surgical ICU)

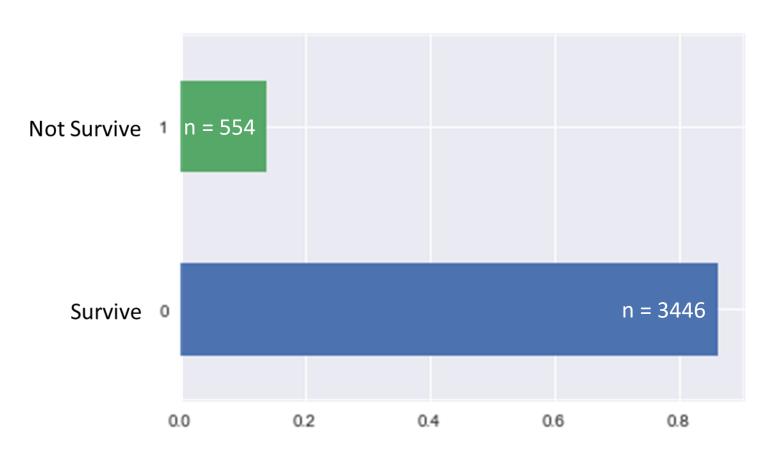


**Survived or Not** 

Outcome

**Predictors** 

## Distribution of patient outcomes



**Imbalanced outcomes in dataset** 

(addressed during modeling via class\_weights "balancing")

% of total ICU patients

### Feature extraction

### Non-time-series data

- One-hot encoding of categorical features (Gender, ICU-type)
- Address missing values (eg: for gender created a new category of "missing")
- Cap "outliers"

### Time-series data

- For numeric features, extract minimum, maximum, median value, change (max-min)
- For categorical features, generate counts/patient
- Address missing values and cap "outliers"

