



Prediction of the Microbial Origin of Presumed Sepsis in PICU Encounters



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Introduction & Background

- Sepsis is an extreme bodily reaction caused from an infection, accounts for ~30% of all hospital mortality.
- Standard treatment is broad-spectrum antibiotics, however, 50% of all sepsis cases are not bacterial in origin, leading to antibiotic overuse.

Objective

To build statistical models for predicting the microbial origin of presumed sepsis in PICU patients by using physiological time series data.

Methods

- Patient data from the JHU ACCM PMAP Database.
- Include if unstable temperature (< 36°C or > 38.5°C)
- Include if physiological time series (heart rate, blood pressure, respiratory rate, blood oxygenation) present.
- Patient labels: **Bacterial (n = 99)** if positive blood test, **Non-Bacterial (n = 642)** if negative blood test, **Not Infected (n = 1,187)** if no test is taken.

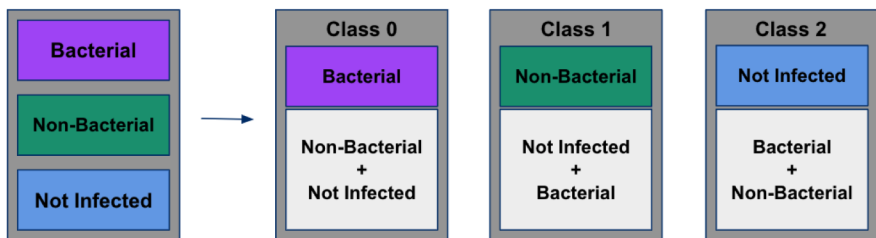


Figure 1. One Vs. Rest Classifier for multi-class classification.

Results

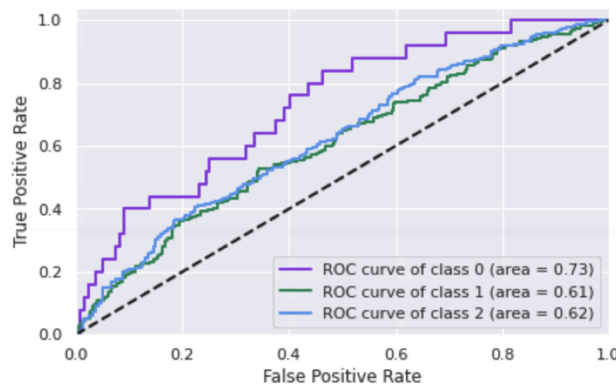


Figure 2. Receiver Operating Characteristic (ROC) curves for each class. Random Forest Classifier.

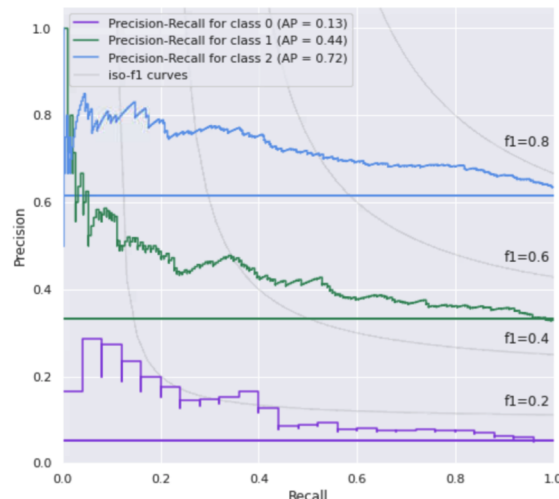


Figure 3. Precision Recall (PR) curves for each of class. Random Forest Classifier.

Rank	Class 0	Class 1	Class 2
1	NIBP Minimum 6	HR Std 9	HR Std 10
2	HR Mean 10	HR Std 10	RR Mean 5
3	RR Mean 10	HR Std 1	RR Mean 9
4	RR Minimum 7	RR Mean 7	NIBP Mean 3
5	RR Minimum 5	HR Std 7	RR Mean 10

Table 1. Top five features for each One Vs. Rest Random Forest classifier calculated across 10-folds. Top features are presented by **signal name, metric, and hour before temperature instability**. NIBP = non-invasive blood pressure, HR = heart rate, RR = respiratory rate.

Discussion & Conclusion

- Based on the ROC curves and PR curves, our model showed promising predictive power for differentiating infections.
- Heart rate and respiratory rate derived features were the top features in predicting the source of infection
- Future work will be focused on the extraction of additional clinical features from physiological signals and model refinement