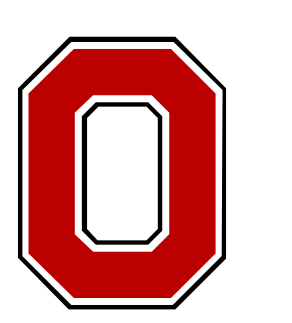


# Predicting Empiric Antibiotic Coverage Based on Patient Factors



THE OHIO STATE UNIVERSITY

WEXNER MEDICAL CENTER

Protiva Rahman, BS<sup>1,3</sup>; Erinn Hade, PhD<sup>1</sup>; Courtney Dewart, PhD<sup>1</sup>; Yuan Gao, MS<sup>1</sup>; Courtney Hebert, MD, MS<sup>1,2</sup>; <sup>1</sup> Department of Biomedical Informatics, <sup>2</sup> Internal Medicine, <sup>3</sup> Department of Computer Science, The Ohio State University, Columbus, OH

## Motivation

- Providers prescribe empiric antibiotics based on patient risk factors and guideline recommendations.
- Prior work has looked at modeling probability of coverage of individual antibiotics based on patient factors<sup>1</sup>.
- However, combining results from multiple models to find the ideal antibiotic is challenging.

## Empiric Prescription

- Antibiotics fall on a spectrum based on their coverage<sup>2</sup>:
  - Prescribing a *narrow-spectrum antibiotic* risks the patient's infection not being treated appropriately.
  - Prescribing a *broad-spectrum antibiotic* can increase antibiotic resistance in the community.
- For any treatment option, we are interested in two metrics:
  - Percentage of infections covered in the entire dataset:
 
$$\frac{\sum \text{Infection Covered}}{\text{Total No. of Patients}}$$
  - Average breadth score (determined by expert survey<sup>2</sup>) for correctly treated patients:
 
$$\frac{\sum (\text{Infection Covered} \times \text{Antibiotic Breadth})}{\sum \text{Infection Covered}}$$
- For each infection:
  - We defined an **ideal antibiotic** as the antibiotic with the lowest breadth score that covered the infection.
  - We defined the **actual empiric antibiotic regimen** as all antibiotics prescribed within 24hrs of admission.