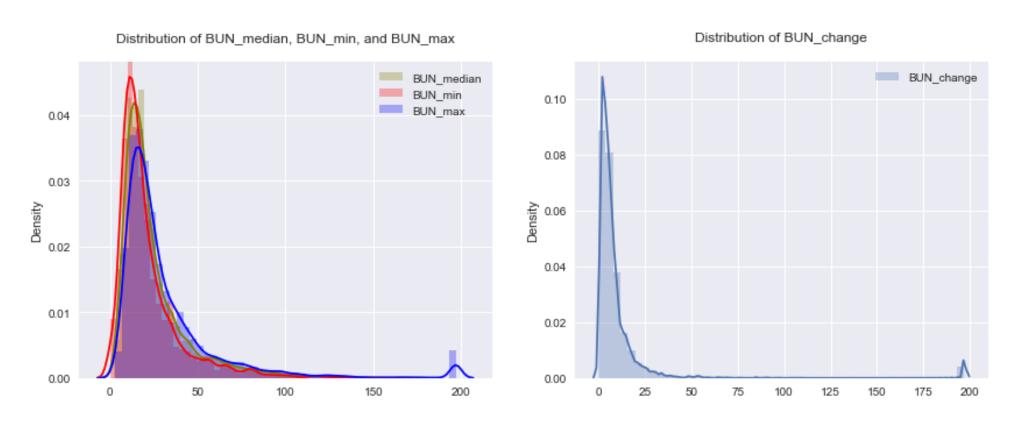
**Predictor Matrix** 

9 features



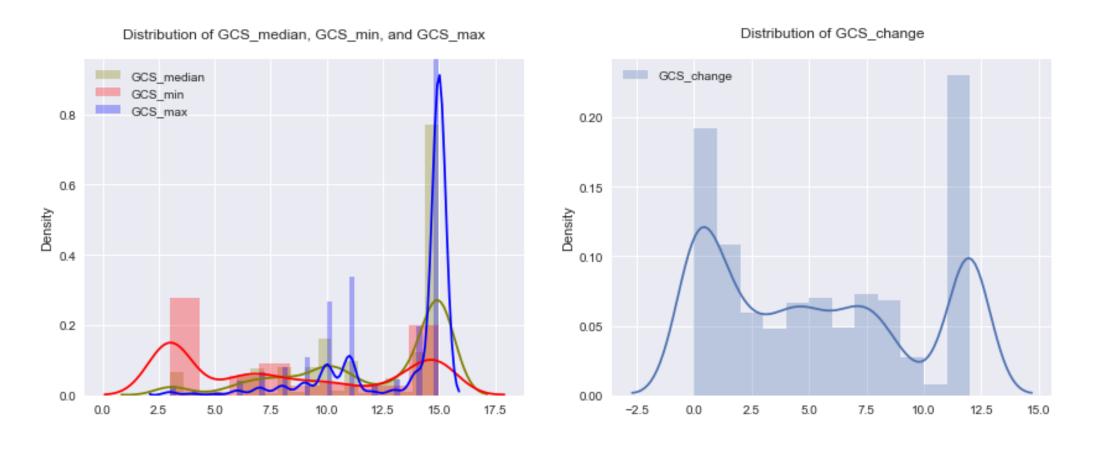
145 features

# Example feature distributions/exploratory analysis - Patient distributions of Blood Urea Nitrogen extracted features



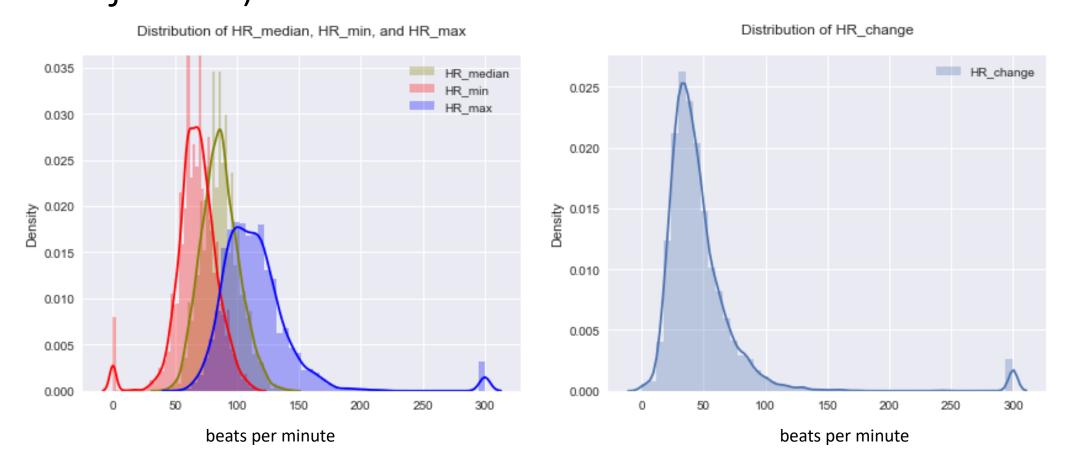
- Nearly overlapping distributions of BUN across median, min, and max.
- Small % of patients show large BUN\_change

## Example feature distributions/exploratory analysis - Distribution of extracted Gleason Coma Scores



Relatively different distributions of GCS\_min vs GCS\_max.

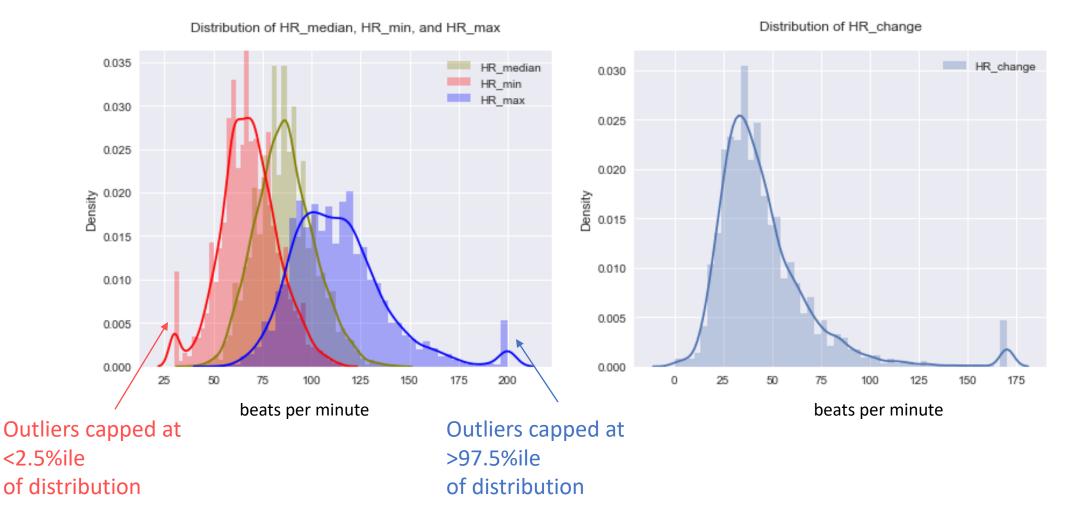
# Example feature distributions/exploratory analysis - Distribution of extracted heart rate features (unadjusted)



