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# MEGATRENDS ARE ABOUT COLLABORATION RATHER THAN ISOLATION: AI & THE BIOREVOLUTION

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In many discussions with investors, we tend to find people want to find the ‘right’ megatrend for their given era.

Usually, since we cannot know returns ahead of time, this means the best, most intense story that involves an expectation of phenomenal performance—at least potentially.

Far less often we find investors seeking to discuss the areas of overlap, meaning examples or cases where the combined impact of two distinct megatrends leads to remarkable results—results that would likely be impossible without the overlaps of these technologies. Usually, people prefer that clear demarcation between megatrends.

Here, we find a case study where [artificial intelligence \(AI\)](#) is used in the domain of the BioRevolution.

While it may be important to show separation between an AI investment strategy and a BioRevolution investment strategy, when it comes to solving real problems, that need for separation tends to melt away.

## Statement of the Problem: Omicron

Many across Europe and the U.S. had a certain picture of their expectations for the 2021 holiday season. That picture was largely shattered on November 26, 2021, when the World Health Organization (WHO) designated a strain of coronavirus in South Africa as a variant of concern—known now as Omicron.<sup>1</sup>

The primary question for the global health system was simple: if we accept that Omicron represents a certain degree of mutation of the coronavirus itself, will the vaccines already widely distributed maintain their efficacy against it?

This is one of those questions that is very intuitive and simple to ask, but far more difficult to answer with any degree of accuracy.

## AI: Creating New Options and Techniques

Scientists use well-known procedures to reveal the three-dimensional structures of proteins, including electron microscopes. The concept is that if you could see how the coronaviruses bind with and enter human cells, then you can learn about and make an initial assessment about the effectiveness of a given vaccine.

The often mentioned ‘spike protein’ is critical in the binding process, thereby lending the intuition that if mutations cause significant changes to the spike protein, it could be more problematic for existing treatments.

If Omicron is very different, there would be less chance the existing vaccines would be as effective. If Omicron is similar, there would be more chance that existing vaccines would work. As a baseline:<sup>2</sup>

- Omicron contains 15 mutations in the receptor-binding domain—how the spike protein binds to neutralizing antibodies
- In contrast, the Delta variant contains seven mutations across the entire spike protein, only two of which are in the receptor-binding domain

But scientists using these techniques have a specific constraint: they need actual physical material to view under the electron microscope.

What if scientists could start answering the question of effectiveness BEFORE receiving any physical supplies? Enter AI.

A researcher in Charlotte, North Carolina, was able to use publicly available AI software to predict the structure of Omicron, with the idea of focusing on the possible effectiveness of antibodies to previous coronavirus strains. This work could be done by early December 2021—after the initial announcements went global on November 26.<sup>1</sup>

By December 21, results from traditional approaches—like those using the electron microscope—became available, and they confirmed that the predictions from the AI software about the Omicron structure were almost exactly right.

This is exciting not because of Omicron, but because of the universal applicability of this concept—we know there are bound to be more viruses and this approach could be used for all of them.<sup>1</sup>

The prediction arising from this work was that existing vaccines would have a tougher time guarding against Omicron because of the changes in the structure, specifically in the region where a person's neutralizing antibody would aim to bind with the spike protein.

As of this writing in mid-January 2022, this appears to have been accurate, even if we recognize experiences of individuals can and do vary.

#### **AI Software Capable of Predicting Protein Structures Is Very New**

In late 2020, competing research between DeepMind and the University of Washington led to AI-based software that could accurately predict protein structures. DeepMind's software in particular, known as AlphaFold, has become fairly well known within the molecular biology community. The 'protein folding problem' had been a grand challenge for scientists over the past 50 years.<sup>1</sup>

The interesting point is that neither software package was originally designed to predict small changes in structure that would be apparent from mutations of an existing virus, and yet the results were still helpful.<sup>1</sup> Instead of just waiting for the physical material and having no options, scientists have the power to make a well-educated guess that can be confirmed with the more traditional techniques.

Importantly, predicting structures does not mean 'immediate cure.' Expert researchers gain a better starting point from which to strategize the design of either a vaccine or treatment therapy.

#### **AI Is Already Contributing in Other Areas of the BioRevolution**

Anywhere there's a massive amount of data to process and (hopefully) gain insights from, it's possible that AI can help.

The WHO estimates that by the year 2050, 10 million people could die annually from drug-resistant infections.<sup>3</sup> To be clear, there is no singular action that could be taken to fully counteract this—as a society we need to try many approaches and likely apply a mixture of different possible strategies.

Recently, an AI algorithm was able to analyze 43,000 peptides in the human body, narrowing these down to 2,603 as proteins secreted from cells. The analysis could help indicate which of these—if any—have antibiotic properties. Researchers synthesized 55 of the most promising, and tests indicated that, at least preliminarily, many were able to stop known antibiotic-resistant bacteria from replicating.<sup>3</sup>

The bottom line: there are a LOT of proteins in the human body, and we do not presently know the properties of all of them. AI can be used to assist on the journey of increased knowledge to solve known medical problems in different ways.

#### **Conclusion: The Powerful Force of Megatrends Collaborating**

In this case, we have shown how the BioRevolution and AI megatrends can work together.

AI becomes less abstract, as we see examples of data, predictions and the value of those predictions all coming together. The BioRevolution, in particular when human health is at stake, is very tangible, especially during a global pandemic.

We will keep searching for examples like this where different megatrends can interact and create force multipliers in terms of their potential impacts.

<sup>1</sup> Source: Simonite, Tom. "This AI Software Nearly Predicted Omicron's Tricky Structure." Wall Street Journal. 10/1/22.

<sup>2</sup> Source for bullets: Ford et al. "Predictions of the SARS-CoV-2 Omicron Variant (B.1.1.529) Spike Protein Receptor-Binding Domain Structure and Neutralizing Antibody Interactions." bioRxiv. 3/12/21.

<sup>3</sup> Source: Levy, Max G. "An AI Finds Superbug-Killing Potential in Human Proteins." WIRED. 30/11/21.

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*Christopher Gannatti is an employee of WisdomTree UK Limited, a European subsidiary of WisdomTree Asset Management Inc.'s parent company, WisdomTree Investments, Inc.*

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