Breakout Session 1: Track B

Measuring and Mitigating the Impact of Biases in Laboratory Testing on Machine Learning Models

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Measuring and Mitigating the Impact of Biases in Laboratory Testing on AI Models

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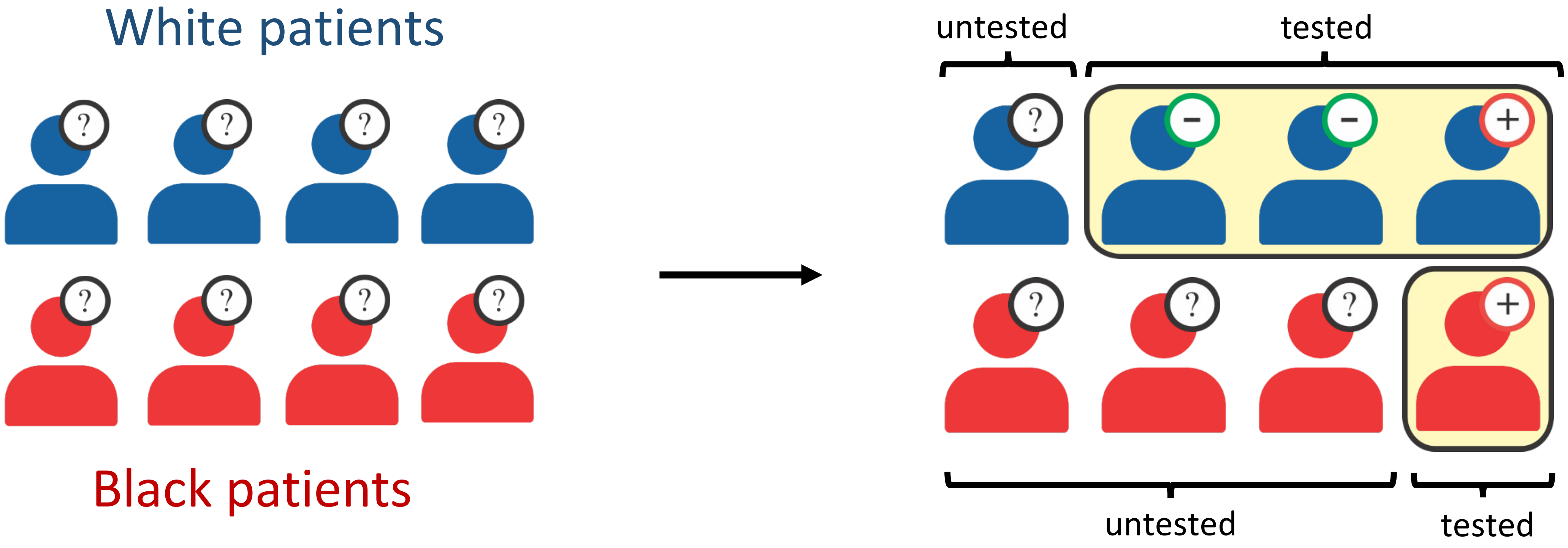
Project Summary & Goals

- Artificial intelligence (AI) tools can potentially assist in diagnostic decision making
- However, AI tools are susceptible to biases, resulting in poor generalization
- We aim to develop techniques and tools for *understanding* and *mitigating* potential biases

Highlights of our work:

