Detecting bacterial sepsis among allogeneic hematopoietic cell transplant (aHCT) recipients with population-specific bedside tools

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BACKGROUND & OBJECTIVES

Background

- aHCT recipients are at in increased risk of developing and dying of sepsis
- Early and accurate sepsis treatment decreases mortality
- Diagnosing sepsis among aHCT recipients remains challenging
  1. Sepsis presents differently in posttransplant patients
  2. Transplantation complications can present similarly to sepsis
- Existing bedside tools were developed among general population patients
- Existing tools perform poorly to moderately and their limitations may be exacerbated among aHCT recipients

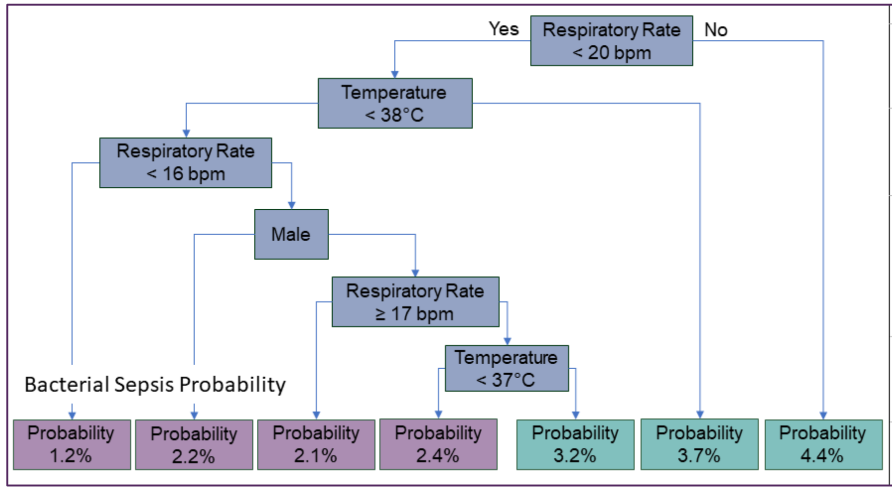
Objectives (Aims)

Goal: Develop bedside bacterial sepsis prediction tools that provide decision support at the time of culture collection for aHCT

Aim 1: Develop two prediction tools: Score - HCT Bacterial Sepsis Score (HSB2), Decision Tree - HCT Bacterial Sepsis Tree (HSBT)

Aim 2: Compare the estimated predictive abilities of HBS2 and HBST to Systemic Inflammatory Response Syndrome (SIRS), quick Sequential Organ Failure Assessment (qSOFA), National Early Warning Score (NEWS)

DEVELOPED TOOLS (HBS2- score, HBST – tree)



Temperature	< 37.5°C	0
	≥ 37.5°C	+ 11
Heart Rate	≤ 93 b/m	0
	> 93 b/m	+ 5
Respiratory Rate	≤ 15 b/m	0
	16 – 17 b/m	+ 3
	18 – 19 b/m	+ 2
	≥ 20 b/m	+ 10
Diastolic Blood Pressure	≤ 70 mmHg	+ 1
	> 70 mmHg	0
Score Range	0 – 27, no 23-25	

METHODOLOGY

STUDY OVERVIEW

Study Period & Location: 2010-2019, Seattle Cancer Care Alliance
Population: Allogeneic HCT recipients with ≥ 1 potential infection (PIs - blood culture)
Cohort: All potential infections that occurred within the 1st 100 days post HCT
Model/Validation Data: Randomly selected 70%/30% of data (randomization done on the patient level)

OUTCOME & PREDICTORS

Outcome: Bacterial sepsis - blood culture confirmed gram-negative, *Staph. aureus*, or *Strep*. species bacteremia
Potential Predictors: Bedside examination factors frequently (≥65%) captured within measurement window (24 hours prior/ 2 hours following culture collection)- measurement closest in time to culture collection used

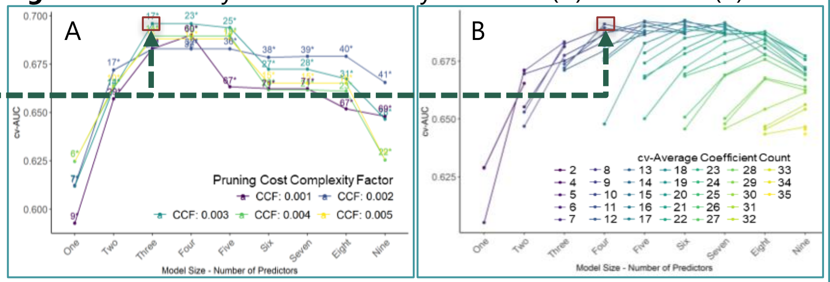
MODEL DEVELOPMENT

Step 1: Determined optimal flexibility (size)
- Estimated cvAUC for all models (HBS2: logistic regression; HBST: classification tree)
- Selected best cvAUC relative to size

Step 2: Identified predictors in best performing (cvAUC) model of optimal size
Step 3: Developed tools in full model dataset
Step 4: Estimated HSB2 scores as 10*betas

* cvAUC (cross validated area under the curve)

Figure 1: cvAUC by Model Flexibility for HBST (A) and HBS2 (B)



TOOL EVALUATION

Numerically: Area under the curve (AUC), sensitivity/specificities (qSOFA/SIRS 2+, NEWS 4+, HBS2/T optimal*)
Visually: Receiver Operating Characteristic (ROC) curve and Decision curve

* Optimal cut points identified using Youden Method

RESULTS

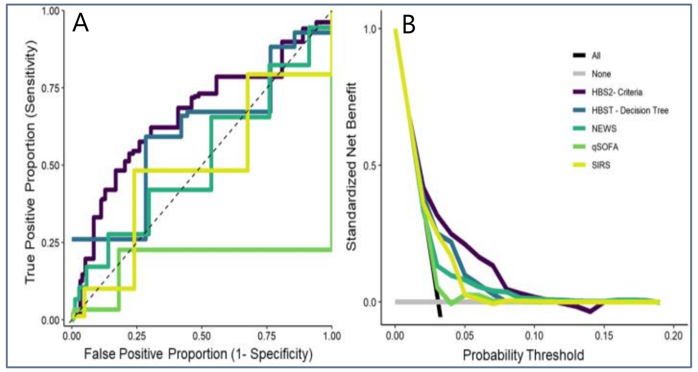
Patient Characteristics

- 1571 aHCT had7755 PIs, 238 sepsis events
- White (73%), male (57%), 135 (8.6%) died

Tool Performance

	AUC	Sensitivity	Specificity
HBS2	71.1 (64.3, 77.9)	60.0 (47.1, 72.0)	74.0 (72.1, 75.8)
HSBT	70.0 (63.7, 67.2)	61.5 (48.6, 73.3)	71.5 (69.6, 73.4)
SIRS	64.7 (57.6, 71.9)	53.8 (41.0, 66.3)	76.0 (74.2, 77.8)
qSOFA	54.4 (48.8, 59.9)	3.1 (0.4, 10.7)	99.7 (99.3, 99.9)
NEWS	58.2 (50.5, 66.0)	40.0 (28.0, 52.9)	70.0 (68.1, 71.9)

Figure 2: ROC Curve (A) and Decision Curve (B)



CONCLUSION

Among aHCT recipients with PIs

- Our tools were better able to predict bacterial sepsis than existing tools
- HBS2 had higher clinical benefits than existing tools (Figure 2b)
- Using our bedside tools could improve early detection and treatment of bacterial sepsis

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