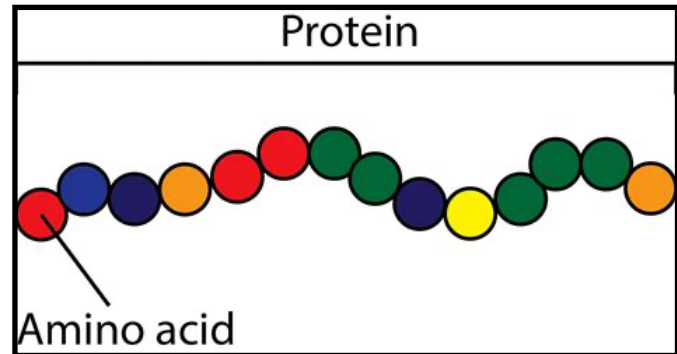# What is AlphaFold?

Let's get Down To Basics, What Are Proteins?

Proteins are essential structures in our body. These structures complete nearly every function in our body, some of these functions include: binding to particles to prevent viruses from entering our body, performing chemical reactions which are used to create new molecules, creating structure for cells… You get the idea, proteins are petty important. So how are they made? Well, proteins are comprised of chains of these things called amino acids, as you add different amino acids, you get different types of proteins. Although this protein on the right might look like a nice chain with amino acids connected to each other, the proteins don't stay that way. They form into very complex shapes.
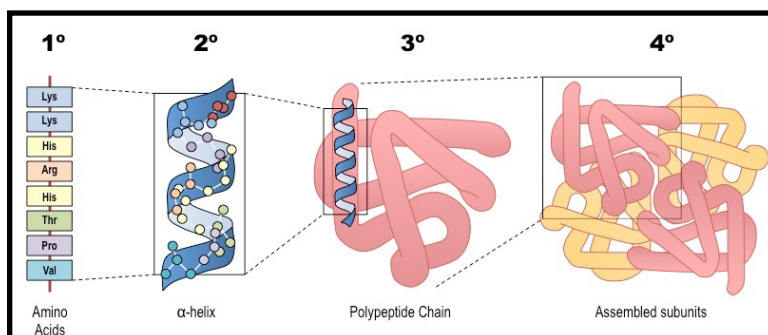

Alright, So Whats The Problem?

These proteins as displayed above are created using genetic code which is stored in our DNA. Any error in these genetic scripts carries over to the proteins; as discussed above, proteins are vital structures which execute fundamental functions, if there's something wrong with the protein, there will be something wrong with the function. Because of this tight link between DNA and proteins, many diseases are linked to abnormalities in protein structures. You might be catching on now, but if you're not its okay. To put it in simple terms, the make up of the proteins dictates the healthiness of a certain individual, if an abnormality is detected in the protein chain, it's a signal of disease and so on.

Why Cant We Just Diagnose Diseases Quicker Then?

Well its not quite that simple. Creating the protein model is much more complicated than it may seam. The digram above is a minuscule segment of a much, much larger chunk of protein.
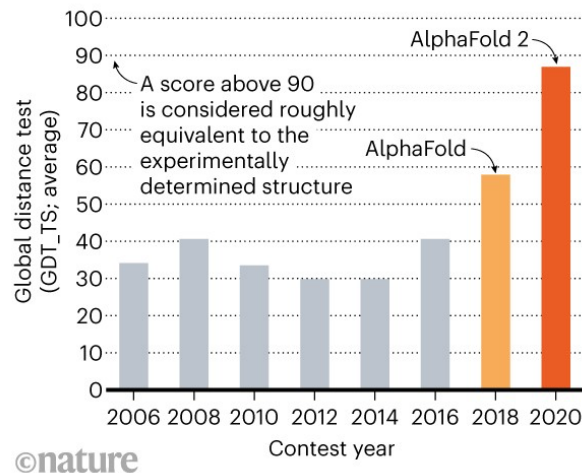

To the left is a diagram of the different levels a protein fold is comprised of. Stage 1 is the same as the strand of amino acids we see in the first digram; as we go further down the chain we see the strand form into a helix, then a fold, then a cluster of folds.

Where does AlphaFold Come in Then?

AlphaFold is essentially an algorithm which uses artificial intelligence in order to predict what the chain will look like. The factor which makes AlphaFold2 (the latest version/ update per se) so distinct is the fact that it is the most accurate algorithm. Below we see a graph of previous attempt made to cracking the chain of amino acids; however, AlphaFold 2 significantly outperformed all of them, putting it in a league of its own. Because of this breakthrough invention, coming up with the structure is no longer the problem. As stated above, with the protein chain in hand, it makes it miles easier to detect abnormalities.

STRUCTURE SOLVER
DeepMind's AlphaFold 2 algorithm significantly outperformed other teams at the CASP14 protein-folding contest — and its previous version's performance at the last CASP.

A score above 90 is considered roughly equivalent to the experimentally determined structure

Global distance test (GDT_TS; average)

Contest year

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Sources

Deepmind. 2021. *AlphaFold: Using AI for scientific discovery*. [online] Available at: <https://deepmind.com/blog/article/AlphaFold-Using-AI-for-scientific-discovery> [Accessed 16 February 2021].

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