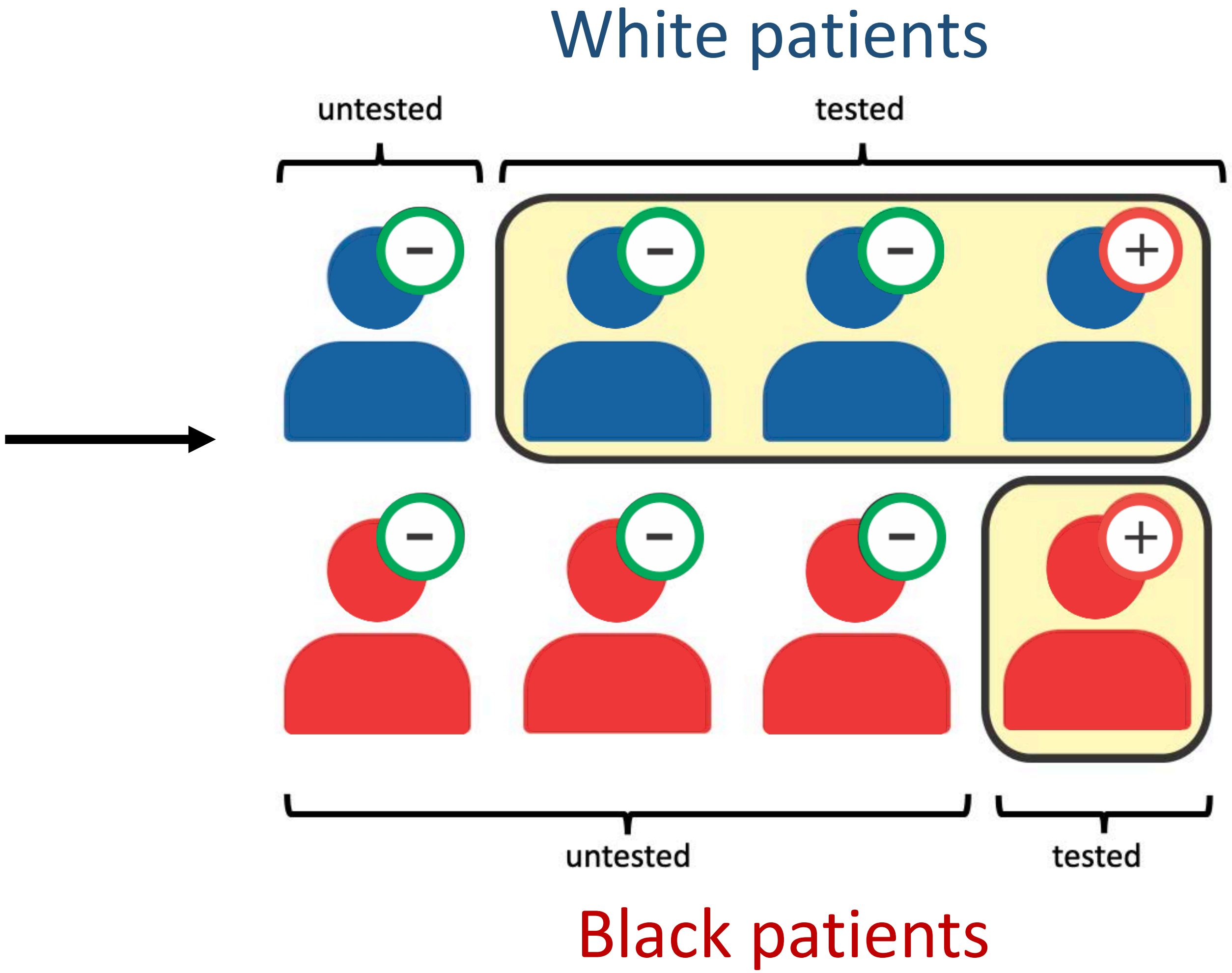
- A large-scale observational study of bias in laboratory testing (*under review*)
- A method for mitigating the impact of laboratory testing bias on AI models (*under review*)

