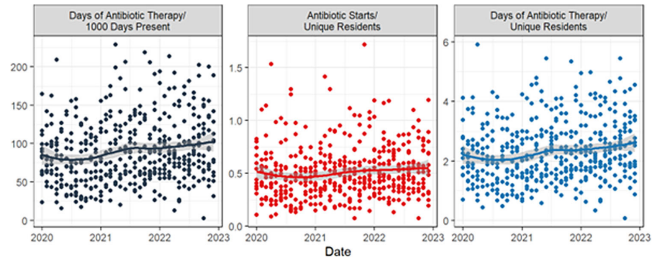

within the same network. After omitting non-pharmacologic items and limiting the data to medications dispensed from 1/2020 – 12/2022, we determined the following metrics by month: days of antibiotic therapy (DOT), number of medications prescribed, number of antibiotic courses prescribed (antibiotic starts), and the number of individual residents issued a prescription for any medication (unique residents). These metrics were assessed for each facility (2020 – 2022) and for prescribers responsible for > 1% of prescriptions within that facility (2022 only). Prescriber-level unique residents was the number of residents issued a prescription by the given provider. We obtained facility-level census data to calculate antibiotic DOT/1000 resident days of care (DOC) as a standard to which we compared novel metrics. **Results:** During the 3-year study period, 1718 prescribers at 13 PALTC settings wrote for 672256 medications, including 31087 antibiotic courses. At the facility level, the correlation between monthly antibiotic starts (courses)/unique residents and antibiotic DOT/1000 DOC was 0.83 ($p < 0.0001$). The correlation between monthly antibiotic DOT/unique residents and antibiotic DOT/1000 DOC was 0.98 ($p < 0.0001$). Trends in monthly values of both novel metrics and DOT/1000 DOC were consistent across the examined period (Figure 1). For individual prescribers, both novel metrics permit assessment and comparison of antibiotic prescription rates over time (Figure 2). **Conclusions:** Pharmacy dispensing data can be used to determine antibiotic DOT/unique residents and antibiotic starts/unique residents at the facility level and for individual providers. The novel metric antibiotic DOT/unique residents demonstrated strong correlation with antibiotic DOT/1000 DOC at the facility level. In addition to supporting tracking and reporting of antibiotic use among PALTC settings, these new metrics permit visualization of the antibiotic prescribing rates of individuals prescribers, as well as peer comparison, which in turn can lead to actionable feedback that helps improve antibiotic use in the care of PALTC.

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Subject Category: Medical Informatics

Multitask Neural Networks to Predict Antimicrobial Susceptibility Results of Escherichia coli Clinical Isolates

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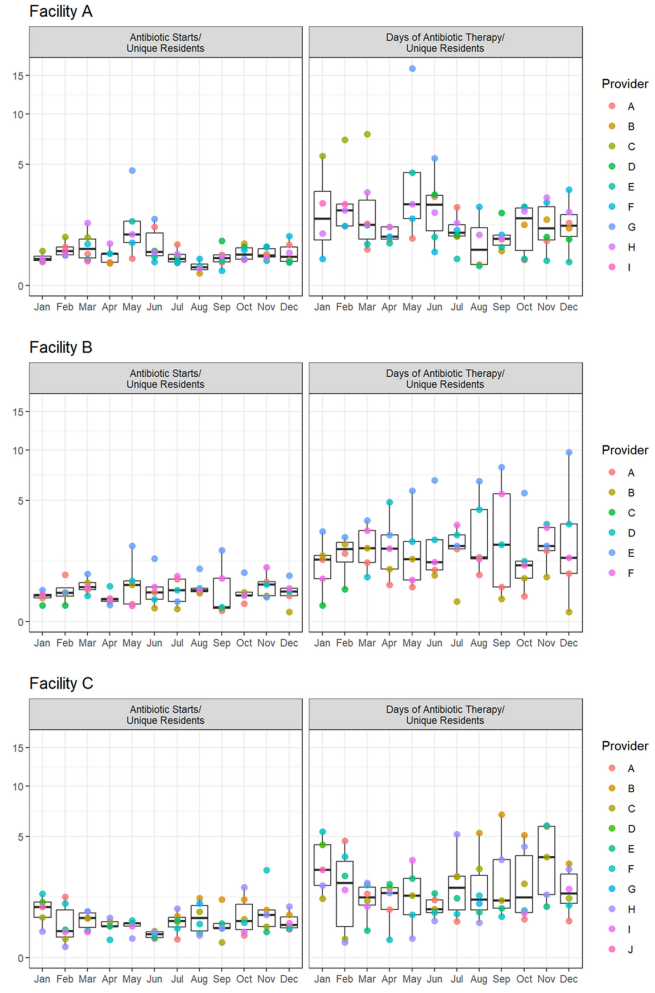