## How does the ideal antibiotic compare with the actual empiric antibiotic regimen for these metrics?

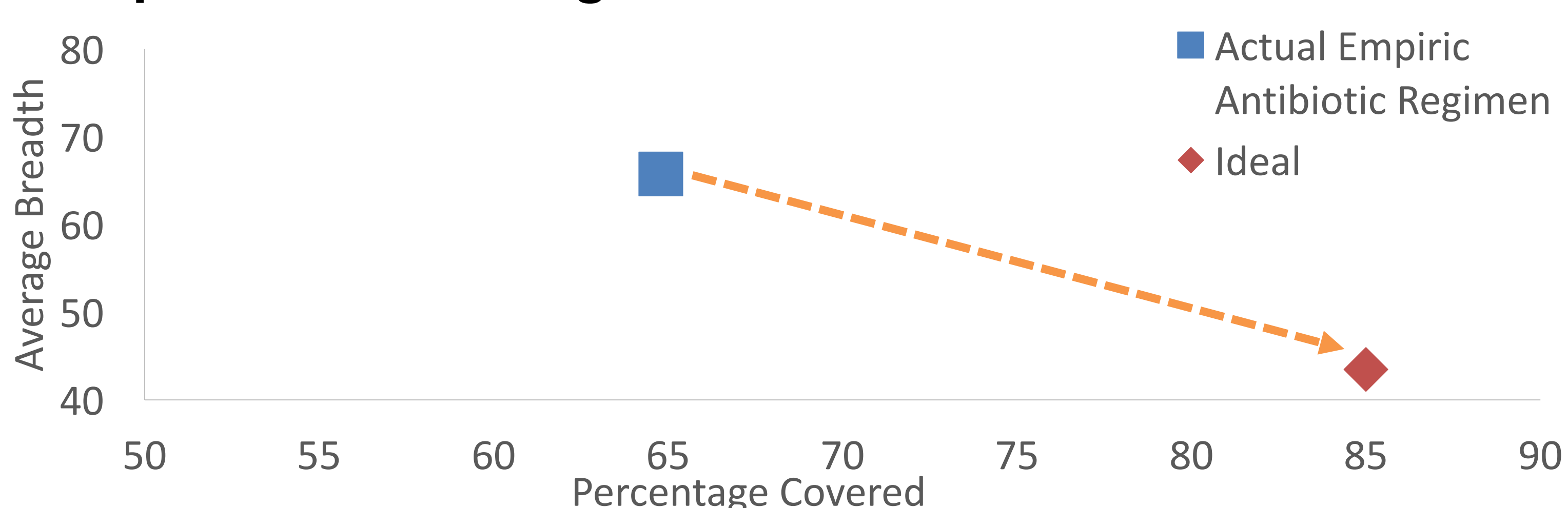


Figure 1: Lots of scope for improving empiric prescription

## Modeling Antibiotic Resistance

- **Dataset:** Hospitalized adult patients with a positive urine culture within 48hrs of admission.
  - N=6,366, train = 5,093, test = 1,273
- Each row in our data corresponds to a patient's infection. We determined the outcome for each antibiotic based on whether this antibiotic would cover the patient's infection<sup>3</sup>.
- We model individual antibiotic coverage with penalized logistic regressions<sup>1</sup>.

Antibiotic	Patient 1	Patient 2	Antibiotic Breadth
Piptazo	95%	90%	~80
Cefepime	86%	65%	~80
Ciprofloxacin	72%	44%	~55
Ceftriaxone	87%	60%	~55
Cefazolin	81%	50%	~35

Figure 2: Model outcomes for 2 example patients.

**Acknowledgement:** This work was supported by the National Institute of Allergy and Infectious Diseases of the National Institutes of Health under Award Number [R01AI116975]; and by Award Number Grant [UL1TR001070] from the National Center For Advancing Translational Sciences.



## Recommending an Antibiotic

- **How do we recommend one antibiotic from Figure 2?**
  1. Pick the antibiotic with highest probability of coverage (gray circle)
  2. Recommending one antibiotic for all patients: For example ceftriaxone (yellow circle) – this is followed by many providers
  3. Choose a threshold: For example, recommend the narrowest antibiotic with at least 0.65 probability of coverage (green circle)