Laboratory testing as a source of bias



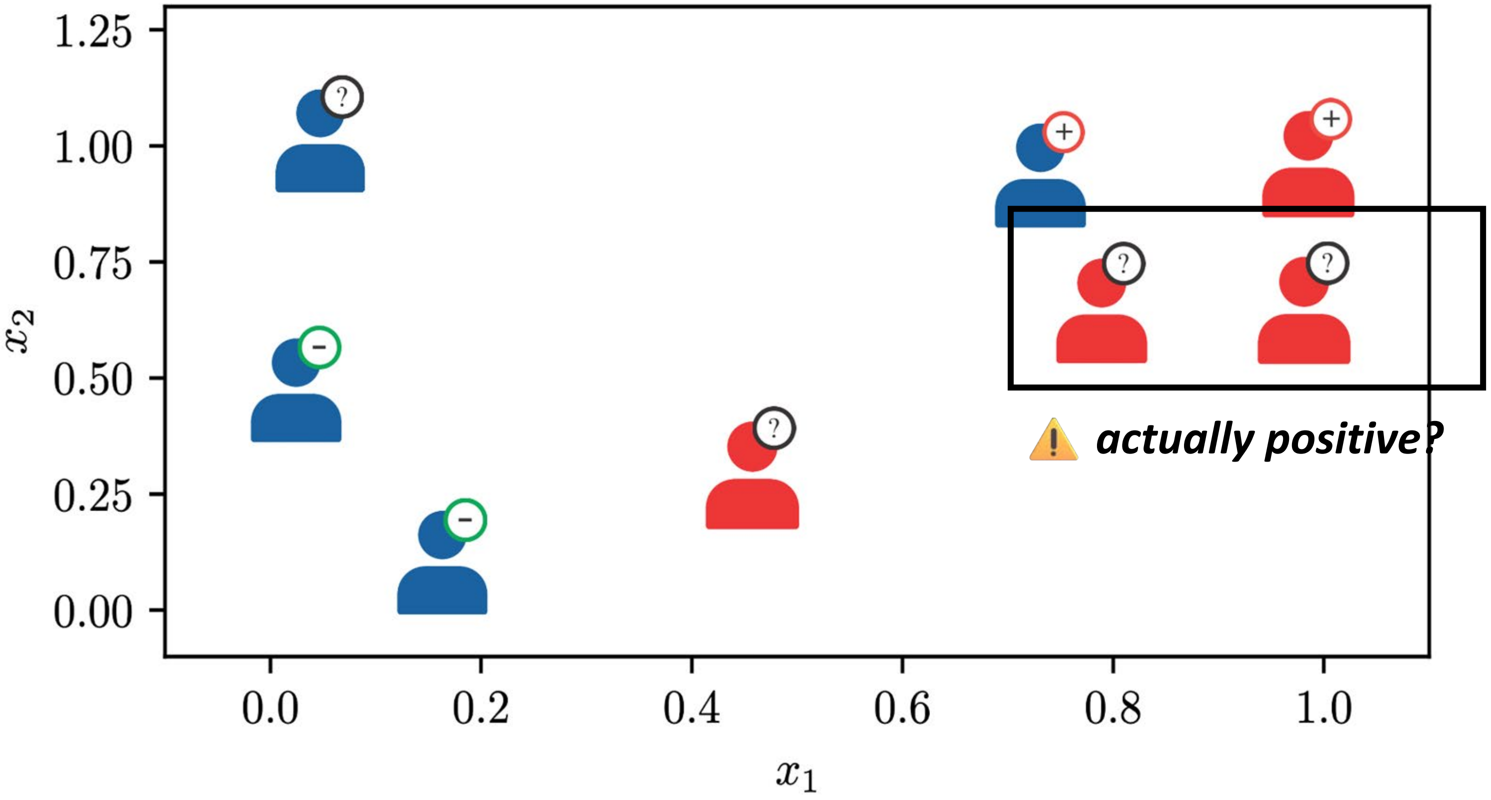
Untested = negative: the default assumption

Many works in practice assumed untested patients are negative:



Impact of testing bias on AI

An AI model might “see” training data as shown below:



⚠️ ***actually positive?***

In this example, an AI model trained on such data may *underpredict* the risk in Black patients.

Is there evidence of such undertesting?

- We conducted a retrospective matched cohort study of 235,830 emergency department (ED) visits
- **Question:** were there significant differences in laboratory testing rates between White vs. Black patients?
- **Cohorts:** All adult ED visits by White and Black patients at Michigan Medicine (U-M), 2015-2022 & Beth Israel Deaconness Medical Center (BIDMC), 2011-2019
- **Race:** as collected during patient registration
- **Main outcomes:** Testing rate difference (% White - % Black) for complete blood count, metabolic panel, arterial blood gas, blood culture, troponin, BNP, and d-dimer. *Secondary outcome:* hospital admission rate.
- **Matching:** exact 1:1 matching on age, biological sex, chief complaint (text), and ED triage score (1 to 5).

Cohort inclusion/exclusion summary

Exclusion criteria:

- Psychiatric visits
- Non-White/non-Black patients (incl. unknown/missing race)
- Patients with unknown biological sex

Before/after exclusion criteria:

Michigan Medicine: 602,650 —> 541,274

BIDMC: 447,109 —> 336,824

Before/after 1:1 exact matching

Michigan Medicine: 541,274 —> 141,510 (26.1% matched)