Background: Machine-learning (ML) models, such as neural networks (NNs), have been proposed to predict antimicrobial susceptibility at the patient level while incorporating patient-level information from electronic medical record (EMR) systems. However, NNs often do not perform well in predicting rare outcomes, such as carbapenem resistance. We aimed to apply a novel multitask NN to create personalized antibiograms for individual patients with Escherichia coli clinical isolates to predict antimicrobial resistance (AMR) for four major antimicrobial classes simultaneously with improved accuracy for carbapenem resistance by using shared hidden layers (Figure 1). **Methods:** We analyzed all E. coli clinical isolates from the US Veterans Health Administration's network from January 1, 2017, to December 31, 2019, focusing on AMR profiles of aminopenicillins, narrow-spectrum (NS) cephalosporins, extended-spectrum (ES) cephalosporins, and carbapenems. Patient-level clinical data (demographics, antimicrobial exposure history, previous isolates (if any), comorbidities, and recent procedures) were extracted from EMR. Antibiograms for all hospitals were generated using standard methods for the preceding calendar years. We employed logistic regression to evaluate the efficacy of conventional antibiograms in predicting AMR profiles. We adopted the ML approach using conventional NNs and novel multitask NNs on all extracted clinical data and hospital antibiograms. The models were trained with data from 2017 and 2018 and then tested on 2019 data, assessing their performance using the area under the receiver-operating curve (AUC). **Results:** The study included 257,968 E. coli isolates, split into 171,391 for training and 86,577 for validation. The prevalence of AMR in the test data from 2019 was 49.8% for aminopenicillins, 28.4% for NS cephalosporins, 10.7% for ES cephalosporins, and 0.2% for carbapenems, respectively. Conventional hospital antibiograms showed low prediction accuracy with AUC scores of 0.56 for aminopenicillins, 0.67 for NS cephalosporins, 0.61 for ES cephalosporin, and 0.67 for carbapenem. AUC scores from preliminary models for conventional and multitask NNs were 0.78/0.78 for aminopenicillins, 0.83/0.82 for NS cephalosporins, 0.84/0.85 for ES cephalosporins, 0.68/0.75 for carbapenems. While producing improved accuracy for carbapenem and comparable accuracies for three other classes, multitask NNs took approximately 66% less time for model training than conventional NNs. **Conclusions:** Integrating EMR data with NNs improved their predictive accuracy, potentially leading to a decision-support tool for better empirical antimicrobial therapy guidance in the

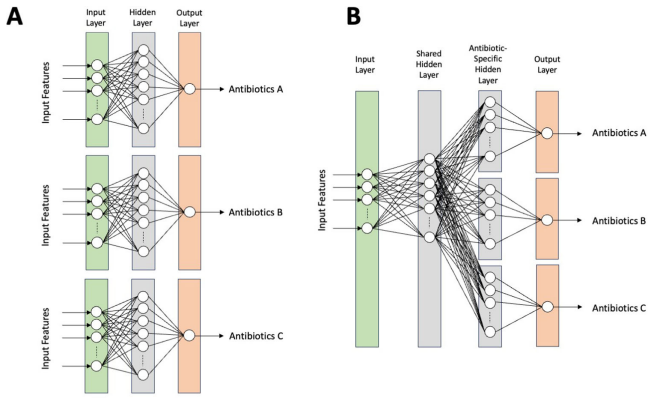

Figure 1: Simplified Diagrams of Conventional Neural Networks (A) and Multitask Neural Network (B)

window between species identification and confirmed susceptibilities. Multitask NNs can potentially improve the prediction accuracy of uncommon AMRs while maintaining comparable prediction accuracies for common AMRs and optimizing the efficiency of model training.

