Deep Learning helps improve gene therapies and antiviral drugs

The nuclease Cas13b associated with the CRISPR gene scissors, which is an enzyme that degrades nucleic acids, has the potential to be used in the future in hereditary diseases to switch off unwanted genes. In the fight against infections, this nuclease is also being researched as an antiviral agent, as Cas13b can specifically intervene in the genetic material of viruses and render them harmless.

Despite these promising properties, an international team of researchers led by the Helmholtz Institute in Würzburg, Germany, in cooperation with the University of Freiburg and King Fahd University in Saudi Arabia, is looking for nuclease inhibitors that can regulate or prevent these effects in order to increase the safety and efficacy of future therapies and help prevent undesirable side effects.

In order to find natural nuclease inhibitors, Prof. Dr. Rolf Backofen from the Department of Computer Science at the University of Freiburg and his team have now used Deep Learning for the first time to identify a protein that blocks the activity of Cas13b. Deep Learning is a subfield of machine learning and examines large amounts of data for patterns and trends. The scientists present their results in the journal Molecular Cell.

In search of Acrs: Deep Learning applied for the first time

Scientists suspect that many undiscovered proteins, known as anti-CRISPR proteins (Acrs), exist that block nucleases. However, these are difficult to find. "Identifying them is like finding a needle in a haystack because Acrs don't resemble each other at all," says Prof. Chase Beisel, Ph.D., who is the lead scientist in the study in cooperation with Backofen and is head of the Synthetic RNA Biology Department at the Helmholtz Institute for RNA-Based Infection Research in Würzburg, Germany.

As a result, the research team members have pushed the use of artificial intelligence to spot new acrs. "With the combination of our deep learning method 'DeepAcr' and the use of a high-throughput screen, we succeeded in discovering the new anti-CRISPR protein," Backofen says. "However, the millions of predictions made by our algorithm not only help to find anti-CRISPR proteins. The developed algorithm shows how neural networks open up effective solution possibilities even for complex problems."

Publication

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