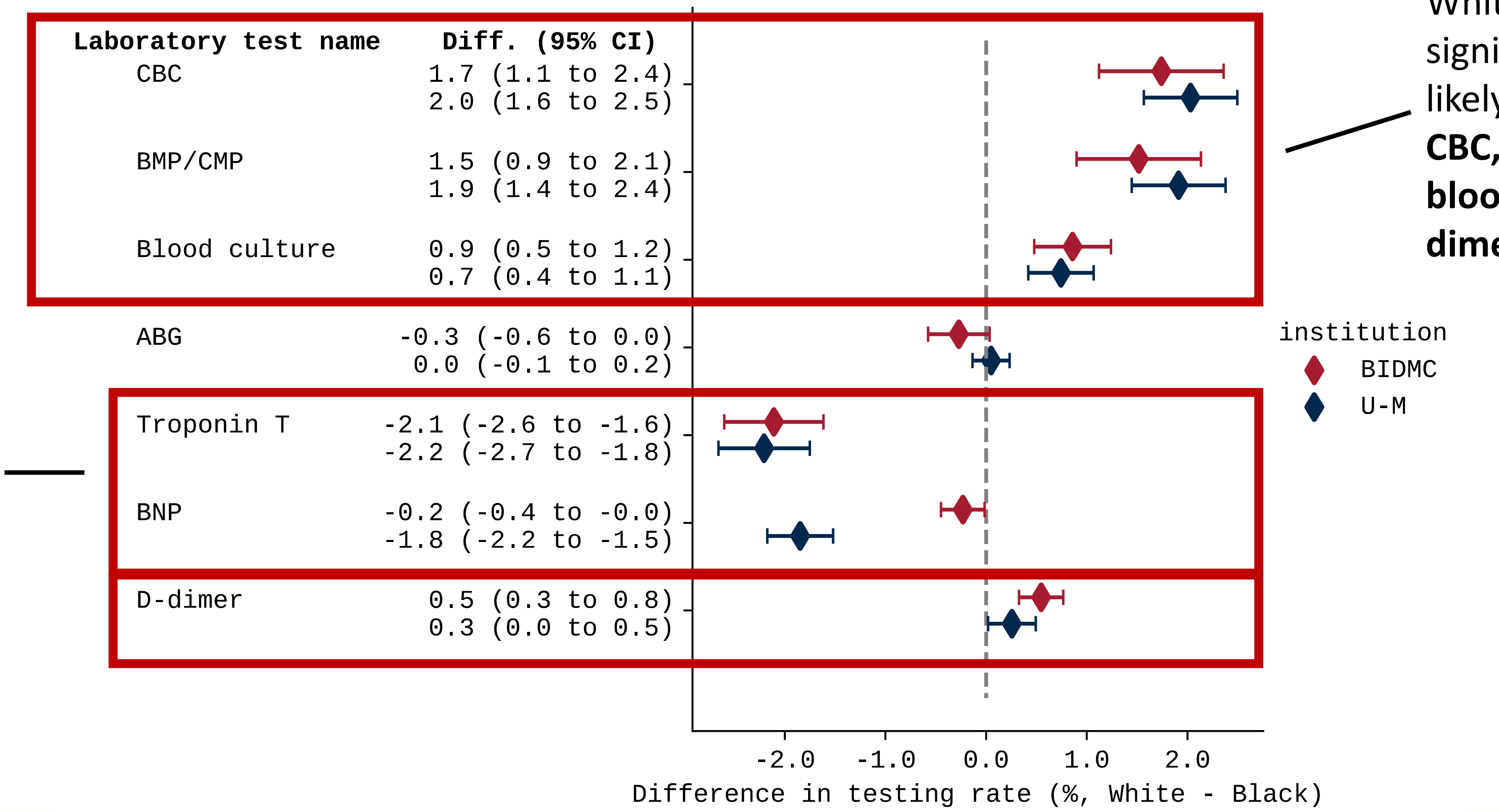
BIDMC: 336,824 —> 94,320 (28.0% matched)

Summary of cohort characteristics (pre-matching)

- **Age:** Black patients were significantly younger than White patients on average (**U-M:** 55 vs. 46 years, p<.001; **BIDMC:** 52 vs. 43 years, p<.001)
- **Biological sex:** Black patients were significantly more likely to be female (**U-M:** 52.0% vs. 62.0%; p<.001, **BIDMC:** 53.1% vs. 57.0%, p<.001)
- **ED triage scores:** Black patients were assessed as less ill on average (lower score; **U-M:** 2.6 vs. 2.7, **BIDMC:** 2.6 vs. 2.8). Chi-sq. test: p<.001.