- Relatively different distributions of HR\_min vs HR\_max.
- Small % of patients show large change in heart rate during ICU stay

## Example feature distributions/exploratory analysis - Distribution of extracted heart rate features (with

outlier "capping")



### Predictive modeling – high level schema

154 extracted features used for model selection without scaling

Select best performing algorithm (based on recall and precision)







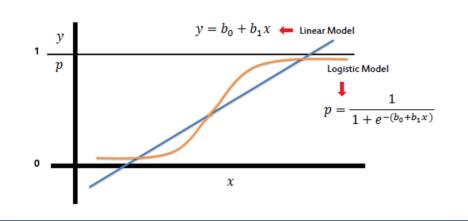


Generate baseline model with all predictors

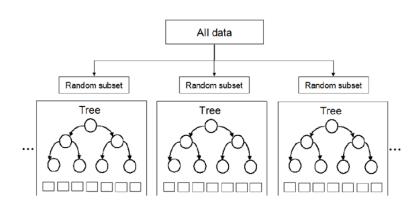
(Compare Logistic Regression vs Random Forest) Refine best performing algorithm towards "final" model (feature selection)

### Logistic Regression vs Random Forest

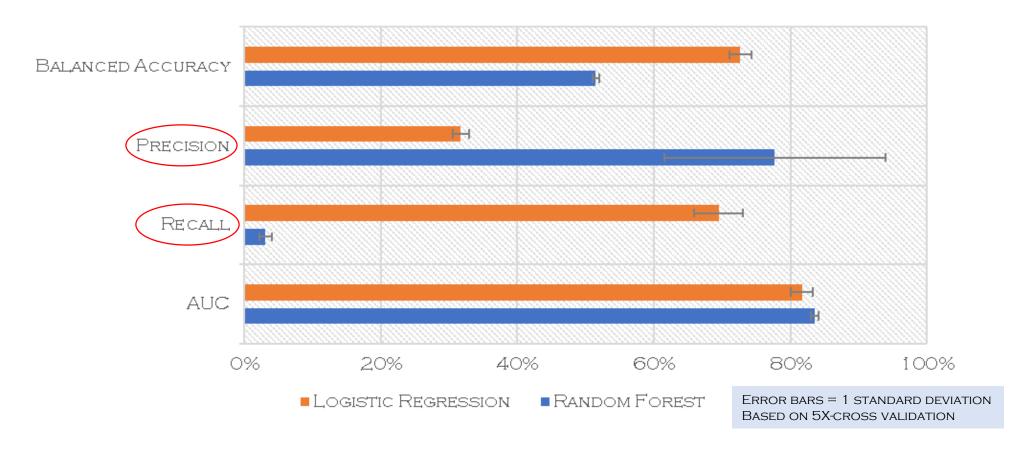
Logistic Regression  Classification based on the probability of odds given a combination of predictor variables



Random Forest  Classification based on an ensemble of decision trees trained on different subsets of features and observations



## Poor recall with out-of-the-box Random Forest compared to Logistic Regression



→Logistic regression algorithm chosen for further refinement towards "final" model

### Logistic regression model refinement schema

Baseline model (with 154 "scaled" features)