Disclosure: Michi Goto: Contracted Research - Merck

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Subject Category: Outbreaks

Investigation and control of an outbreak of methicillin-susceptible Staphylococcus aureus skin and soft tissue infections in a level IV NICU

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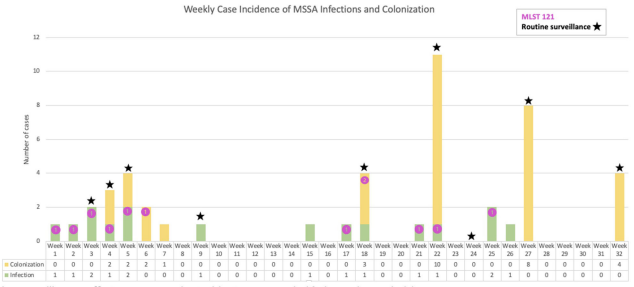
Background: Neonatal intensive care units (NICU) outbreaks caused by methicillin-susceptible Staphylococcus aureus (MSSA) are less commonly reported than outbreaks caused by methicillin-resistant S. aureus. We report an unusual outbreak of MSSA skin and soft tissue infections (SSTIs) in a level IV NICU investigated by whole genome sequencing (WGS) and molecular typing. **Methods:** An investigation was initiated in a 56-single-bed NICU after four patients developed MSSA SSTIs in Week 1. Case-patients had positive MSSA cultures identified by clinical cultures or surveillance sampling (bilateral nares, axillae, umbilicus, and groin), and antibiotic susceptibility testing was performed. WGS and assessment of isolate relatedness through mutation event analysis and multi-locus sequence typing (MLST) was performed by the NYS DOH. Demographic and isolate characteristics were compared using Wilcoxon rank sum test, Fisher's exact test and Pearson's Chi-squared test, as appropriate. **Results:** From Week 2 to Week 32, 9 rounds of surveillance for MSSA colonization were conducted. In all, 30 case-patients had MSSA colonization and 16 infants developed infections including impetigo (n=7), pustules (n=5), staphylococcal scalded skin syndrome (SSSS, n=2), abscess (n=1), and bacteremia (n=1). All SSTI cases presented on infants' faces, all of whom were on non-invasive respiratory support. MLST identified 4 distinct types including MLST 121 (n=12), MLST 398 (n=10), MLST 30 (n=6), and MLST 15 (n=6). Eight isolates were unrelated to other isolates. MLST 398 and MLST 30 included isolates not closely related (>9 mutation events). The 12 MLST 121 isolates were closely related (≤9 mutational events between all isolates), harbored the mupA gene, and were mupirocin-resistant (MIC>1024 ug/ml). Clinical infection and mupirocin resistance were associated with MLST 121 (Table 1). Multiple infection control measures were implemented, including increased availability of alcohol-based hand sanitizers, introducing bare-below-the-elbows practice for staff, contact precautions for case-patients, decolonization with mupirocin and chlorhexidine baths, environmental cleaning/disinfection, and removing excess equipment and supplies. No new cases of mupirocin-resistant or MLST 121 SSTIs occurred after Week 25. **Conclusion:** We report a MSSA outbreak associated with multiple MLST types and a predominant mupirocin-resistant strain. This report highlights the ability of molecular typing to characterize strains causing infections versus colonization and the potential loss of mupirocin as a control measure when outbreaks are caused by mupirocin-resistant strains. WGS analysis allows for increased discrimination of mutation events allowing for improved resolution of case relatedness compared to other typing methods. Successful control of this outbreak was achieved with a multitude of infection prevention and control.

Table 1. Characteristics of case-patients by MLST 121 compared to other MLST[1]

	MLST 121 (n=12)	Not MLST 121 (n=30)	*P-value*
Demographic characteristics			
Median age (IQR) at first MSSA detection, days	18 (12, 22)	26 (14, 54)	0.14
Median gestational age (IQR), weeks	34 (28, 38)	31 (28, 35)	0.3
Median birth weight (IQR), grams	1,865 (1058, 2722)	1,460 (942, 1890)	0.2
Infection or Colonization			<0.001
Infection	10 (83%)	5 (17%)	
Colonization	2 (17%)	25 (83%)	
Site of infection (N=15)			<0.001
Impetigo	6 (60%)	1 (3.3%)	
Pustule	2 (20%)	2 (6.7%)	
SSSS	2 (20%)	0 (0%)	
Abscess	0 (0%)	1 (3.3%)	
Bacteremia	0 (0%)	1 (3.3%)	
Mupirocin susceptibility (N=41)			<0.001
MIC >1024 µg/ml	12 (100%)	0 (0%)	
MIC ≤1024 µg/ml	0 (0%)	29 (100%)	

[1]4 case-patients' isolates unavailable for sequencing.



*No surveillance efforts were conducted between week 10 through week 14

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