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AI can help predict responses to specific tuberculosis treatments, paving way for personalized care

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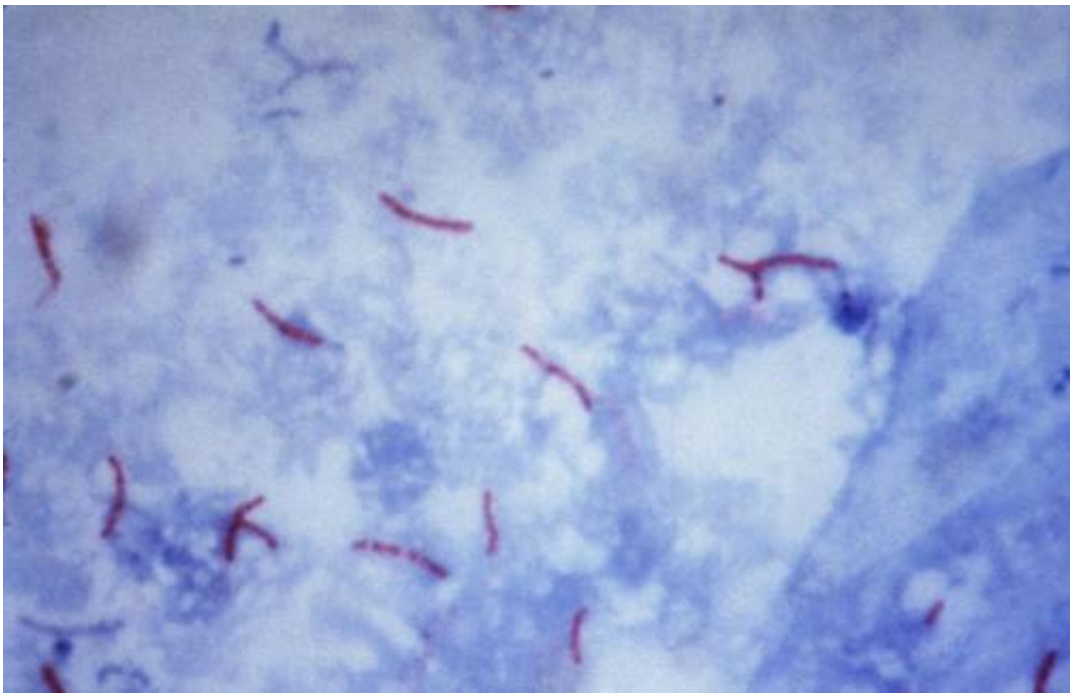

This photomicrograph reveals Mycobacterium tuberculosis bacteria using acid-fast Ziehl-Neelsen stain; Magnified 1000 X. The acid-fast stains depend on the ability of mycobacteria to retain dye when treated with mineral acid or an acid-alcohol solution such as the Ziehl-Neelsen, or the Kinyoun stains that are carbolfuchsin methods specific for M. tuberculosis. Credit: public domain

Tuberculosis is the world's deadliest bacterial infection. It afflicted over 10 million people and took 1.3 million lives in 2022. These numbers are predicted to increase dramatically because of the spread of multidrug-resistant TB.

Why does one TB patient recover from the infection while another succumbs? And why does one drug work in one patient but not another, even if they have the same disease?

People have been battling TB for millennia. For example, researchers have found Egyptian mummies from 2400 BCE that show signs of TB. While TB infections occur worldwide, the countries with the highest number of multidrug-resistant TB cases are Ukraine, Moldova, Belarus and Russia.

Researchers predict that the ongoing war in Ukraine will result in an increase in multidrug-resistant TB cases because of health care disruptions. Additionally, the COVID-19 pandemic reduced access to TB diagnosis and treatment, reversing decades of progress worldwide.

Rapidly and holistically analyzing available medical data can help optimize treatments for each patient and reduce drug resistance. In our recently published research, my team and I describe a new AI tool we developed that uses worldwide patient data to guide more personalized and effective treatment of TB.

Predicting success or failure

My team and I wanted to identify what variables can predict how a patient responds to TB treatment. So we analyzed more than 200 types of clinical test results, medical imaging and drug prescriptions from over

5,000 TB patients in 10 countries. We examined demographic information such as age and gender, prior treatment history and whether patients had other conditions. Finally, we also analyzed data on various TB strains, such as what drugs the pathogen is resistant to and what genetic mutations the pathogen had.

Looking at enormous datasets like these can be overwhelming. Even most existing AI tools have had difficulty analyzing large datasets. Prior studies using AI have focused on a single data type—such as imaging or age alone—and had limited success predicting TB treatment outcomes.

We used an approach to AI that allowed us to analyze a large and diverse number of variables simultaneously and identify their relationship to TB outcomes. Our AI model was transparent, meaning we can see through its inner workings to identify the most meaningful clinical features. It was also multimodal, meaning it could interpret different types of data at the same time.

Once we trained our AI model on the dataset, we found that it could predict treatment prognosis with 83% accuracy on newer, unseen patient data and outperform existing AI models. In other words, we could feed a new patient's information into the model and the AI would determine whether a specific type of treatment will either succeed or fail.

We observed that clinical features related to nutrition, particularly lower BMI, are associated with treatment failure. This supports the use of interventions to improve nourishment, as TB is typically more prevalent in undernourished populations.

We also found that certain drug combinations worked better in patients with certain types of drug-resistant infections but not others, leading to treatment failure. Combining drugs that are synergistic, meaning they enhance each other's potency in the lab, could result in better outcomes.

Given the complex environment in the body compared with conditions in the lab, it has so far been unclear whether synergistic relationships between drugs in the lab hold up in the clinic. Our results suggest that using AI to weed out antagonistic drugs, or drugs that inhibit or counteract each other, early in the drug discovery process can avoid treatment failures down the line.

Ending TB with the help of AI

Our findings may help researchers and clinicians meet the World Health Organization's goal to end TB by 2035, by highlighting the relative importance of different types of clinical data. This can help prioritize public health efforts to mitigate TB.

While the performance of our AI tool is promising, it isn't perfect in every case, and more training is needed before it can be used in the clinic. Demographic diversity can be high within a country and may even vary between hospitals. We are working to make this tool more generalizable across regions.

Our goal is to eventually tailor our AI model to identify drug regimens suitable for individuals with certain conditions. Instead of a one-size-fits-all treatment approach, we hope that studying multiple types of data can help physicians personalize treatments for each patient to provide the best outcomes.

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