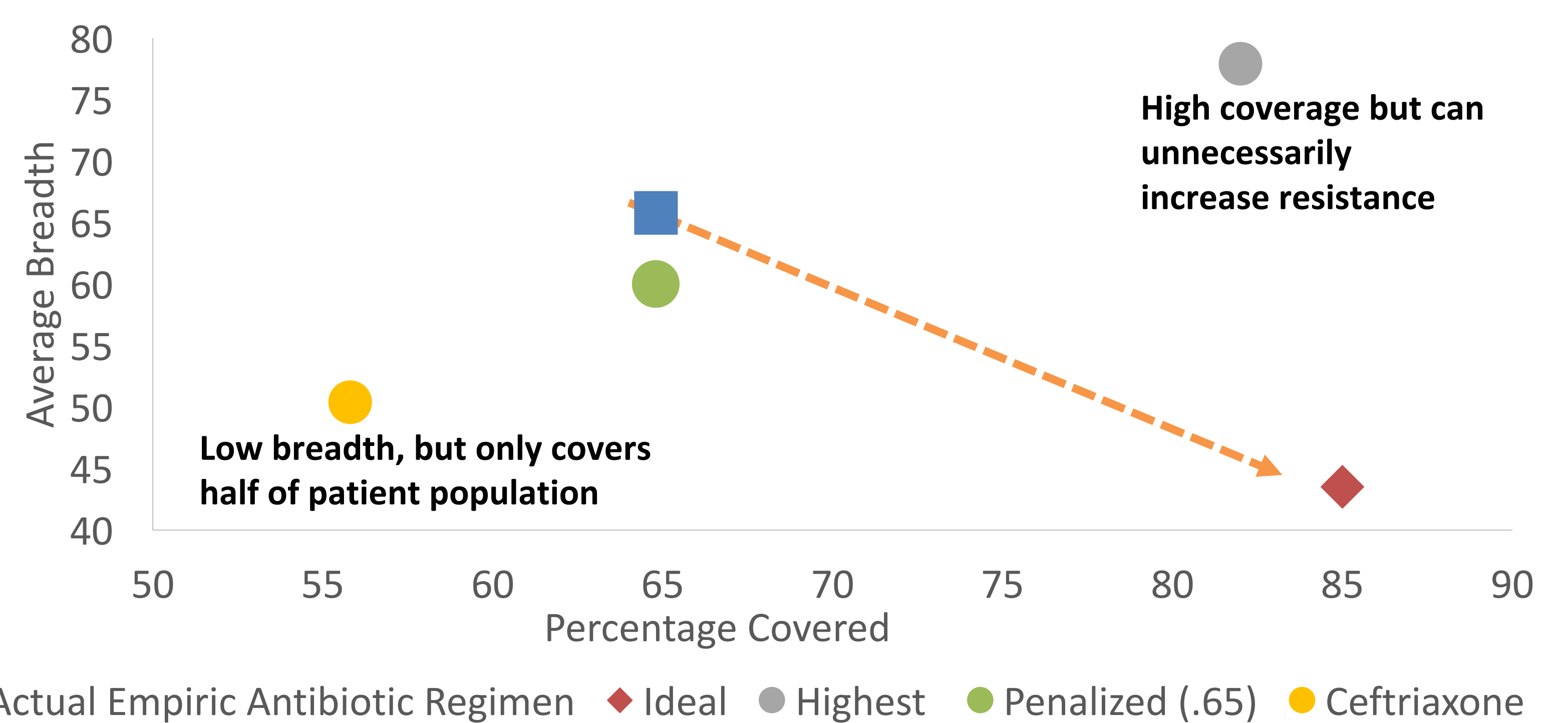


Figure 3

- **Can we do better?**
  - Picking different thresholds for each antibiotic varies the two metrics (green circles in Figure 4).
  - Increasing coverage requires increasing breadth, as expected.
- **Neural Network:** As a first step in directly modelling the ideal antibiotic, we used a hierarchical feedforward network:
  - Three fully connected layers
  - Dropout rate of 0.2 after each layer
  - Binary crossentropy loss function
  - Sigmoid activation
- The results from the neural network (purple crosses) are comparable to the penalized models.

