Megatrends are about collaboration rather than isolation: A case study of AI & Biorevolution

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

Far less often we find investors seeking to discuss areas where megatrends overlap, meaning examples or cases where the combined impact of two distinct megatrends could potentially lead to significant 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 utilised in the domain of the the technological revolution known as 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 will tend to melt away in its importance.

Statement of the Problem: Omicron

Many across Europe and the United States had a certain picture of their expectations for the 2021 holiday season—a picture that was largely shattered on 26th November 2021 when the World Health Organization designated a strain of coronavirus in South Africa as a ‘variant of concern’—known now as ‘Omicron[1].’

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, would the vaccines already widely distributed maintain their efficacy?

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

AI: Creating New Options & Techniques

There are well known procedures that scientists use to reveal the three-dimensional structure of proteins. Sometimes, electron microscopes are used, the concept being that if there could be a picture of how the coronaviruses bind with and enter human cells, then you can learn about and assess an initial view 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 still be as effective. If Omicron is similar, there would be more chance that existing vaccines would work. As a baseline[2]:

- Omicron contains 15 mutations in the receptor binding domain, specifically how the spike protein binds to neutralising 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 be sent in order to view under the electron microscope.

What if scientists could start answering the question of effectiveness before receiving any physical supplies? Enter artificial intelligence.

There was a researcher in Charlotte, North Carolina, able to use publicly available artificial intelligence software to predict the structure of Omicron, with the idea of focusing on the possible effectiveness of antibodies to previous Coronavirus strains. This work was able to be done by early December 2021—after the initial announcements went global on 26th November[3].

By 21st December, results from traditional approaches—like those using the electron microscope—became available, and they confirmed that the predictions from the AI software of 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 very well be utilised for all of them[4].

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 human’s neutralising antibody would aim to bind with the spike protein.

As of writing this in mid-January 2022, this appears to have been accurate, even if we recognise experiences of individuals can 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 has ‘Alphafold’ has become fairly well known within the molecular biology community, as the ‘protein folding problem’ had been a grand challenge for scientists over the past 50 years[5].

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[6].

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 more traditional techniques.

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

AI is Already Contributing in Other Areas of the Biorevolution

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

The World Health Organisation estimates that by the year 2050, 10 million people could die annually from drug-resistant infections[7]. 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 analyse 43,000 peptides in the human body, narrowing things down to 2,603 of these being proteins secreted from cells. The analysis could indicate which of these—if any—had antibiotic properties. Researchers synthesised 55 of the most promising, and tests indicated that, at least preliminarily, many were able to stop known antibiotic resistant bacteria from replicating[8].

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.

[1] Source: Simonite, Tom. "This AI Software Nearly Predicted Omicron's Tricky Structure." Wall Street Journal. 10 January 2022.

[2] 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 December 2021.

[3] Source: Simonite, 2022.

[4] Source: Simonite, 2022.

[5] Source: Simonite, 2022.

[6] Source: Simonite, 2022.

[7] Source: Levy, Max G. “An AI Finds Superbug-Killing Potential in Human Proteins.” WIRED. 30 November 2021.

[8] Source: Levy, 2021.

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