Machine Learning-Based Prediction of ICU Admission in Febrile Oncology Patients

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1. PROBLEM & OBJECTIVE

The Problem

- Febrile illness affects up to 80% of chemotherapy patients
- Some patients rapidly deteriorate and require ICU admission
- Current scores (MASCC, qSOFA) not designed for ICU prediction

Research Question

Can a machine learning model using routinely available clinical features predict ICU admission in febrile oncology patients more accurately than existing clinical scores?

Hypotheses

- **H1:** XGBoost model will achieve AUROC ≥ 0.80
- **H2:** Model will outperform MASCC and qSOFA
- **H3:** Consistent performance across subgroups

2. APPROACH & METHODS

Study Design

- **Population:** 149 oncology patients with febrile illness
- **Outcome:** ICU admission (54.4% rate)
- **Features:** 10 clinical variables (MASCC, qSOFA, hypotension, tumor type, neutropenia, etc.)

Model Development

- **Algorithm:** XGBoost classifier
- **Validation:** 10×5-fold cross-validation
- **Confidence intervals:** 1000-iteration bootstrap

Sensitivity Analysis

- Separate model trained **excluding hypotension**
- Tests if model provides value beyond obvious clinical triggers

3. KEY RESULTS

0.934
AUROC (Full)

0.887
AUROC (No Hypo)

85.9%
Accuracy

Model	AUROC	Sensitivity	Specificity
XGBoost	**0.934**	**87.7%**	**88.2%**
MASCC+qSOFA	0.864	96.3%	55.9%
qSOFA alone	0.838	86.4%	55.9%
MASCC alone	0.656	98.8%	32.4%

Key Finding: Even without hypotension, model achieves AUROC 0.887, demonstrating value beyond obvious clinical triggers.

4. CONCLUSIONS & IMPACT

Hypotheses Supported

- ✓ **H1:** AUROC 0.934 > 0.80 threshold
- ✓ **H2:** Outperforms MASCC (+42%) and qSOFA (+11%)
- ✓ **H3:** Consistent across tumor type & neutropenia status

Clinical Applications

- Triage tool for high-risk patient identification
- Resource allocation in ICU-limited settings
- Decision support for intermediate-risk patients

Limitations & Future Work

- Single-center data (n=149) — needs external validation
- Retrospective design — prospective study needed
- Future: multi-center validation, biomarker integration