A New Way to Predict Immune Response to Viruses

A mathematical technique called matrix completion could speed up the development of vaccines for flu and COVID-19 variants.

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As we know well by now, vaccines must be updated periodically because viruses constantly evolve new strains that may or may not bind to our existing antibodies. The influenza vaccine, for example, is updated every year; it seems likely that the SARS-CoV-2 vaccine will follow the same cadence. To develop and update these vaccines, researchers must test how panels of antibodies respond to panels of viruses. The number of possible antibody-virus combinations makes testing every interaction impractical, so even the most laborious studies have to settle for non-exhaustive data.

But at Fred Hutchinson Cancer Research Center, Damon Runyon Quantitative Biology Fellow Tal Einav, PhD, and his colleagues are taking a different approach. Using a mathematical technique called matrix completion, in which a relatively small number of data points is used to infer missing values, Dr. Einav has figured out how to predict an antibody's response to a new virus strain based on its response to others.

Courtesy of Damon Runyon

This is possible, he explains, because large datasets of antibody-virus interactions can be reduced to relatively simple patterns. Virus strains from the same genetic lineage, for example, tend to elicit similar antibody responses. Different antibodies targeting the same epitope—the portion of an antigen to which an antibody binds—can likewise be grouped together. Dr. Einav developed his approach using influenza virus and HIV data, but it might be understood through the lens of COVID-19: an antibody that works against an existing Delta variant is more likely to work against a new Delta variant than, say, an Omicron variant. Matrix completion could tell us exactly how much more likely, accelerating the race to test each new variant against the current vaccine.

“In essence, while the scale and scope of experiments has exponentially increased over time, the way we analyze experiments has stayed relatively constant,” Dr. Einav explains. “Our framework tackles this often-overlooked aspect of data analysis and demonstrates that leveraging all existing

measurements can help probe the rich diversity of antibody-virus interactions.” With this framework, Dr. Einav and his team have paved the way for immunology studies that need only to measure a small fraction of antibody-virus interactions to know them all. This will allow for far more efficient vaccine development, addressing more than one global crisis as a result.

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