L1 regularization

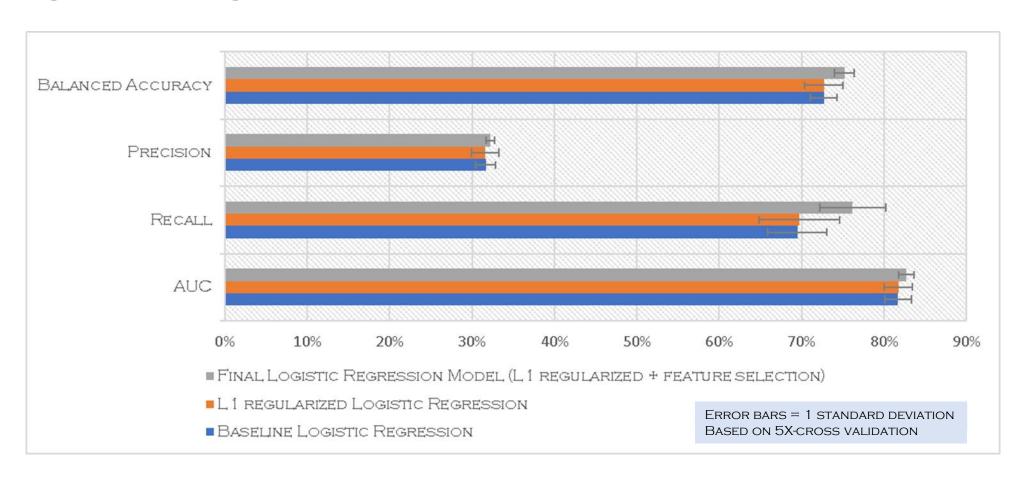
Feature selection by odds-ratios of L1 regularized model Report model performance with cross-validation

**154 predictors** 

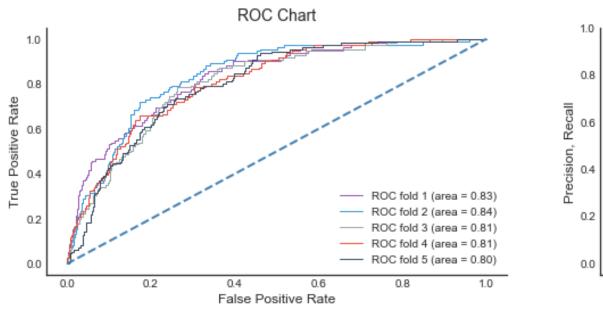
28 predictors

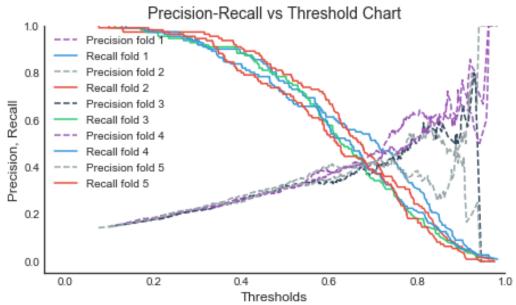
18 predictors

## Comparison of performance metrics for all (logistic regression) models



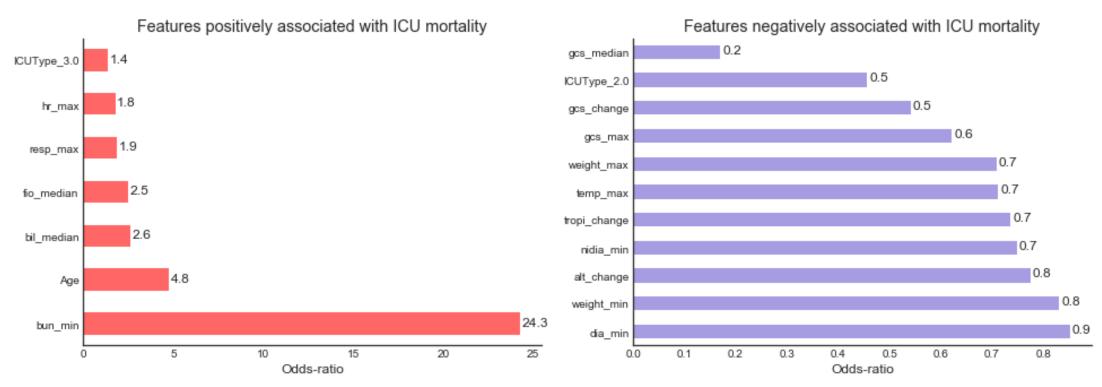
### ROC and Precision-Recall vs Threshold Chart





 $\rightarrow$  Opportunity exists to improve model sensitivity via reducing probability threshold < 0.5 (at cost of precision)

