

Let us celebrate the European idea

Laudatio of the President of the Max-Planck-Gesellschaft

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Ladies and Gentleman,

Did you know that in the German language there is no word that rhymes with the word "Mensch", human being. The human being as an outlier. It is true: humans can be odd.

For example, how is it that humans throughout the ages have created archives? The treasures in such archives outlast their own lives, their own centuries and perhaps even their own civilization. So why all these efforts?

Clearly, it is our sympathy for the future. It is that somehow we know that what we collect cannot yet be fully explored. And that the collection could be important for those who come after us.

Simply put: archives can change the world of the future. Believe it or not, we just witnessed such a world-changing event.

The company DeepMind released their program AlphaFold. It predicts the 3D structure of proteins based only on their coding DNA sequences. This solves a decades-old Grand Challenge in biology.

If you like gardening, imagine the following: Just by looking at a tiny seed you know what the flower will look like when blooming in your garden. Even if you've neither seen the seed nor the type of flower ever before!

Quite unbelievable, but this is what AlphaFold does with proteins.



So how did this become possible? AlphaFold was trained on all known 200,000 protein structures in the Protein Data Bank – an archive that is the result of decades of work of thousands of molecular biologists around the globe.

Now the European Molecular Biology Laboratory – EMBL - comes into play. Not only is it the European node of the legendary Protein Data Bank. But more so, EMBL partnered with DeepMind to build a new archive. One that makes all protein structure predictions freely available. Open Science at its best!

In merely two years, the new database arrived at around 200 million predicted proteins – that's basically the entire catalogue of life. This new service accelerates basic research, biotech applications and drug discovery.

Now EMBL takes the next step, developing their own computational framework: AlphaDesign. Soon you can plan your protein from scratch, and even find solutions that nature hasn't come up with.

There are close ties between EMBL and the Max Planck Society. Countless Max Planck scientists started their careers at EMBL. I am one of them. So allow me to end on a more personal note.

I think that tonight we should not only celebrate EMBL, but as much the idea behind it, the European idea.

At a time when many people seem to have lost track of what they should actually make of the European idea, I can only say: Look at EMBL! 28 member states are committed to it. Science has been transformed by it, communities were built on it. EMBL has always been a number one training hub – and now it also makes the next generation of biologists AI ready.

EMBL is many things at once: a scientific, a social, and a peace project.

The idea behind it was born 60 years ago by a few scientists from different countries. Amongst them the founding father John Kendrew, one of my heroes, who solved the first protein structure, that of the muscle protein myoglobin.

The current Director-General of EMBL, Edith Heard, is a star in the field of genetics. EMBL's stunning Al-related achievements and many other projects are being realized under her leadership – and that of Ewan Birney, head of EMBL's site near Cambridge, the EBI.

By the way, remember that two years ago the prize went to ELLIS. ELLIS transfers the idea of EMBL to the field of machine learning. Bernhard Schölkopf is here tonight. I know how much EMBL is an inspiration for him.



This brings me full circle to the beginning of my talk: human beings can not only build archives, they can change the world when they work together across space and time.

Ladies and gentlemen!

In recognition of unleashing a new era in biology, and in recognition of its central role in shaping the European life sciences, I wholeheartedly congratulate EMBL on the "Deutscher KI-Preis 2023" in the category of AI applications!