A WHO worker opens a box the Canadian-made Ebola vaccine at the Geneva Hospital on Oct. 22, 2014. THE CANADIAN PRESS/HO - WHO, Mathilde Missioneiro

MATHILDE MISSIONEIRO/THE CANADIAN PRESS

JORDANA DIVON
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When an Ebola outbreak hit West Africa last year, scientists feared it might take years to find an effective treatment. In March, Toronto biomedical startup Atomwise identified two existing medications that were found to significantly reduce the virus' infection rate and have moved to the next stage of clinical trials. The entire discovery process took four months.

The speed at which Atomwise isolated a potential treatment is significant: Developing a new medicine can take an average of 15 years and, while estimates vary, can cost up to $2-billion. But when a pandemic like Ebola, MERS, or H1N1 strikes, there's no time to waste.

Atomwise CEO Abraham Heifets, a Toronto-based machine learning and computational biology expert, has capitalized on recent advancements in artificial intelligence in order to come up with the most accurate and rapid predictive models to date.

When applied to biology, his "supercomputers" can analyze molecules found in millions of different medications already on the market and determine how well the molecules are going to "stick to a disease target" – and ultimately switch it off – with the fewest side effects.

"The impact of our work is that it's a general tool for discovering medicines," says Mr. Heifets. "The fact we began with medicines that had already been in people made us hopeful that the medicines are going to be good results."

Much like the revelation that Aspirin can double as a treatment for managing heart disease, the Toronto biomedical startup hopes its technology can also find multiple uses for existing treatments. Ideally, it's a process that would save a huge amount of time and money by identifying the optimal medicines for patients fast enough to quell an outbreak.

But its applications go beyond well-traveled germs. Mr. Heifets is currently investigating potential treatments for chronic conditions like multiple sclerosis.

"We tested every molecule you could find on the market because we didn't know what would work. The kind of scope of that project would not be possible to do physically so you'd have to guess what could work and you'd never know if you missed something. In the computer, it's possible," he says.

The idea of using computers to facilitate the pharmaceutical process is hardly a new one. Biomedical engineers have been playing around with the idea for years, with mixed results.

When it comes to the human body, however, there's no room for error: What works for one patient may harm another. Mr. Heifets says the timing is right for his ambitious platform.

Unlike previous biomedical prediction models, which required experts to analyze the results of these kinds of searches by hand, Atomwise is using a subfield of artificial intelligence called deep learning, which is a technology that effectively teaches a computer how to learn and utilize information much like a human brain would. While deep learning is still in its infancy, engineers like Mr. Heifets use sophisticated algorithms that can process massive amounts of data, an advantage that gives Atomwise's predictive model a higher accuracy rate while reducing the time, increasing the breadth and eliminating the margin of error from a human analysis.

"People have had the dream of using computers for biology for decades as well," Mr. Heifets acknowledges. "I want to give credit to the people who came before us. These were bright people who had great ideas and in many cases had the appropriate

ideas for the kind of data and computers that were available," he says, but the technology had not caught up to the concept until recently.

It appears as though investors are taking note. Atomwise recently raised $6-million in seed money and the team recently uprooted from the University of Toronto incubator to began a residency at the prestigious Y-Combinator in Silicon Valley.

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