Significant testing disparities in the ED

Difference in testing rates by race, matched analysis



Laboratory test name	Diff. (95% CI)
CBC	1.7 (1.1 to 2.4) 2.0 (1.6 to 2.5)
BMP/CMP	1.5 (0.9 to 2.1) 1.9 (1.4 to 2.4)
Blood culture	0.9 (0.5 to 1.2) 0.7 (0.4 to 1.1)
ABG	-0.3 (-0.6 to 0.0) 0.0 (-0.1 to 0.2)
Troponin T	-2.1 (-2.6 to -1.6) -2.2 (-2.7 to -1.8)
BNP	-0.2 (-0.4 to -0.0) -1.8 (-2.2 to -1.5)
D-dimer	0.5 (0.3 to 0.8) 0.3 (0.0 to 0.5)

White patients significantly more likely to be tested: **CBC, BMP/CMP, blood culture, d-dimer**

Black patients significantly more likely to be tested: **Troponin T, BNP**

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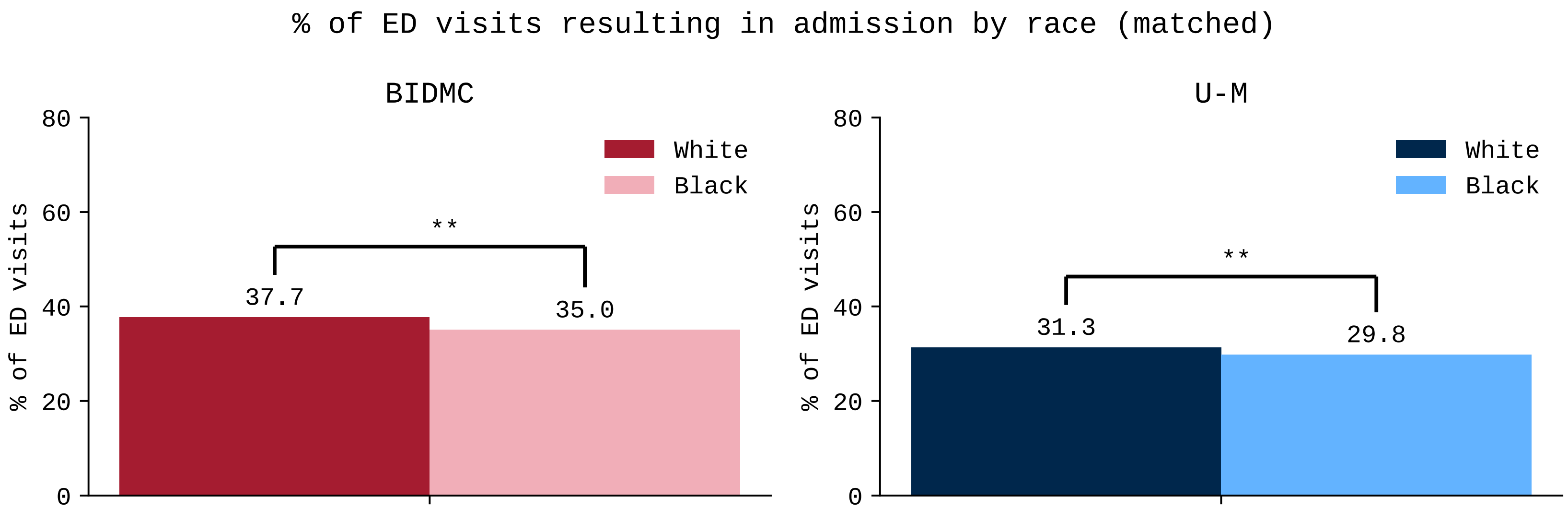
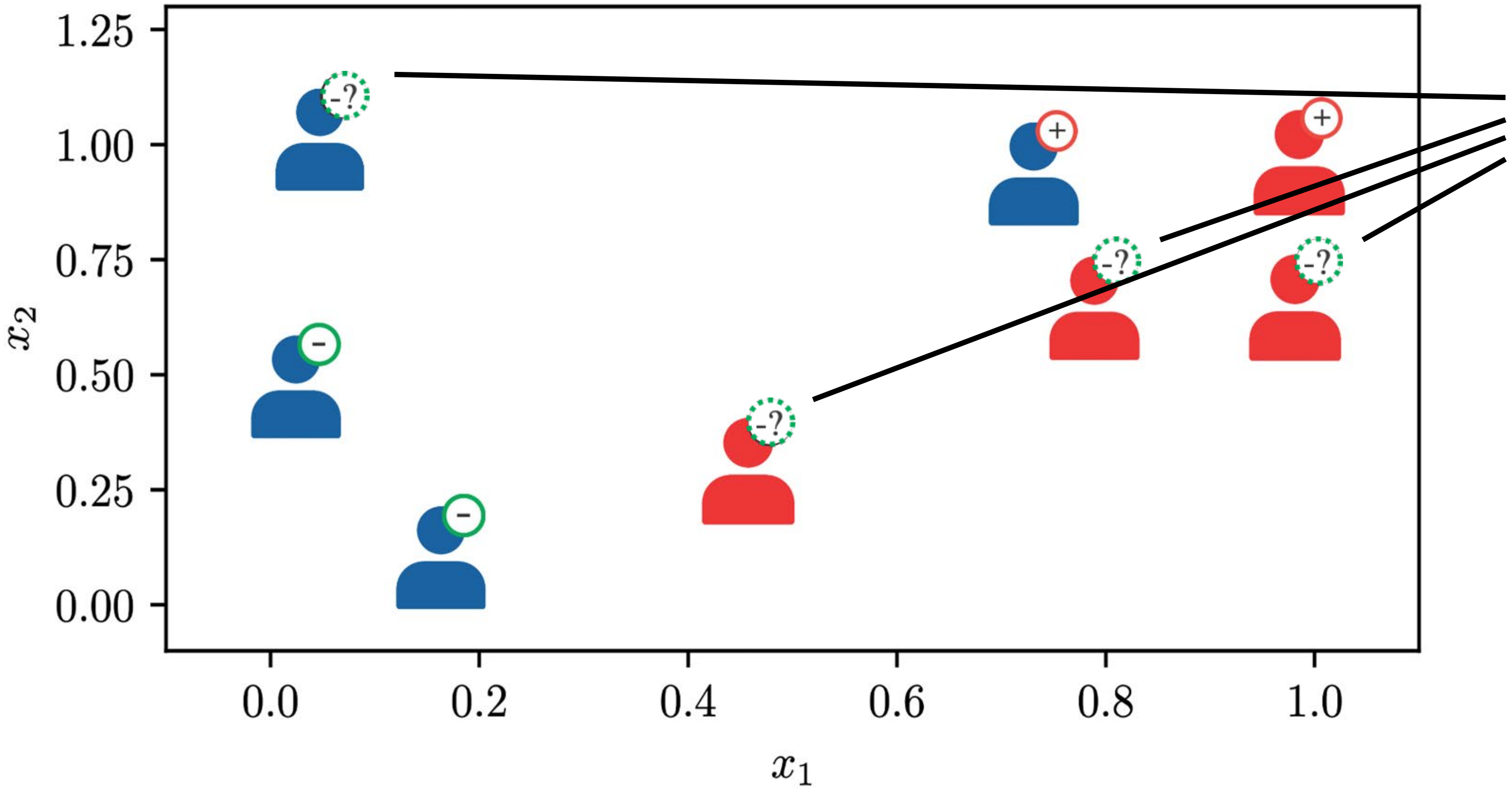
Hospital admission rate disparities



