

To the media representatives

PRESS RELEASE

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Predictive genetics through artificial intelligence

Neuchâtel, 10 June 2021. Using artificial intelligence to predict the chromosomal rearrangements that can occur spontaneously during the reproduction of an organism! This is the feat achieved by a team from the University of Neuchâtel (Switzerland) who 'trained' a computer programme to predict the location of DNA modifications in the offspring of a pathogenic fungus. Its results are published in the journal *Nature Communications*.

This is a first of its kind! Applying machine learning to genetics, which consists of 'training' a software to deliver results for which it was not originally specifically programmed. This artificial intelligence method was used to predict the location of genetic code changes in the offspring of a pathogenic fungus.

The team led by Daniel Croll, a professor at the Laboratory of Evolutionary Genetics at the University of Neuchâtel, first tested it on *Zymoseptoria tritici*, the fungus that causes septoria in wheat, a scourge that is responsible for 5 to 10% of annual crop losses in Europe alone.

These losses are the result of the pathogen's resistance to various pesticides, the emergence of which is linked to chromosomal rearrangements in the fungus. Hence the interest of post-doctoral student Thomas Badet and his colleagues in testing a predictive genetics approach on this fungal pathogen.

To do this, the biologists from the University of Neuchâtel submitted to a computer programme some thirty chromosomal characteristics collected from several individuals of the fungus. These characteristics are likely to be at the origin of chromosomal rearrangements that would occur in future generations. After the learning process, the programme was able to predict, by looking at a given genome, exactly where rearrangements in the DNA of successive generations of the fungus would be found.

Daniel Croll and his colleagues produced lines of fungi to compare the results. It was a complete success! "After analysing the DNA of the offspring, we were able to predict 99% of certain types of spontaneous changes that occurred," says Daniel Croll.

Following this, the biologists tested the method on *Arabidopsis thaliana*, known as a laboratory guinea pig plant. But with a more fundamental objective: to ask the machine to predict, after compiling eight 'perfect' genomes of the plant, where rearrangements could appear in a randomly selected *Arabidopsis* plant. And the results were excellent. "The computer model was able to predict more than 74% of the chromosomal rearrangements," continues Daniel Croll.

The prediction method may not be limited to plant biology and could be applied to human medicine in the future. Daniel Croll makes no secret of the fact: "Spontaneous changes in DNA occurring during cell multiplication are often the cause of hereditary diseases and cancers. Being able to predict them would be a great help to medicine."

However, the University of Neuchâtel's method depends on one imperative condition: the genome of the organism being studied must be known in great detail for a reliable prediction. This is indeed the case for the pathogenic fungus and *Arabidopsis*. But not yet for the human being, although a very large part of its DNA has already been decoded.

Scientific reference :

Badet T, Fouché S, Hartmann FE, Zala M, Croll D. 2021. *Machine-learning predicts genomic determinants of meiosis-driven structural variation in a eukaryotic pathogen*. Nature Communications.

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