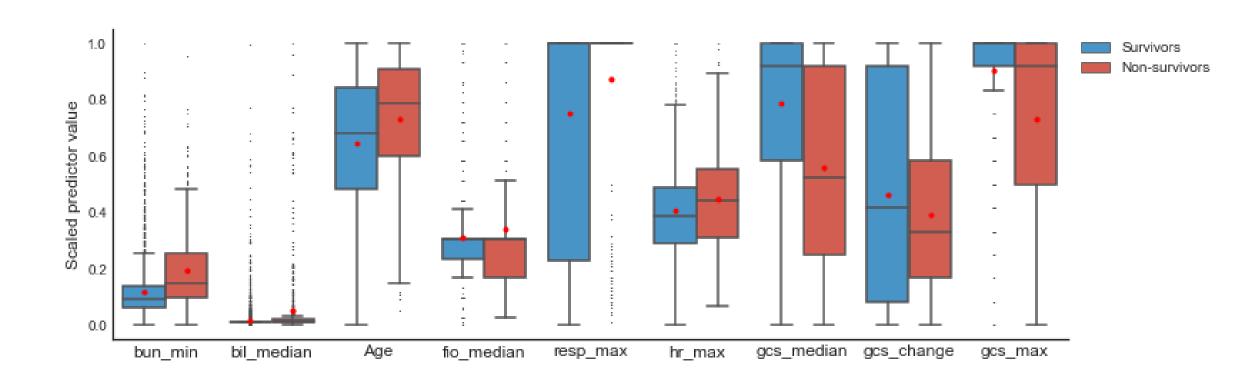
# "Final" model predictors of in-hospital mortality for ICU patients and odds-ratios\*



<sup>\*</sup>for predictors scaled between 0-1.

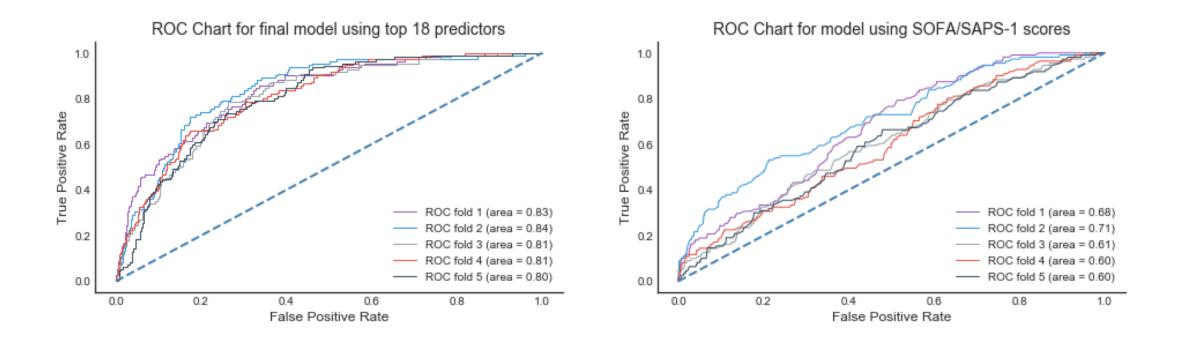
→\*Thus, an odds-ratio of 24.3 for BUN\_min (Blood Urea Nitrogen minimum) indicates increase in odds of on-hospital mortality as BUN\_min increases from lowest to highest value of its measured range.

## Distributions of top predictors in survivors vs non-survivors



→Positive predictors of mortality have generally higher values in non-survivors (bun\_min, bil\_median, age, fio\_median) and negative predictors have mortality have generally lower values in non-survivors.

# Comparison of "final" model to "benchmark" model using SOFA/SAPS-1 scores



→Across multiple test-train subsets, "final" model generated in this study outperforms models developed using SOFA/SAPS-1 scores

### Summary/Conclusions

A parsimonious logistic regression model based on 18/154 total features was developed to predict in-house mortality of ICU patients. Most important predictors are:

- Blood urea nitrogen levels
- Gleason Coma Score level
- Age
- Bilirubin levels

Model shows superior performance to benchmark models using current measures of mortality. It may be possible to further improve model performance by:

- Addition of more features (eg: past medical history)
- Addition of more data
- Increase of model sensivity (at cost of precision) via lowering of probability thresholds