After exact 1:1 matching, racial differences in hospital admission rate following an ED visit also persisted.

A method for mitigating the impacts

- We can interpret predicting missing laboratory test results as a ***missing outcome problem*** —well-studied area in machine learning

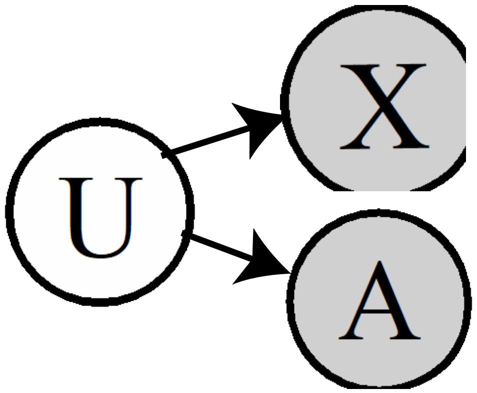


Can we “fill in the blanks?”

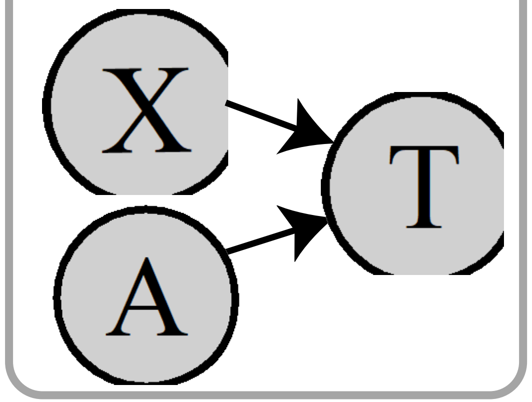
Overview of our approach

- We propose a probabilistic model for bias in laboratory testing and use an *expectation-maximization* algorithm to impute the missing test results

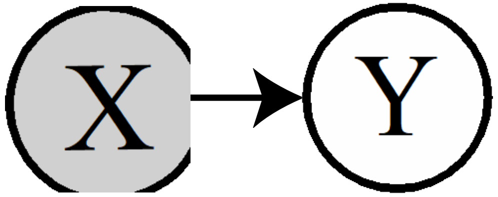
Demographic **groups (A)** might have different observed **features (X)**



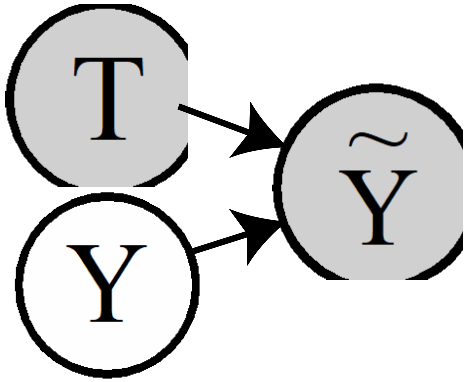
Testing decisions (T) can be **biased (depend on A)**



Ground truth (Y) does **not** directly depend on **demographics (A)**



Observed label is negative if **untested;** equal to **Y** if tested



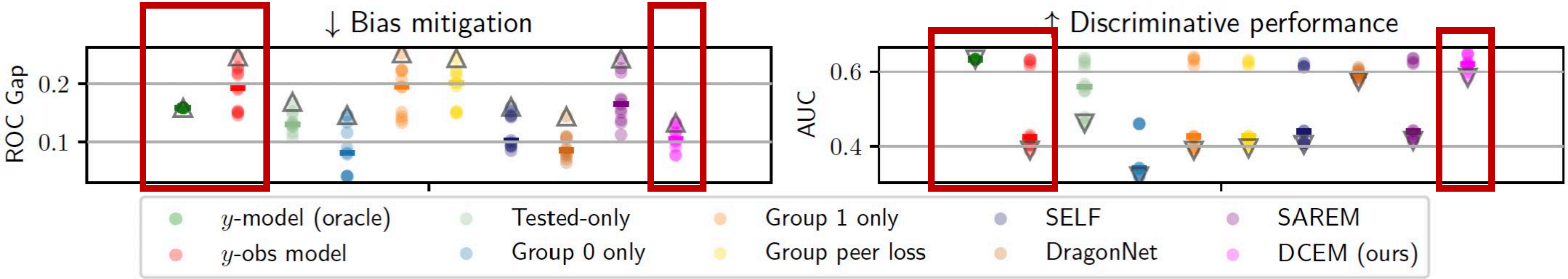
Case study: sepsis classification

- Many sepsis definitions (*e.g.,* Sepsis-3) are dependent on laboratory test results (blood culture) — no test = no diagnosis
- We aim to predict whether a patient will ever develop sepsis during a hospital stay
- We simulate multiple hypothetical testing decisions based on features used by the qSOFA score + report results across all replications
- We evaluate bias mitigation (similar performance across patient groups) and discriminative performance (can ”separate” positive vs. negative) with respect to true sepsis labels

Empirical results

Key methods:

- **green** = train on actual labels (best possible discriminative performance)
- **red** = *default (assume untested = negative)*
- **magenta** = our imputation-based method



Compared to baselines, our method *mitigates bias* and *improves discriminative performance.*

Future Work

- **Improved methods.** The proposed approach eventually fails when testing rates are too low — can we improve the robustness of our method to low testing rates?
- **Evaluation.** Data is often missing in biased ways. Can we design a benchmark/dataset that allows us to evaluate modeling approaches in practice?