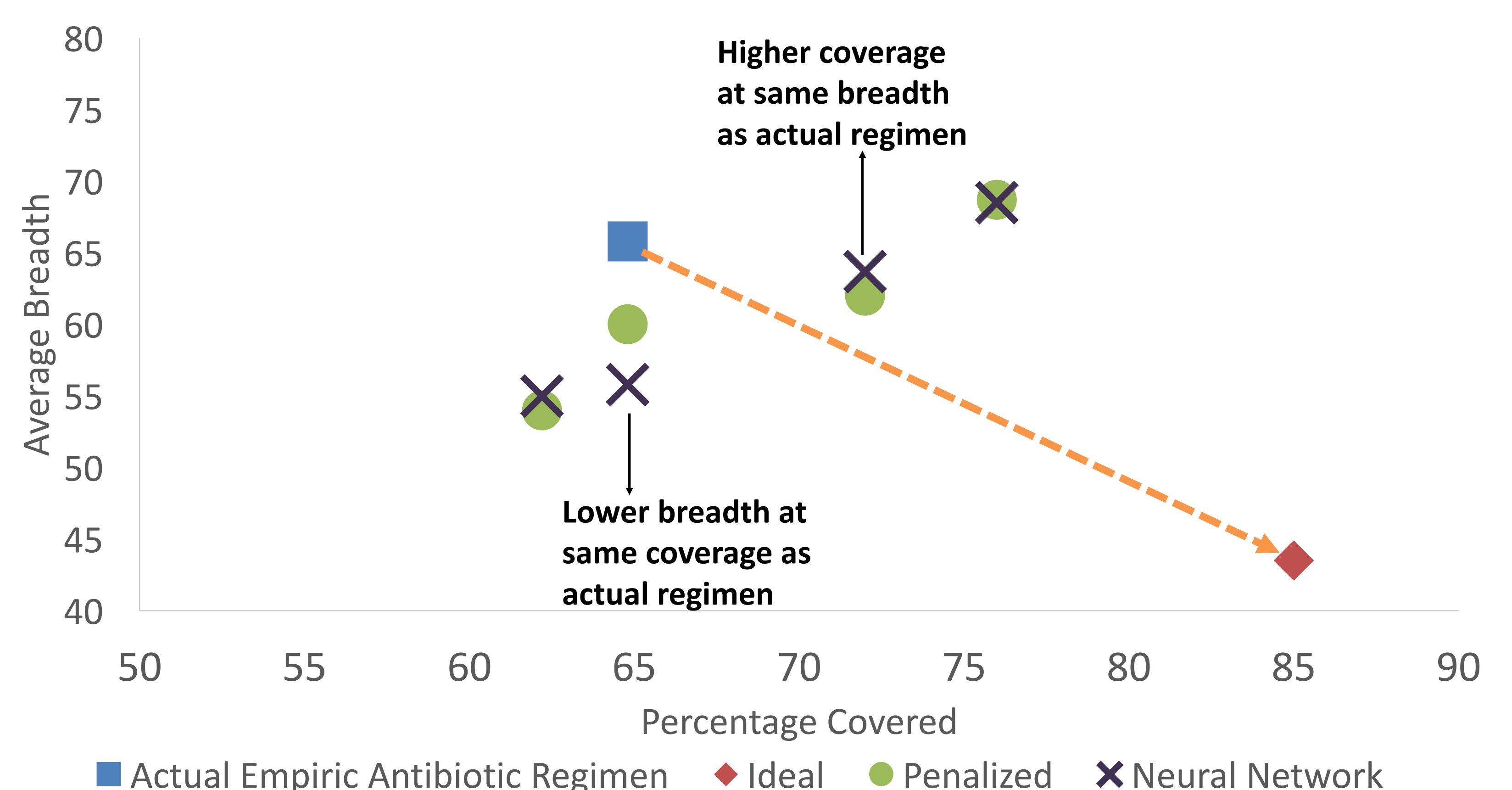


Figure 4

## Limitations and Future Directions

- Actual empiric treatment is based on other factors that may not have been taken into account in this analysis: allergies, drug-drug interactions, severity of infection (sepsis), concurrent infections.
- Data-driven models have the potential to cover the same number of infections with narrower-spectrum antibiotics.
- Deploying these models to decision-makers requires additional studies on when, what and how to present this information.

## References

1. Hebert C, Gao Y, Rahman P, Dewart CM, Shah N, Lustberg M, Stevenson K, Pancholi P, Hade E. 1433. Predictive Models for Antibiotic Coverage of Gram-Negative Urinary Tract Infections. In Open Forum Infectious Diseases 2019 Oct 2 (Vol. 6).
2. Patterson et al. A Mixed Methods Approach to Tailoring Evidence-Based Guidance for Antibiotic Stewardship to One Medical System. Human Factors and Ergonomics in Health Care 2018.
3. Rahman P, Hebert C, Nandi A. ICARUS: Minimizing Human Effort in Iterative Data Completion. Proceedings of the VLDB Endowment. 2018 Sep 1;11(13):2263-76.

